

STIC-Biotech/ChemLib

139347

mej

From: Whiteman, Brian  
Sent: Thursday, December 02, 2004 1:49 PM  
To: STIC-Biotech/ChemLib  
Subject: oligonucleotide search

DEC-2 2004  
STIC-Biotech/ChemLib  
(610)

09/786,436, US filing date 7/16/01, priority 9/3/98

Wagner et al.

oligonucleotide search an oligonucleotide 10-50 nucleotides in length, and the oligonucleotide comprises a sequence chosen from GGGGG, GAGGG, GGGAG, GTGGG, and GGGTG; and the oligonucleotide does not comprise a CG dinucleotide (CpG motif).

the oligonucleotides are used in a method of treating a tumor in a subject

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 1-10 \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GAGGG  
Perfect score: 5  
Sequence: 1 gaggg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	5	100.0	10	6	AR029981 Sequence
C 3	5	100.0	10	6	AR030010 Sequence
C 4	5	100.0	10	6	AR030099 Sequence
C 5	5	100.0	10	6	AR030218 Sequence
C 6	5	100.0	10	6	AR043159 Sequence
C 7	5	100.0	10	6	AR049732 Sequence
C 8	5	100.0	10	6	AR053555 Sequence
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C 10	5	100.0	10	6	AR065882 Sequence
C 11	5	100.0	10	6	AR074659 Sequence
C 12	5	100.0	10	6	AR075515 Sequence
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C 22	5	100.0	10	6	AR175404 Sequence
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24	5	100.0	10	6	BD177264 Method fo
25	5	100.0	10	6	BD238590 Preparati
C 26	5	100.0	10	6	BD238635 Preparati
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C 37	5	100.0	10	6	BD239034 Preparati
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C 82	5	100.0	10	6	I38658 Sequence 18
C 83	5	100.0	10	6	I79742 Sequence 38
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c 192	5	100.0	10	6	BD083209	Human mat
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LOCUS	AR016043	Sequence 11	from patent	US 5776679.	10 bp	DNA	linear	PAT 05-DEC-1998											
DEFINITION	Sequence 11	from patent	US 5776679.																
ACCESSION	AR016043																		
VERSION	AR016043.1	GI:3972320																	
KEYWORDS																			
SOURCE	Unknown.																		
ORGANISM	Unknown.																		
REFERENCE	1	(bases 1 to 10)																	
AUTHORS	Villeponteau,B.,	Feng,J.,	Funk,W.	and	Andrews,W.H.														
TITLE	Assays for the	DNA component of	human telomerase																
JOURNAL	Patent: US 5776679-A	11	07-JUL-1998;																
FEATURES	Location/Qualifiers																		
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9 GAGGG 5

RESULT 2  
AR029981/c  
LOCUS AR029981 linear PAT 29-SEP-1999  
DEFINITION Sequence 170 from patent US 5861244.  
ACCESSION AR029981  
VERSION AR029981.1 GI:5943195  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang, C.-G. and Hepburn, A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 170 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Db 7 GAGGG 3

RESULT 3  
AR030010/c  
LOCUS AR030010 linear PAT 29-SEP-1999  
DEFINITION Sequence 199 from patent US 5861244.  
ACCESSION AR030010  
VERSION AR030010.1 GI:5943224  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang, C.-G. and Hepburn, A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 199 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Db 7 GAGGG 3

RESULT 4  
AR030099/c  
LOCUS AR030099 linear PAT 29-SEP-1999  
DEFINITION Sequence 288 from patent US 5861244.  
ACCESSION AR030099  
VERSION AR030099.1 GI:5943313  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)

AUTHORS Wang, C.-G. and Hepburn, A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 288 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
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Db 9 GAGGG 5

RESULT 5  
AR030218  
LOCUS AR030218 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 29 from patent US 5861246.  
ACCESSION AR030218  
VERSION AR030218.1 GI:5943432  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman, S.M., Nallur, G.N. and Kulkarni, P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 29 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
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Db 5 GAGGG 9

RESULT 6  
AR043159/c  
LOCUS AR043159 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 43 from patent US 5814453.  
ACCESSION AR043159  
VERSION AR043159.1 GI:5964167  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Beck, J. Joseph.  
TITLE Detection of fungal pathogens using the polymerase chain reaction  
JOURNAL Patent: US 5814453-A 43 29-SEP-1998;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
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Db 5 GAGGG 9

Db 10 GAGGG 6  
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RESULT 7  
AR049732 LOCUS AR049732 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 35 from patent US 5824770.  
ACCESSION AR049732  
VERSION AR049732.1 GI:5971724  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros polypeptides  
JOURNAL Patent: US 5824770-A 35 20-OCT-1998;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAGGG 5

RESULT 8  
AR053555/c LOCUS AR053555 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5834248.  
ACCESSION AR053555  
VERSION AR053555.1 GI:5978417  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchd534, a gene upregulated by shear stress  
JOURNAL Patent: US 5834248-A 20 10-NOV-1998;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 GAGGG 4

RESULT 9  
AR059204/c LOCUS AR059204 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5837857.  
ACCESSION AR059204  
VERSION AR059204.1 GI:5984781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5837857-A 11 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..10  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
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Db 9 GAGGG 5

RESULT 10  
AR065882/c LOCUS AR065882 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5849578.  
ACCESSION AR065882  
VERSION AR065882.1 GI:5996098  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular using RCHD528 as a target  
JOURNAL Patent: US 5849578-A 20 15-DEC-1998;  
FEATURES Location/Qualifiers  
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Qy 1 GAGGG 5  
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Db 8 GAGGG 4

RESULT 11  
AR074659/c LOCUS AR074659 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 43 from patent US 5955274.  
ACCESSION AR074659  
VERSION AR074659.1 GI:10001412  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Ligon,J.M. and Beck,J.J.  
TITLE Detection of fungal pathogens using the polymerase chain reaction  
JOURNAL Patent: US 5955274-A 43 21-SEP-1999;  
FEATURES Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





QY 1 GAGGG 5  
Db 7 GAGGG 3

RESULT 17  
AR098905  
LOCUS AR098905 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 41 from patent US 6077685.  
ACCESSION AR098905  
VERSION AR098905.1 GI:12808671  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.  
TITLE Tumor suppressor merlin and antibodies thereof  
JOURNAL Patent: US 6077685-A 41 20-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 18  
AR147933  
LOCUS AR147933 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 102 from patent US 6225054.  
ACCESSION AR147933  
VERSION AR147933.1 GI:15112023  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Frudakis,T.N., Smith,J.M. and Reed,S.G.  
TITLE Compositions and methods for the treatment and diagnosis of breast cancer  
JOURNAL Patent: US 6225054-A 102 01-MAY-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
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QY 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 19  
AR148319/c  
LOCUS AR148319 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 20 from patent US 6225084.  
ACCESSION AR148319  
VERSION AR148319.1 GI:15112409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd534 as a target  
JOURNAL Patent: US 6225084-A 20 01-MAY-2001;  
FEATURES Location/Qualifiers  
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QY 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 20  
AR149626  
LOCUS AR149626 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 35 from patent US 6228611.  
ACCESSION AR149626  
VERSION AR149626.1 GI:15114217  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros: A T cell pathway regulatory gene  
JOURNAL Patent: US 6228611-A 35 08-MAY-2001;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
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QY 1 GAGGG 5  
Db 1 GAGGG 5

RESULT 21  
AR161913/c  
LOCUS AR161913 10 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 11 from patent US 6258535.  
ACCESSION AR161913  
VERSION AR161913.1 GI:16228931  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 6258535-A 11 10-JUL-2001;  
FEATURES Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 22  
AR175404/c  
LOCUS AR175404 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 127 from patent US 6309823.  
ACCESSION AR175404  
VERSION AR175404.1 GI:17916703  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.  
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes and methods of using the same  
JOURNAL Patent: US 6309823-A 127 30-OCT-2001;  
FEATURES Location/Qualifiers  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 23  
BD176154/c  
LOCUS BD176154 10 bp DNA linear PAT 18-MAR-2003  
DEFINITION Mammalian telomerase.  
ACCESSION BD176154  
VERSION BD176154.1 GI:29121858  
KEYWORDS JP 2002272489-A/13.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: JP 2002272489-A 13 24-SEP-2002;  
COMMENT GERON CORP  
OS Unidentified  
PN JP 2002272489-A/13  
PD 24-SEP-2002  
PF 06-MAR-2002 JP 2002061125  
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR  
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 PI BRYANT  
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC  
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC  
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CC Topology: Linear;  
CC Mammalian telomerase  
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ORIGIN

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QY 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 24  
BD177264  
LOCUS BD177264 10 bp DNA linear PAT 16-APR-2003  
DEFINITION Method for discriminating individuals by the RAPD process.  
ACCESSION BD177264  
VERSION BD177264.1 GI:30014525  
KEYWORDS JP 2002291475-A/5.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsuda,M., Kojima,E., Izumi,K. and Murakami,K.  
TITLE Method for discriminating individuals by the RAPD process  
JOURNAL Patent: JP 2002291475-A 5 08-OCT-2002;  
COMMENT NIPPON PAPER INDUSTRIES CO LTD  
OS Artificial Sequence  
PN JP 2002291475-A/5  
PD 08-OCT-2002  
PF 29-MAR-2001 JP 2001097703  
PI MANABU MATSUDA,EIJI KOJIMA,KIMIKO IZUMI,KUNICHIKA MURAKAMI PC  
C12N15/09,C12Q1/68//A01H1/00,C12N15/00  
CC primer for PCR  
FH Key Location/Qualifiers  
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ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 2 GAGGG 6

RESULT 25  
BD238590  
LOCUS BD238590 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238590  
VERSION BD238590.1 GI:33048360  
KEYWORDS JP 2002534056-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 8 15-OCT-2002;  
COMMENT GENZYME CORP  
OS Homo sapiens (human)  
PN JP 2002534056-A/8  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR









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Db          |||||
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RESULT 35
BD238973
LOCUS      BD238973              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238973
VERSION    BD238973.1  GI:33048743
KEYWORDS  JP 2002534056-A/391.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 391 15-OCT-2002;
          GENZYME CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002534056-A/391
          PD 15-OCT-2002
          PF 18-JUN-1999 JP 2000554749
          PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GAGGG 7

RESULT 36
BD239002
LOCUS      BD239002              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239002
VERSION    BD239002.1  GI:33048772
KEYWORDS  JP 2002534056-A/420.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 452 15-OCT-2002;
          GENZYME CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002534056-A/420
          PD 15-OCT-2002
          PF 18-JUN-1999 JP 2000554749
          PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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          08-DEC-1998 US 60/111715
          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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          PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GAGGG 7

RESULT 37
BD239034/c
LOCUS      BD239034              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239034
VERSION    BD239034.1  GI:33048804
KEYWORDS  JP 2002534056-A/452.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 452 15-OCT-2002;
          GENZYME CORP
COMMENT   OS Homo sapiens (human)
          PN JP 2002534056-A/452
          PD 15-OCT-2002
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          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
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Db 3 GAGGG 7
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 660 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/660  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
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C12N1/19,  
G01N37/00,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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QY 1 GAGGG 5  
Db |||||  
5 GAGGG 9  
RESULT 43  
BD239296  
LOCUS BD239296 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239296  
VERSION BD239296.1 GI:33049066  
KEYWORDS JP 2002534056-A/714.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 714 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/714  
PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
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19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
G01N37/00,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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CC Preparation and use of superior vaccines  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
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QY 1 GAGGG 5  
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RESULT 44  
BD239347  
LOCUS BD239347 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239347  
VERSION BD239347.1 GI:33049117  
KEYWORDS JP 2002534056-A/765.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 765 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/765  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
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C12N1/19,  
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G01N37/00,  
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1 GAGGG 5  
RESULT 45  
BD239356/c  
LOCUS BD239356 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239356  
VERSION BD239356.1 GI:33049126  
KEYWORDS JP 2002534056-A/774.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
REFERENCE  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 774 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/774  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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LOCUS BD239356 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239356  
VERSION BD239356.1 GI:33049126  
KEYWORDS JP 2002534056-A/774.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 10)  
REFERENCE  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 774 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/774  
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19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
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08-DEC-1998 US 60/111715  
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CC Preparation and use of superior vaccines  
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RESULT 46  
BD239370  
LOCUS BD239370 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239370  
VERSION BD239370.1 GI:33049140  
KEYWORDS JP 2002534056-A/788.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
REFERENCE  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 788 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/788  
PD 15-OCT-2002  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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CC Preparation and use of superior vaccines  
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RESULT 46  
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LOCUS BD239370 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239370  
VERSION BD239370.1 GI:33049140  
KEYWORDS JP 2002534056-A/788.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
REFERENCE  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 788 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/788  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
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19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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CC Preparation and use of superior vaccines  
FH Key Location/Qualifiers

QY 1 GAGGG 5  
Db 1 GAGGG 5

RESULT 47  
BD239497/c  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239497  
VERSION BD239497.1 GI:33049267  
KEYWORDS JP 2002534056-A/915.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 915 15-OCT-2002;  
GENZYME CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/915  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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QY 1 GAGGG 5  
Db 6 GAGGG 2

RESULT 48  
BD239582  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239582  
VERSION BD239582.1 GI:33049352

KEYWORDS JP 2002534056-A/1000.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1000 15-OCT-2002;  
GENZYME CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/1000  
PD 15-OCT-2002  
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Db 4 GAGGG 8

RESULT 49  
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LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239620  
VERSION BD239620.1 GI:33049390  
KEYWORDS JP 2002534056-A/1038.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1038 15-OCT-2002;  
GENZYME CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/1038

PD 15-OCT-2002 JP 2000554749  
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08-DEC-1998 US 60/111715  
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QY 1 GAGGG 5  
Db 3 GAGGG 7  
RESULT 50  
BD239646  
LOCUS BD239646 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239646  
VERSION BD239646.1 GI:33049416  
KEYWORDS JP 2002534056-A/1064.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1064 15-OCT-2002;  
GENZYME CORP  
OS Homo sapiens (human)  
PN JP 2002534056-A/1064  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR  
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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CC Preparation and use of superior vaccines  
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QY 1 GAGGG 5  
Db 5 GAGGG 9  
Search completed: January 7, 2005, 07:55:11  
Job time : 524 secs

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:35:05 ; Search time 254.4 Seconds  
(without alignments)  
103.173 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3979404

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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277	5	100.0	10	3	AAF19178	Aaf19178 Human ade
278	5	100.0	10	3	AAF19135	Aaf19135 Human ade
279	5	100.0	10	3	AAF19088	Aaf19088 Human ade
280	5	100.0	10	3	AAF19157	Aaf19157 Human ade
281	5	100.0	10	3	AAF19198	Aaf19198 Human ade
282	5	100.0	10	3	AAF19112	Aaf19112 Human ade
C 283	5	100.0	10	3	AAZ88020	Aaz88020 Human umb
284	5	100.0	10	3	AAAG1013	Aaa61013 Protein b
285	5	100.0	10	3	AAC68567	Aac68567 Green flu
286	5	100.0	10	3	AAA95171	Aaa95171 Primer #1
C 287	5	100.0	10	3	AAA74377	Aaa74377 Mouse tra
C 288	5	100.0	10	3	AAH74368	Aaa74368 Mouse tra
C 289	5	100.0	10	4	AAH18990	Aah18990 UCP3 poly
290	5	100.0	10	4	AAH19960	Aah19960 Mouse Tre
C 291	5	100.0	10	4	AAH19987	Aah19987 Mouse Tre
C 292	5	100.0	10	4	AAI67375	Aai67375 Human FKB
293	5	100.0	10	4	AAI67352	Aai67352 Human FKB
C 294	5	100.0	10	4	AAI67369	Aai67369 Human FKB
C 295	5	100.0	10	4	AAI67354	Aai67354 Human FKB
296	5	100.0	10	4	AAI67355	Aai67355 Human FKB
297	5	100.0	10	4	AAI67380	Aai67380 Human FKB
298	5	100.0	10	4	AAF58695	Aaf58695 DNA segme
299	5	100.0	10	4	AAD06118	Aad06118 Human b3
C 300	5	100.0	10	4	AAH27548	Aah27548 Ligation
C 301	5	100.0	10	4	AAH27547	Aah27547 Ligation
302	5	100.0	10	4	AAF77673	Aaf77673 Rice S-5
303	5	100.0	10	4	AAS04436	Aas04436 Human DAX
304	5	100.0	10	4	AAS04440	Aas04440 Human DAX
305	5	100.0	10	4	AAS04443	Aas04443 Human DAX
C 306	5	100.0	10	4	AAS04420	Aas04420 Human DAX
307	5	100.0	10	4	AAH63433	Aah63433 Human ubi
308	5	100.0	10	4	AAH63629	Aah63629 Human ubi
309	5	100.0	10	4	AAH63735	Aah63735 Human ubi
310	5	100.0	10	4	AAH63739	Aah63739 Human ubi
C 311	5	100.0	10	4	AAH63956	Aah63956 Human ubi
312	5	100.0	10	4	AAH64152	Aah64152 Human ubi
C 313	5	100.0	10	4	AAH63406	Aah63406 Human can

314	5	100.0	10	4	AAH63653	Aah63653 Human ubi
315	5	100.0	10	4	AAH63183	Aah63183 Human col
C 316	5	100.0	10	4	AAH63802	Aah63802 Human ubi
C 317	5	100.0	10	4	AAH63211	Aah63211 Human col
C 318	5	100.0	10	4	AAH64264	Aah64264 Human ubi
C 319	5	100.0	10	4	AAH64574	Aah64574 Human ubi
C 320	5	100.0	10	4	AAH63412	Aah63412 Human can
321	5	100.0	10	4	AAH63840	Aah63840 Human ubi
322	5	100.0	10	4	AAH64708	Aah64708 Human hig
C 323	5	100.0	10	4	AAH63801	Aah63801 Human ubi
324	5	100.0	10	4	AAH64621	Aah64621 Human col
325	5	100.0	10	4	AAH63466	Aah63466 Human ubi
C 326	5	100.0	10	4	AAH64099	Aah64099 Human ubi
327	5	100.0	10	4	AAH64338	Aah64338 Human ubi
328	5	100.0	10	4	AAH63689	Aah63689 Human ubi
329	5	100.0	10	4	AAH63757	Aah63757 Human ubi
330	5	100.0	10	4	AAH63841	Aah63841 Human ubi
331	5	100.0	10	4	AAH63462	Aah63462 Human ubi
332	5	100.0	10	4	AAH64021	Aah64021 Human ubi
333	5	100.0	10	4	AAH63839	Aah63839 Human ubi
C 334	5	100.0	10	4	AAH64500	Aah64500 Human ubi
C 335	5	100.0	10	4	AAH63176	Aah63176 Human col
C 336	5	100.0	10	4	AAH63179	Aah63179 Human col
C 337	5	100.0	10	4	AAH63307	Aah63307 Human col
C 338	5	100.0	10	4	AAH63435	Aah63435 Human ubi
C 339	5	100.0	10	4	AAH63528	Aah63528 Human ubi
C 340	5	100.0	10	4	AAH57282	Aah57282 Human CHR
C 341	5	100.0	10	4	AAH57284	Aah57284 Human CHR
C 342	5	100.0	10	4	AAH57310	Aah57310 Human CHR
C 343	5	100.0	10	4	AAH57286	Aah57286 Human CHR
C 344	5	100.0	10	4	AAH57303	Aah57303 Human CHR
345	5	100.0	10	4	AAF16618	Aaf16618 Gastric a
346	5	100.0	10	4	AAF70100	Aaf70100 Human TNF
C 347	5	100.0	10	4	AAH28600	Aah28600 Human int
348	5	100.0	10	4	AAH28624	Aah28624 Human int
349	5	100.0	10	4	AAH32933	Aah32933 LPS activ
350	5	100.0	10	4	AAH32701	Aah32701 LPS activ
351	5	100.0	10	4	AAH32861	Aah32861 LPS activ
C 352	5	100.0	10	4	AAH32868	Aah32868 LPS activ
C 353	5	100.0	10	4	AAH32908	Aah32908 LPS activ
354	5	100.0	10	4	AAH32790	Aah32790 LPS activ
355	5	100.0	10	4	AAH32892	Aah32892 LPS activ
356	5	100.0	10	4	ABA81675	Aba81675 Human pho
357	5	100.0	10	4	ABA81650	Aba81650 Human pho
358	5	100.0	10	4	ABA81634	Aba81634 Human pho
359	5	100.0	10	5	AAH41727	Aah41727 Anti-PEP
360	5	100.0	10	5	AAH41710	Aah41710 Anti-PEP
C 361	5	100.0	10	5	ABA06213	Aba06213 Human nor
362	5	100.0	10	5	ABA06157	Aba06157 Human nor
363	5	100.0	10	5	AAF70443	Aaf70443 Human DRD
364	5	100.0	10	5	AAF70431	Aaf70431 Human DRD
C 365	5	100.0	10	5	AAF69606	Aaf69606 Human IL4
C 366	5	100.0	10	5	AAF69623	Aaf69623 Human IL4
367	5	100.0	10	5	AAF74011	Aaf74011 Human SLC
C 368	5	100.0	10	5	AAF74010	Aaf74010 Human SLC
369	5	100.0	10	5	ABA83151	Aba83151 Glutathio
370	5	100.0	10	5	AAF37150	Aaf37150 Yeast NOR
371	5	100.0	10	5	AAF37652	Aaf37652 Yeast NOR
C 372	5	100.0	10	5	AAF40937	Aaf40937 Yeast NOR
C 373	5	100.0	10	5	AAF42839	Aaf42839 Yeast NOR
C 374	5	100.0	10	5	AAF42840	Aaf42840 Yeast NOR
C 375	5	100.0	10	5	AAF43929	Aaf43929 Yeast NOR
376	5	100.0	10	5	AAF36456	Aaf36456 Yeast NOR
C 377	5	100.0	10	5	AAF40041	Aaf40041 Yeast NOR
378	5	100.0	10	5	AAF42573	Aaf42573 Yeast NOR
C 379	5	100.0	10	5	AAF35078	Aaf35078 Yeast NOR
C 380	5	100.0	10	5	AAF36719	Aaf36719 Yeast NOR
C 381	5	100.0	10	5	AAF40953	Aaf40953 Yeast NOR
382	5	100.0	10	5	AAF38210	Aaf38210 Yeast NOR
383	5	100.0	10	5	AAF39594	Aaf39594 Yeast NOR
C 384	5	100.0	10	5	AAF41459	Aaf41459 Yeast NOR
385	5	100.0	10	5	AAF42052	Aaf42052 Yeast NOR
386	5	100.0	10	5	AAF43475	Aaf43475 Yeast NOR

387	5	100.0	10	5	AAE34727	Aaf34727	Yeast	NOR
388	5	100.0	10	5	AAF40147	Aaf40147	Yeast	NOR
C 389	5	100.0	10	5	AAF36707	Aaf36707	Yeast	NOR
390	5	100.0	10	5	AAF42054	Aaf42054	Yeast	NOR
391	5	100.0	10	5	AAF43110	Aaf43110	Yeast	NOR
392	5	100.0	10	5	AAF35023	Aaf35023	Yeast	NOR
C 393	5	100.0	10	5	AAF39184	Aaf39184	Yeast	NOR
C 394	5	100.0	10	5	AAF339670	Aaf339670	Yeast	NOR
395	5	100.0	10	5	AAF40445	Aaf40445	Yeast	NOR
C 396	5	100.0	10	5	AAF40954	Aaf40954	Yeast	NOR
397	5	100.0	10	5	AAF42060	Aaf42060	Yeast	NOR
398	5	100.0	10	5	AAF39595	Aaf39595	Yeast	NOR
C 399	5	100.0	10	5	AAF41373	Aaf41373	Yeast	NOR
400	5	100.0	10	5	AAF34231	Aaf34231	Yeast	NOR
401	5	100.0	10	5	AAF34236	Aaf34236	Yeast	NOR
402	5	100.0	10	5	AAF38902	Aaf38902	Yeast	NOR
403	5	100.0	10	5	AAF41487	Aaf41487	Yeast	NOR
C 404	5	100.0	10	5	AAF43778	Aaf43778	Yeast	NOR
405	5	100.0	10	5	AAF36243	Aaf36243	Yeast	NOR
406	5	100.0	10	5	AAF36308	Aaf36308	Yeast	NOR
407	5	100.0	10	5	AAF41116	Aaf41116	Yeast	NOR
408	5	100.0	10	5	AAF42058	Aaf42058	Yeast	NOR
409	5	100.0	10	5	AAF34447	Aaf34447	Yeast	NOR
410	5	100.0	10	5	AAF40966	Aaf40966	Yeast	NOR
411	5	100.0	10	5	AAF42051	Aaf42051	Yeast	NOR
412	5	100.0	10	5	AAF42056	Aaf42056	Yeast	NOR
413	5	100.0	10	5	AAF42057	Aaf42057	Yeast	NOR
C 414	5	100.0	10	5	AAF34444	Aaf34444	Yeast	NOR
C 415	5	100.0	10	5	AAF39165	Aaf39165	Yeast	NOR
416	5	100.0	10	5	AAF39583	Aaf39583	Yeast	NOR
417	5	100.0	10	5	AAF41444	Aaf41444	Yeast	NOR
418	5	100.0	10	5	AAF36526	Aaf36526	Yeast	NOR
419	5	100.0	10	5	AAF37174	Aaf37174	Yeast	NOR
C 420	5	100.0	10	5	AAF42478	Aaf42478	Yeast	NOR
421	5	100.0	10	5	AAF35927	Aaf35927	Yeast	NOR
422	5	100.0	10	5	AAF41180	Aaf41180	Yeast	NOR
C 423	5	100.0	10	5	AAF41287	Aaf41287	Yeast	NOR
424	5	100.0	10	5	AAF42053	Aaf42053	Yeast	NOR
425	5	100.0	10	5	AAF42059	Aaf42059	Yeast	NOR
C 426	5	100.0	10	5	AAF42398	Aaf42398	Yeast	NOR
427	5	100.0	10	5	AAF43406	Aaf43406	Yeast	NOR
C 428	5	100.0	10	5	AAF34314	Aaf34314	Yeast	NOR
C 429	5	100.0	10	5	AAF34867	Aaf34867	Yeast	NOR
430	5	100.0	10	5	AAF37794	Aaf37794	Yeast	NOR
431	5	100.0	10	5	AAF38424	Aaf38424	Yeast	NOR
C 432	5	100.0	10	5	AAF38718	Aaf38718	Yeast	NOR
C 433	5	100.0	10	5	AAF41800	Aaf41800	Yeast	NOR
434	5	100.0	10	5	AAF42055	Aaf42055	Yeast	NOR
C 435	5	100.0	10	5	AAF42682	Aaf42682	Yeast	NOR
436	5	100.0	10	6	AAS19589	Aas19589	Primer-ex	
437	5	100.0	10	6	AAS19657	Aas19657	Primer-ex	
C 438	5	100.0	10	6	AAS19649	Aas19649	Primer-ex	
439	5	100.0	10	6	AAI72971	Aai72971	Purine ri	
440	5	100.0	10	6	AAS18742	Aas18742	Primer-ex	
C 441	5	100.0	10	6	AAS18741	Aas18741	Primer-ex	
442	5	100.0	10	6	AAS98374	Aas98374	Galanin r	
C 443	5	100.0	10	6	AAS98385	Aas98385	Galanin r	
C 444	5	100.0	10	6	AAS98387	Aas98387	Galanin r	
445	5	100.0	10	6	AAS98380	Aas98380	Galanin r	
446	5	100.0	10	6	AAS98370	Aas98370	Galanin r	
447	5	100.0	10	6	AAS98378	Aas98378	Galanin r	
448	5	100.0	10	6	AAS98372	Aas98372	Galanin r	
449	5	100.0	10	6	AAS98376	Aas98376	Galanin r	
C 450	5	100.0	10	6	AAS98383	Aas98383	Galanin r	
C 451	5	100.0	10	6	AAD26710	Aad26710	Human GPR	
C 452	5	100.0	10	6	AAD26716	Aad26716	Human GPR	
453	5	100.0	10	6	ABK24243	Abk24243	Retinalde	
C 454	5	100.0	10	6	AAI45321	Aal45321	Human KCN	
C 455	5	100.0	10	6	AAI45320	Aal45320	Human KCN	
C 456	5	100.0	10	6	ABK68693	Abk68693	Human SCN	
457	5	100.0	10	6	ABK96684	Abk96684	Interleuk	
C 458	5	100.0	10	6	AAS18288	Aas18288	Primer-ex	
459	5	100.0	10	6	AAD25432	Aad25432	Human GNR	

C 460	5	100.0	10	6	ABL88325	Ab188325	Human	CHR
C 461	5	100.0	10	6	ABK14245	Abk14245	Human	RRA
C 462	5	100.0	10	6	AAD32206	Aad32206	Human	NFK
463	5	100.0	10	6	AAD32202	Aad32202	Human	NFK
464	5	100.0	10	6	ABL52165	Ab152165	Human	PER
C 465	5	100.0	10	6	ABL52189	Ab152189	Human	PER
C 466	5	100.0	10	6	ABL52189	Ab152189	Oligonuc1	
467	5	100.0	10	6	ABL38366	Ab138366	Human	CYP
C 468	5	100.0	10	6	ABK81953	Abk81953	Human	AKR
C 469	5	100.0	10	6	ABL01179	Ab101179	Human	AKR
470	5	100.0	10	6	ABL01221	Ab101221	Human	AKR
C 471	5	100.0	10	6	AAS98896	Aas98896	Colony st	
C 472	5	100.0	10	6	AAS98852	Aas98852	Colony st	
473	5	100.0	10	6	AAD25885	Aad25885	Primer #7	
C 474	5	100.0	10	6	AAS99670	Aas99670	Breast tu	
C 475	5	100.0	10	6	ABL42863	Ab142863	Human mat	
476	5	100.0	10	6	ABL42756	Ab142756	Human mat	
C 477	5	100.0	10	6	ABL42716	Ab142716	Human mat	
478	5	100.0	10	6	ABL99006	Ab199006	Mouse neu	
479	5	100.0	10	6	ABL57659	Ab157659	Human SCN	
480	5	100.0	10	6	ABL57662	Ab157662	Human SCN	
C 481	5	100.0	10	6	ABL57671	Ab157671	Human SCN	
482	5	100.0	10	6	ABK70541	Abk70541	Human G p	
483	5	100.0	10	6	ABL60194	Ab160194	Human MUC	
484	5	100.0	10	6	ABL60200	Ab160200	Human MUC	
C 485	5	100.0	10	6	ABK89140	Abk89140	RNA seque	
C 486	5	100.0	10	6	ABS51966	Ab51966	Human FMO	
C 487	5	100.0	10	6	ABS51949	Ab51949	Human FMO	
C 488	5	100.0	10	6	ABS51956	Ab51956	Human FMO	
C 489	5	100.0	10	6	ABS51960	Ab51960	Human FMO	
490	5	100.0	10	6	AAD45283	Aad45283	Human PON	
491	5	100.0	10	6	ABK81400	Abk81400	SCYA21 ge	
492	5	100.0	10	6	ABK96075	Abk96075	Human LIP	
493	5	100.0	10	6	ABK96052	Abk96052	Human LIP	
494	5	100.0	10	6	AAS96200	Aas96200	Human Ace	
C 495	5	100.0	10	6	AAS96191	Aas96191	Human Ace	
C 496	5	100.0	10	6	ABA97044	Ab97044	ZFP36 ext	
C 497	5	100.0	10	6	ABA97036	Ab97036	ZFP36 ext	
498	5	100.0	10	6	AAD26176	Aad26176	Human end	
C 499	5	100.0	10	6	AAD26165	Aad26165	Human end	
C 500	5	100.0	10	12	ABK16982	Abk16982	Pyridoxal	
					AD113702	Ad113702	Cytoplasm	

ALIGNMENTS

RESULT 1  
AAN92503  
ID AAN92503 standard; DNA; 10 BP.  
XX  
AC AAN92503;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-MAY-1990 (first entry)  
XX  
DE Sequence corresponding to ribosome binding region.  
XX  
KW Ribosome binding region; anti-hyperlipidaemia agent;  
KW anti-arteriosclerosis agent; ss.  
OS Escherichia coli.  
XX  
PN EP345155-A.  
XX  
PD 06-DEC-1989.  
XX  
PF 31-MAY-1989; 89EP-00401495.  
XX  
PR 31-MAY-1988; 88JP-00133549.  
PR 26-APR-1989; 89JP-00107027.  
XX  
PA (MITU ) MITSUBISHI KASEI CORP.  
XX



PI Shibul T, Kamizono M, Teranishi Y;  
XX WPI; 1989-358519/49.  
DR  
XX Prodn. of natural human apolipoprotein E or related protein - using a  
PT vector contg. the coding sequence fused to a secretory signal peptide.  
PT  
XX Claim 12; Page 13; 32pp; English.  
PS  
XX This sequence is present in the vector and is complementary to the 3'  
CC terminal base sequence of ribosomal RNA. When DNA sequences encoding  
CC human apolipoprotein E (I) and E-like proteins and a secretory peptide  
CC are inserted into the vector the resultant products are expressed at  
CC least 1000 times more efficiently than previously. E3-type (I) is useful  
CC as an anti-hyperlipidaemia and anti-arteriosclerosis agent. (Updated on  
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR  
CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
DB 3 GAGGG 7  
RESULT 2  
AAQ79358/c  
ID AAQ79358 standard; DNA; 10 BP.  
XX  
AC AAQ79358;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Sequence of AP2 regulatory sequence located at posn. 896 in hEpsLH.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UJNY ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table I, p. 12; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
CC 5' flanking region and includes all the 5' regulatory elements. This  
CC region, consisting of the first 3892 of AAQ79353, was not found in the  
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362

CC show several of these elements and their positions. The nucleotide  
CC position of these elements is measured from the BamHI site at the 5' end  
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
DB 8 GAGGG 4  
RESULT 3  
AAQ71100  
ID AAQ71100 standard; cDNA; 10 BP.  
XX  
AC AAQ71100;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 12 splice donor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX  
PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GCHO ) GEN HOSPITAL CORP.  
XX  
PI Trofatter JA, Maccollin MM, Gusella JF;  
XX  
DR WPI; 1994-272992/34.  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
PT tumours and neurofibromatosis (NF2).  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance

CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

Db |||||

3 GAGGG 7

RESULT 4

AAQ71097/c

ID AAQ71097 standard; cDNA; 10 BP.

XX AC AAQ71097;

XX DT 25-MAR-2003 (revised)

DT 20-APR-1995 (first entry)

XX DE Merlin exon 11 splice acceptor site.

XX KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;

KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;

KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;

KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;

KW merlin-associated tumour; D22S1; posterior capsular lens opacity;

KW deafness; balance disorder; paralysis; ss.

XX OS Homo sapiens.

XX PN EP613945-A2.

XX PD 07-SEP-1994.

XX PF 25-FEB-1994; 94EP-00301367.

XX PR 25-FEB-1993; 93US-00022034.

PR 04-MAR-1993; 93US-00026063.

PR 19-AUG-1993; 93US-00108808.

PR 22-DEC-1993; 93US-00171718.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PI Trofatter JA, Maccollin MM, Gusella JF;

XX DR WPI; 1994-272992/34.

XX PT The tumour suppressor gene merlin - for treatment and diagnosis of

PT tumours and neurofibromatosis (NF2).

XX PS Example 6; Page 26; 86pp; English.

XX CC The sequences given in AAQ71078-109 represent the splice donor and

CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2

CC "gene" has been shown by linkage studies to be assigned to chromosome 22.

CC The missing or mutated gene in NF2 patients has been shown to be the

CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-

CC like protein), which possesses tumour suppressor activity, and whose

CC tumour suppressor activity is mediated by inter- actions with the

CC cytoskeleton. The merlin gene is found on chromosome 22 between the known

CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene

CC is either lost or mutated. A mutant merlin protein may be encoded by a

CC gene in which a mutation of A to T at the first position of the codon

CC encoding amino acid 220 causes the substitution of Tyr for Asn. The

CC merlin gene may be used in gene therapy for the treatment of a merlin-

CC associated tumour or NF2, or for prevention of schwannoma, meningioma,

CC posterior capsular lens opacities, deafness or hearing loss, balance

CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

Db |||||

6 GAGGG 2

RESULT 5

AAQ71099/c

ID AAQ71099 standard; cDNA; 10 BP.

XX AC AAQ71099;

XX DT 25-MAR-2003 (revised)

DT 20-APR-1995 (first entry)

XX DE Merlin exon 12 splice acceptor site.

XX KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;

KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;

KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;

KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;

KW merlin-associated tumour; D22S1; posterior capsular lens opacity;

KW deafness; balance disorder; paralysis; ss.

XX OS Homo sapiens.

XX PN EP613945-A2.

XX PD 07-SEP-1994.

XX PF 25-FEB-1994; 94EP-00301367.

XX PR 25-FEB-1993; 93US-00022034.

PR 04-MAR-1993; 93US-00026063.

PR 19-AUG-1993; 93US-00108808.

PR 22-DEC-1993; 93US-00171718.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PI Trofatter JA, Maccollin MM, Gusella JF;

XX DR WPI; 1994-272992/34.

XX PT The tumour suppressor gene merlin - for treatment and diagnosis of

PT tumours and neurofibromatosis (NF2).

XX PS Example 6; Page 26; 86pp; English.

XX CC The sequences given in AAQ71078-109 represent the splice donor and

CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2

CC "gene" has been shown by linkage studies to be assigned to chromosome 22.

CC The missing or mutated gene in NF2 patients has been shown to be the

CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-

CC like protein), which possesses tumour suppressor activity, and whose

CC tumour suppressor activity is mediated by inter- actions with the

CC cytoskeleton. The merlin gene is found on chromosome 22 between the known

CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene

CC is either lost or mutated. A mutant merlin protein may be encoded by a

CC gene in which a mutation of A to T at the first position of the codon

CC encoding amino acid 220 causes the substitution of Tyr for Asn. The

CC merlin gene may be used in gene therapy for the treatment of a merlin-

CC associated tumour or NF2, or for prevention of schwannoma, meningioma,

CC posterior capsular lens opacities, deafness or hearing loss, balance

CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
      |||||  
Db 7 GAGGG 3

RESULT 6  
AAQ64610/c  
ID AAQ64610 standard; cDNA; 10 BP.  
XX  
AC AAQ64610;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-DEC-1994 (first entry)  
XX  
DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.  
XX  
KW Mitochondrial DNA mutation; associated with Alzheimer's;  
KW Parkinson's disease; mismatch primers; PCR; amplification;  
KW polymerase chain reaction; ss.  
XX Homo sapiens.  
OS  
XX WO9409162-A1.  
PN  
XX  
PD 28-APR-1994.  
XX  
PF 20-OCT-1993; 93WO-US010072.  
XX  
PR 20-OCT-1992; 92US-00963723.  
XX  
PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
XX  
PI Wallace DC;  
XX  
DR WPI; 1994-151346/18.  
XX  
PT Detection of mitochondrial DNA mutation associated with Alzheimer's  
PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-  
PT disposition to Alzheimer's disease and/or Parkinson's disease in a  
PT patient.  
XX  
PS Disclosure; Page 36; 83pp; English.  
XX  
CC A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene  
CC insertion. Direct sequence analysis revealed that the insertion consisted  
CC of approximately five cytosines within AAQ64610. This mitochondrial DNA  
CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The  
CC detection of the mutations is useful for diagnosing or predicting a pre-  
CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
      |||||  
Db 7 GAGGG 3

RESULT 7  
AAQ88295/c  
ID AAQ88295 standard; DNA; 10 BP.  
XX  
AC AAQ88295;  
XX  
DT 12-DEC-1995 (first entry)  
XX

XX Primer sequence 9 for detection of fruit species by PCR.  
DE  
XX  
KW Polymerase chain reaction amplification; fruit juice; fruit pulp;  
KW species detection; apple; orange; grapefruit; RAPD technique; ss.  
XX  
OS Synthetic.  
XX  
PN FR2711143-A1.  
XX  
PD 21-APR-1995.  
XX  
PF 13-OCT-1994; 94FR-00012235.  
XX  
PR 13-OCT-1993; 93GB-00021113.  
XX  
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.  
XX  
PI Lindsey K, Twell D;  
XX  
DR WPI; 1995-157154/21.  
XX  
PT Identifying species, variety etc. of fruits by PCR amplification - then  
PT comparing products with standards, also new test kits, primers and  
PT hybridisation probes, partic. to detect fraudulent use in food prodn.  
XX  
PS Claim 8; Page 17; 20pp; French.  
XX  
CC Primers have been identified which give useful results for identification  
CC of genus, species or variety of fruits (see AAQ88293-Q88298);  
CC amplification profiles are established using several of the primers,  
CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of  
CC the target sequences which are amplified. Using the primers it was  
CC possible to distinguish between e.g. different varieties of Navel oranges  
CC and also between "red" apples and "Granny Smith" apples  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
      |||||  
Db 8 GAGGG 4

RESULT 8  
AAQ88289  
ID AAQ88289 standard; DNA; 10 BP.  
XX  
AC AAQ88289;  
XX  
DT 27-AUG-2003 (revised)  
DT 12-DEC-1995 (first entry)  
XX  
DE 5'-target sequence 3 for detection of fruit species by PCR.  
XX  
KW Polymerase chain reaction amplification; fruit juice; fruit pulp;  
KW species detection; apple; orange; grapefruit; RAPD technique; ss.  
XX  
OS Citrus.  
XX  
PN FR2711143-A1.  
XX  
PD 21-APR-1995.  
XX  
PF 13-OCT-1994; 94FR-00012235.  
XX  
PR 13-OCT-1993; 93GB-00021113.  
XX  
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.  
XX

PI Lindsey K, Twell D;  
XX WPI; 1995-157154/21.  
XX  
PT Identifying species, variety etc. of fruits by PCR amplification - then  
PT comparing products with standards, also new test kits, primers and  
PT hybridisation probes, partic. to detect fraudulent use in food prodn.  
XX  
PS Claim 7; Page 17; 20pp; French.  
XX  
CC Primers have been identified which give useful results for identification  
CC of genus, species or variety of fruits (see AAQ88293-Q88298);  
CC amplification profiles are established using several of the primers,  
CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of  
CC the target sequences which are amplified. Using the primers it was  
CC possible to distinguish between e.g. different varieties of Navel oranges  
CC and also between "red" apples and "Granny Smith" apples. (Updated on 27-  
CC AUG-2003 to correct OS field.)  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
3 GAGGG 7  
  
RESULT 9  
AAQ81904/c  
ID AAQ81904 standard; RNA; 10 BP.  
XX  
AC AAQ81904;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-SEP-1995 (first entry)  
XX  
DE Interferon-gamma binding oligonucleotide 34.  
XX  
KW Interferon gamma; IFN-gamma; inhibition; binding; immunomodulation;  
KW septic shock; rheumatoid arthritis; HIV infection; ss.  
XX  
OS Synthetic.  
XX  
PN WO9500529-A1.  
XX  
PD 05-JAN-1995.  
XX  
PF 17-JUN-1994; 94WO-US006897.  
XX  
PR 18-JUN-1993; 93US-00079677.  
PR 17-MAR-1994; 94US-00210222.  
XX  
PA (PHAR-) PHARMAGENICS INC.  
XX  
PI Coppola GR, Beutel BA, Bertelsen AH;  
XX  
DR WPI; 1995-051993/07.  
XX  
PT Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating,  
PT inhibiting or enhancing the activity or function of interferon-gamma.  
XX  
PS Claim 4; Page 32; 43pp; English.  
XX  
CC Oligonucleotides which bind to interferon-gamma are useful for  
CC modulating, inhibiting or enhancing the activity or function of the IFN.  
CC Particularly, they are useful for treatment of septic shock, rheumatoid  
CC arthritis and HIV infection. Preferred oligonucleotides are given in  
CC AAQ81894-Q81909 and AAQ81913-Q81932; esp. the oligo- nucleotides comprise  
CC at least one of the sequences AAGUUG, UGANGCUC, GCACNC, AAQ81903 or  
CC AAQ81904. (Updated on 25-MAR-2003 to correct PN field.)

XX  
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 0 T; 1 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
9 GAGGG 5  
  
RESULT 10  
AAT05374/c  
ID AAT05374 standard; DNA; 10 BP.  
XX  
AC AAT05374;  
XX  
DT 04-JUN-1996 (first entry)  
XX  
DE Setoria tritici RAPD primer OPE-6.  
XX  
KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;  
KW pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;  
KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;  
KW internal transcribed region; strain; capture; colourimetric assay;  
KW isolate; development; population; random amplified polymorphic DNA; ss.  
XX  
OS Synthetic.  
XX  
PN WO9529260-A2.  
XX  
PD 02-NOV-1995.  
XX  
PF 19-APR-1995; 95WO-US004712.  
XX  
PR 25-APR-1994; 94US-00233608.  
XX  
PA (CIBA ) CIBA GEIGY AG.  
XX  
PI Ligon JM, Beck JJ;  
XX  
DR WPI; 1995-383005/49.  
XX  
PT DNA encoding intervening transcribed sequence - used for detection of  
PT plant fungal pathogens.  
XX  
PS Claim 9; Page 16; 65pp; English.  
XX  
CC A novel method for the detection of plant pathogenic strains of fungi  
CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,  
CC Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR  
CC amplification of sequences found in the internal transcribed region (ITS)  
CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93  
CC and AAT05357-72. These primers are derived from the ITS sequences of  
CC these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The  
CC amplification products of the reactions using these primers can be used  
CC with the capture primers AAT05378-93 in colourimetric assays. The primers  
CC and ITS DNAs can be used for the detection of specific fungal pathogen  
CC isolates and in monitoring disease development in plant populations. The  
CC primers AAT05373-7 were obtained from purchased random amplified  
CC polymorphic DNA (RAPD) primer libraries and used to PCR amplify ITS  
CC sequences in conjunction with the primers AAQ94390-3. This primer  
CC amplified a 1.0 kb region from S.tritici  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||

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Db          10 GAGGG 6

RESULT 11
AAT45290/c
ID AAT45290 standard; DNA; 10 BP.
XX
AC AAT45290;
XX
DT 06-FEB-1997 (first entry)
XX
DE Gypsy moth FS-2 RAPD primer.
XX
KW Gypsy moth; Lymantria dispar; Asian; North American; European; genotype;
KW assay; RAPD primer; FS-2 fragment; diagnostic marker;
KW randomly amplified polymorphic DNAs; ss.
XX
OS Synthetic.
XX
PN US5571672-A.
XX
PD 05-NOV-1996.
XX
PF 20-SEP-1994; 94US-00308894.
XX
PR 20-SEP-1994; 94US-00308894.
XX
PA (USDA ) US SEC OF AGRIC.
XX
PI Garner KJ, Slavicek JM, Schreiber DE;
XX WPI; 1996-505395/50.
XX
PT Genotype assay for gypsy moth strains - to differentiate between Asian
PT and North American/European strains using specific primers to produce
PT diagnostic PCR amplification prods.
XX
PS Claim 1; Col 19; 17pp; English.
XX
CC Three RAPD (randomly amplified polymorphic DNAs) primers, designated
CC primers FS-1, FS-2 and FS-3, have been identified that generate
CC diagnostic fragment markers from gypsy moth (Lymantria dispar) DNA.
CC Comparison of marker size, e.g. by gel electrophoresis, allows the Asian
CC strain to be distinguished from the North American/European strain. RAPD
CC primers are 10 bp primers that are designed to be used individually, as
CC opposed to the usual primer pair; they can prime both ends of a
CC diagnostic fragment. The present sequence is that of primer FS-2 which
CC generates a fragment of 800 bp from North American/European moths that is
CC absent in control Asian moths
XX
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
8 GAGGG 4

RESULT 12
AAT98848
ID AAT98848 standard; DNA; 10 BP.
XX
AC AAT98848;
XX
DT 20-MAR-1998 (first entry)
XX
DE Binding site BSN6 identified using the method of the invention.
XX
KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.

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XX Synthetic.
OS
XX WO9727330-A1.
PN
XX 31-JUL-1997.
PD
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYYA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX WPI; 1997-393714/36.
DR
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
5 GAGGG 9

RESULT 13
AAX83301
ID AAX83301 standard; DNA; 10 BP.
XX
AC AAX83301;
XX
DT 31-AUG-1999 (first entry)
XX
DE Breast cancer tumour specific cDNA isolation primer #16.
XX
KW Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9725426-A2.
XX
PD 17-JUL-1997.
XX
PF 10-JAN-1997; 97WO-US000485.

```

```
XX 11-JAN-1996; 96US-00585392.
PR 20-AUG-1996; 96US-00700014.
XX (CORI-) CORIXA CORP.
XX Frudakis TN, Smith JM, Reed SG;
PI WPI; 1997-372865/34.
XX Breast cancer-related DNA from retrovirus antigen (s) - useful for
PT diagnosis and treatment of breast cancer.
XX Example 1; Page 103; 221pp; English.
XX Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
CC specific clones (AAX83201-X83285 and AAX83331-X83415) which are expressed
CC from a genomic region containing a human endogenous retrovirus
CC (AAX83330). Detection of the clone sequences allows determination of the
CC presence of breast cancer in a mammal. Progression of breast cancer can
CC be monitored by detecting the level of clone expression. Polypeptides
CC encoded by the clones can be used in vaccines to inhibit or prevent
CC breast cancer
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
3 GAGGG 7

RESULT 14
AAV62568/c
ID AAV62568 standard; DNA; 10 BP.
XX
AC AAV62568;
XX
DT 17-DEC-1998 (first entry)
XX
DE Septoria tritici species specific RAPD primer OPE-6.
XX Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;
KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KW Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;
KW random amplified polymorphic DNA; PCR; nucleic acid detection; RAPD;
KW PCR primer; ss.
XX
OS Synthetic.
OS Mycosphaerella graminicola.
XX
PN US5814453-A.
XX
PD 29-SEP-1998.
XX
PF 02-JUL-1997; 97US-00887480.
XX
PR 19-APR-1995; 95WO-US004712.
PR 15-OCT-1996; 96US-00722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
PA Beck JJ;
XX
PI WPI; 1998-541745/46.
XX
PT DNA isolated from fungal RNA, and its internal transcribed spacer
PT sequence - used for detecting fungal pathogens in plant tissue.
XX
PS Example 7; Col 19; 56pp; English.
```

```
XX Sequences AAV62567 to AAV62571 represent random amplified polymorphic DNA
CC (RAPD) primers used in the course of the invention for detection of
CC Septoria species. The invention provides a DNA molecule isolated from the
CC ribosomal RNA gene region of a fungal pathogen, where the DNA molecule
CC consists of an internal transcribed spacer (ITS) sequence selected from
CC ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
CC moniliforme, Septoria avenae or Microdochium nivale. A method for
CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
CC avenaceum and M. nivale isolates is also provided which comprises
CC isolating DNA from a plant leaf infected with at least one of the above
CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
CC PCR using specific primers from within these sequences. The pathogen(s)
CC are detected by visualising the amplified part of the ITS sequence
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
10 GAGGG 6

RESULT 15
AAV47256
ID AAV47256 standard; DNA; 10 BP.
XX
AC AAV47256;
XX
DT 10-NOV-1998 (first entry)
XX
DE Antisense oligonucleotide 756, targeting adenosine A1 receptor.
XX Secondary structure; mRNA; phosphorothioate backbone; G-protein;
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;
KW allergy; emphysema; cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /tag= a
FT /note= "contains phosphorothioate internucleotide
XX linkages"
PN WO9823294-A1.
XX
XX 04-JUN-1998.
XX
PF 26-NOV-1997; 97WO-US022017.
XX
PR 26-NOV-1996; 96US-00757024.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1998-322464/28.
XX
PT Treating respiratory disease with antisense sequences directed against
PT adenosine or bradykinin receptors - with localised delivery to the
PT respiratory system, suitable for long term treatment of asthma, adult
PT respiratory distress syndrome etc.
XX
PS Claim 12; Page 8-24; 47pp; English.
XX
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
CC human adenosine A1 receptor, the design of which required the secondary
CC structure of this targets mRNA. The adenosine receptor mRNA secondary
```



CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db 1 GAGGG 5  
|||||  
  
RESULT 16  
AAV47215  
ID AAV47215 standard; DNA; 10 BP.  
XX  
AC AAV47215;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 715, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
PN W09823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC oligonucleotides are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The

CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db 3 GAGGG 7  
|||||  
  
RESULT 17  
AAV47236  
ID AAV47236 standard; DNA; 10 BP.  
XX  
AC AAV47236;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 736, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
PN W09823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The

CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis

SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 2 GAGGG 6

RESULT 18  
AAV47170  
ID AAV47170 standard; DNA; 10 BP.  
XX  
AC AAV47170;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 670, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
PN WO9823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they

CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis

SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 5 GAGGG 9

RESULT 19  
AAV47193  
ID AAV47193 standard; DNA; 10 BP.  
XX  
AC AAV47193;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 693, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
PN WO9823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-



CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 4 GAGGG 8  
RESULT 20  
AAV47146  
ID AAV47146 standard; DNA; 10 BP.  
XX  
AC AAV47146;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 646, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
PN WO9823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung

CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 6 GAGGG 10  
RESULT 21  
AAV20923  
ID AAV20923 standard; DNA; 10 BP.  
XX  
AC AAV20923;  
XX  
DT 27-AUG-2003 (revised)  
DT 07-JUL-1998 (first entry)  
XX  
DE Aloe specific universal PCR primer OPAE-01.  
XX  
KW Aloe; detection; identification; amplification; PCR primer; antioxidant;  
KW differentiation; anti-tumour; anti-diabetic; tyrosine inhibiting; ss.  
XX  
OS Synthetic.  
OS Aloe.  
XX  
PN WO9804741-A1.  
XX  
PD 05-FEB-1998.  
XX  
PF 24-JUL-1997; 97WO-US013001.  
XX  
PR 26-JUL-1996; 96US-0022611P.  
XX  
PA (UNIV-) UNIVERA PHARM INC.  
XX  
PI Toothman P;  
XX  
DR WPI; 1998-159152/14.  
XX  
PT Detection and assay of Aloe - by extraction of DNA from a sample and  
PT amplification by polymerase chain reaction using primers specific for  
PT Aloe.  
XX  
PS Claim 3; Page 15; 37pp; English.  
XX  
CC The present sequence represents an Aloe specific universal PCR primer  
CC from the present invention. The present invention describes a method for  
CC identifying Aloe using polymerase chain reaction (PCR). The method  
CC comprises: (a) extracting DNA from a sample containing Aloe; (b)  
CC amplifying the DNA using PCR, and (c) comparing the sequence of the  
CC amplified DNA obtained from PCR with the sequence of DNA obtained from a  
CC known sample of Aloe. Also described are: (1) a nucleotide sequence  
CC comprising sequences given in the specification or a fragment; (2) a  
CC method for differentiating between different species of Aloe comprising:  
CC (a) extracting DNA from an unknown sample containing Aloe, and (b)  
CC amplifying the DNA by PCR using primers specific for a particular species  
CC of Aloe, and (3) a method for determining the amount of Aloe present in a  
CC mixture comprising: (a) extracting DNA from an unknown sample with  
CC internal controls for recovery of DNA, and (b) simultaneous amplification  
CC of DNA with primers specific to a particular Aloe species and  
CC amplification of non-homologous DNA added to a sample to internally  
CC quantify the amplification. The methods can be used for detecting and  
CC assaying Aloe in samples and for differentiating between different  
CC species of Aloe. The Aloe compounds have diverse biological activities,  
CC including anti-tumour activity, anti-acid activity, anti-diabetic  
CC activity, tyrosine inhibiting activity and antioxidant activity. (Updated  
CC on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
11111

Db 2 GAGGG 6

RESULT 22  
AAV45390  
ID AAV45390 standard; DNA; 10 BP.  
XX  
AC AAV45390;  
XX  
DT 11-JAN-1999 (first entry)  
XX  
DE Mouse CD3-epsilon enhancer binding site for Ikaros.  
XX  
KW Ikaros; mIK; transcription factor; mouse; lymphocyte;  
KW cell differentiation; T cell; cancer; immunodeficiency;  
KW Alzheimer's disease; therapy; diagnosis; CD3-epsilon; enhancer; ss.  
XX  
OS Mus sp.  
XX  
PN CA2194256-A.  
XX  
PD 05-MAR-1998.  
XX  
PF 02-JAN-1997; 97CA-02194256.  
XX  
PR 05-SEP-1996; 96US-00711417.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Georgopoulos K;  
XX  
DR WPI; 1998-378292/33.  
XX  
PT New nucleic acid encoding Ikaros protein involved in early  
PT differentiation of lymphocytes - existing in several isoforms, and  
PT related products, used to treat e.g. immune diseases or cancer and to  
PT control cell differentiation.  
XX  
PS Disclosure; Page 38; 158pp; English.  
XX  
CC This oligonucleotide from the mouse CD3-epsilon gene enhancer was  
CC identified as a potential high affinity binding site for Ikaros proteins  
CC (see AAW70963-71). It partially includes the core motif GGGAA found in  
CC consensus recognition sequences for murine Ikaros isoforms mIK-1, mIK-2  
CC and mIK-3 (see AAV52830-32). High affinity binding sites for Ikaros have  
CC been found in enhancer and promoter regions of the regulatory domains of  
CC the TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal  
CC repeat and in the regulatory domains of other T cell restricted antigens  
CC (see AAV45358-402) by gel retardation assay. Ikaros is involved in early  
CC differentiation of lymphocytes. The invention provides Ikaros nucleic  
CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host  
CC cells. These are used to treat T and B cell diseases, to control  
CC expression of heterologous genes placed under control of an Ikaros-  
CC responsive element, to treat nervous system diseases and to modulate cell  
CC division, amplification or differentiation, especially in haematopoietic  
CC cells  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
11111

Db 1 GAGGG 5  
11111

RESULT 23  
AAV67001  
ID AAV67001 standard; cDNA; 10 BP.  
XX  
AC AAV67001;  
XX  
DT 14-JAN-1999 (first entry)  
XX  
DE CD3-epsilon enhancer oligonucleotide #3.  
XX  
KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;  
KW differentiation marker; immune system; corpus striatum; AIDS;  
KW Alzheimer's disease; ss.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN US5824770-A.  
XX  
PD 20-OCT-1998.  
XX  
PF 05-JUN-1995; 95US-00465590.  
XX  
PR 14-SEP-1992; 92US-00946233.  
PR 14-SEP-1993; 93US-00121438.  
PR 02-MAY-1994; 94US-00238212.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Georgopoulos K;  
XX  
DR WPI; 1998-582621/49.  
XX  
PT Ikaros poly:peptide(s) - useful for treating disorders of immune system  
PT or corpus striatum.  
XX  
PS Disclosure; Col 27; 111pp; English.  
XX  
CC The present invention describes a purified peptide having at least one of  
CC the following properties: (a) it stimulates transcription of a DNA  
CC sequence under the control of a delta A element, an NFKB element or an  
CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of  
CC a delta A element, an NFKB element or an Ikaros binding oligonucleotide  
CC consensus sequence; (c) it competitively inhibits the binding of a  
CC naturally occurring Ikaros isoform to any of a delta A element, an NFKB  
CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it  
CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
CC (e) it inhibits protein-protein interactions of transcriptional complexes  
CC formed with naturally occurring Ikaros isoforms. The proteins, provided  
CC that they stimulate gene transcription under the control of delta A  
CC elements, NFKB elements and/or Ikaros-binding oligonucleotides, bind to  
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
CC inhibit protein-protein interactions of transcriptional complexes with  
CC naturally occurring Ikaros isoforms, can be used to treat immune system  
CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
CC given in the present invention  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
11111

Db 1 GAGGG 5

RESULT 24  
AAV69060  
ID AAV69060 standard; DNA; 10 BP.  
XX  
AC AAV69060;  
XX  
DT 22-JAN-1999 (first entry)  
XX  
DE Human breast tumour cDNA PCR primer #16.  
XX  
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;  
KW vaccine; epitope; endogenous; retroviral element; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9845328-A2.  
XX  
PD 15-OCT-1998.  
XX  
PF 09-APR-1998; 98WO-US0006939.  
XX  
PR 09-APR-1997; 97US-00838762.  
PR 11-DEC-1997; 97US-00991789.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Frudakis TN, Smith JM, Reed SG;  
XX  
DR WPI; 1998-557473/47.  
XX  
PT New DNA sequences isolated from endogenous human retroviral element - and  
PT related vectors, transformed cells, proteins and antibodies, useful for  
PT diagnosis, treatment and prevention of breast cancer.  
XX  
PS Example 1; Page 69; 173pp; English.  
XX  
CC The present sequence represents a PCR primer for human breast tumour cDNA  
CC nucleotide sequences. The present invention describes nucleotide  
CC sequences which encode human breast tumour specific polypeptides.  
CC Detection or measurement of human breast tumour specific polypeptides and  
CC nucleotide sequences, or the corresponding RNA in a sample, is used for  
CC diagnosis and monitoring of breast cancer. Human breast tumour specific  
CC polypeptides and nucleotide sequences, and the vectors containing the  
CC DNAs, are also useful in vaccines for inhibiting development (for  
CC prevention or therapy) of breast cancer. The polypeptides may also be  
CC used to raise monoclonal antibodies, used as immunoassay reagents  
XX  
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 25  
AAV35962  
ID AAV35962 standard; DNA; 10 BP.  
XX  
AC AAV35962;  
XX  
DT 26-AUG-1998 (first entry)  
XX  
DE Primer used in RAPD assay of the invention.  
XX  
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;

muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
Synthetic.  
Sus sp.  
WO9815837-A1.  
16-APR-1998.  
07-OCT-1997; 97WO-GB002741.  
07-OCT-1996; 96GB-00020904.  
18-FEB-1997; 97GB-00003350.  
20-MAR-1997; 97GB-00005796.  
09-SEP-1997; 97GB-00019002.  
(MEAT-) MEAT & LIVESTOCK COMMISSION.  
Maltin CA, Steven J, Warkup CC;  
WPI; 1998-240968/21.  
Assay for alleles or muscle fibre composition characteristic of Duroc  
type pigs - comprises determination of genotype or muscle fibre  
properties, used to identify animals for breeding programs and to assess  
meat quality.  
Example 3; Page 33; 56pp; English.  
PCR primers AAV35877-996 were used in a rapid amplification of  
polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
is used to determine if an animal has an allele for, or muscle fibre  
composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
meat of superior quality (particularly tenderness) but are normally less  
efficient feed converters and fatter than other types. The assay  
comprises analysing a tissue sample to determine if the genotype  
comprises the allele, and genetic features typical of animals with Duroc-  
type MFC are present. The method is used to select animals that have  
Duroc characteristics for use in breeding programmes (to develop the  
animals with Duroc pig characteristics), and to assess meat quality  
Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 6 GAGGG 10

RESULT 26  
AAV35969/c  
ID AAV35969 standard; DNA; 10 BP.  
XX  
AC AAV35969;  
XX  
DT 26-AUG-1998 (first entry)  
XX  
DE Primer used in RAPD assay of the invention.  
XX  
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX  
OS Synthetic.  
OS Sus sp.  
XX  
PN WO9815837-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 07-OCT-1997; 97WO-GB002741.

XX 07-OCT-1996; 96GB-00020904.  
PR 18-FEB-1997; 97GB-00003350.  
PR 20-MAR-1997; 97GB-00005796.  
PR 09-SEP-1997; 97GB-00019002.  
XX (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX Maltin CA, Steven J, Warkup CC;  
PI WPI; 1998-240968/21.  
XX Assay for alleles or muscle fibre composition characteristic of Duroc  
PT type pigs - comprises determination of genotype or muscle fibre  
PT properties, used to identify animals for breeding programs and to assess  
PT meat quality.  
XX Example 3; Page 33; 56pp; English.  
XX PCR primers AAV35877-996 were used in a rapid amplification of  
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
CC is used to determine if an animal has an allele for, or muscle fibre  
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
CC meat of superior quality (particularly tenderness) but are normally less  
CC efficient feed converters and fatter than other types. The assay  
CC comprises analysing a tissue sample to determine if the genotype  
CC comprises the allele, and genetic features typical of animals with Duroc-  
CC type MFC are present. The method is used to select animals that have  
CC Duroc characteristics for use in breeding programmes (to develop the  
CC animals with Duroc pig characteristics), and to assess meat quality  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
7 GAGGG 3  
  
RESULT 27  
AAV35908/c  
ID AAV35908 standard; DNA; 10 BP.  
XX  
AC AAV35908;  
XX  
DT 26-AUG-1998 (first entry)  
XX  
DE Primer used in RAPD assay of the invention.  
XX  
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX  
OS Synthetic.  
OS Sus sp.  
XX  
PN WO9815837-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 07-OCT-1997; 97WO-GB002741.  
XX  
KW 07-OCT-1996; 96GB-00020904.  
PR 18-FEB-1997; 97GB-00003350.  
PR 20-MAR-1997; 97GB-00005796.  
PR 09-SEP-1997; 97GB-00019002.  
XX  
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX  
PI Maltin CA, Steven J, Warkup CC;  
XX

DR WPI; 1998-240968/21.  
XX Assay for alleles or muscle fibre composition characteristic of Duroc  
PT type pigs - comprises determination of genotype or muscle fibre  
PT properties, used to identify animals for breeding programs and to assess  
PT meat quality.  
XX Example 3; Page 32; 56pp; English.  
PS  
XX PCR primers AAV35877-996 were used in a rapid amplification of  
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
CC is used to determine if an animal has an allele for, or muscle fibre  
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
CC meat of superior quality (particularly tenderness) but are normally less  
CC efficient feed converters and fatter than other types. The assay  
CC comprises analysing a tissue sample to determine if the genotype  
CC comprises the allele, and genetic features typical of animals with Duroc-  
CC type MFC are present. The method is used to select animals that have  
CC Duroc characteristics for use in breeding programmes (to develop the  
CC animals with Duroc pig characteristics), and to assess meat quality  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
5 GAGGG 1  
  
RESULT 28  
AAV35980/c  
ID AAV35980 standard; DNA; 10 BP.  
XX  
AC AAV35980;  
XX  
DT 26-AUG-1998 (first entry)  
XX  
DE Primer used in RAPD assay of the invention.  
XX  
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX  
OS Synthetic.  
OS Sus sp.  
XX  
PN WO9815837-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 07-OCT-1997; 97WO-GB002741.  
XX  
PR 07-OCT-1996; 96GB-00020904.  
PR 18-FEB-1997; 97GB-00003350.  
PR 20-MAR-1997; 97GB-00005796.  
PR 09-SEP-1997; 97GB-00019002.  
XX  
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX  
PI Maltin CA, Steven J, Warkup CC;  
XX  
DR WPI; 1998-240968/21.  
XX  
PT Assay for alleles or muscle fibre composition characteristic of Duroc  
PT type pigs - comprises determination of genotype or muscle fibre  
PT properties, used to identify animals for breeding programs and to assess  
PT meat quality.  
XX  
PS Example 3; Page 33; 56pp; English.  
XX PCR primers AAV35877-996 were used in a rapid amplification of

CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
CC is used to determine if an animal has an allele for, or muscle fibre  
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
CC meat of superior quality (particularly tenderness) but are normally less  
CC efficient feed converters and fatter than other types. The assay  
CC comprises analysing a tissue sample to determine if the genotype  
CC comprises the allele, and genetic features typical of animals with Duroc-  
CC type MFC are present. The method is used to select animals that have  
CC Duroc characteristics for use in breeding programmes (to develop the  
CC animals with Duroc pig characteristics), and to assess meat quality  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 5 GAGGG 1

RESULT 29  
AAx60193/c  
ID AAX60193 standard; DNA; 10 BP.

XX AAX60193;

XX 10-AUG-1999 (first entry)

XX Pyrimidinone derivative of the invention.

XX Pyrimidinone derivative; labeled binding partner; diagnostic assay;  
KW antisense; transfection complex; primer; probe; ss.

XX Synthetic.

XX WO9924452-A2.

XX 20-MAY-1999.

XX 30-OCT-1998; 98WO-US023119.

XX 07-NOV-1997; 97US-00966392.

XX 10-NOV-1997; 97US-00966875.

XX (ISIS-) ISIS PHARM INC.

XX Lin K, Matteucci MD;

XX WPI; 1999-370671/31.

XX Composition comprising pyrimidinone derivatives for diagnostic and  
XX analytical labels.

XX Example 4; Page 87; 101pp; English.

XX The specification describes pyrimidinone derivatives. These derivatives  
CC are used as labeled binding partners, particularly as labels for  
CC diagnostic, analytical and therapeutic applications. The derivatives are  
CC used as detectable labels for diagnostic assays, to enhance diagnostic  
CC assays that use oligonucleotides and to improve potency of  
CC oligonucleotides as antisense reagents that affect gene expression by  
CC altering intracellular metabolism of complementary RNA sequences encoding  
CC a target gene. They are also used in transfection complexes to deliver  
CC oligonucleotides into cell cytoplasm and in PCR e.g. as primers, and  
CC ligase chain reaction (LCR) e.g. as probes. The derivatives have  
CC increased affinity and specificity for their complementary sequences and  
CC facilitate PCR and LCR processes. The present sequence represents a  
CC pyrimidinone derivative of the invention

XX Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 30  
AAV08397  
ID AAV08397 standard; DNA; 10 BP.

XX AAV08397;

XX 01-MAR-1999 (first entry)

XX Fsh16 antisense oligonucleotide.

XX Bipolar affective disorder; BAD; fsh16 gene; human;  
KW neuropsychiatric disorder; schizophrenia; mood disorder;  
KW attention deficit disorder; schizoaffective disorder;  
KW unipolar affective disorder; depression; therapy; antisense; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9842726-A1.

XX 01-OCT-1998.

XX 27-MAR-1998; 98WO-US006210.

XX 27-MAR-1997; 97US-00828009.

XX (MILL-) MILLENNIUM PHARM INC.

XX (REGC ) UNIV CALIFORNIA.

XX Chen H, Freimer NB;

XX WPI; 1999-045133/04.

XX New isolated human fsh16 gene - used to develop products for treating  
PT neuropsychiatric disorders, e.g. schizophrenia, attention deficit  
PT disorder or bipolar affective disorder.

XX Disclosure; Page 55; 91pp; English.

XX Oligonucleotides (see AAV08397-402) are provided that comprise antisense  
CC molecules complementary to the human fsh16 gene (see AAV08396). This gene  
CC has been shown to be associated with neuropsychiatric disorders. The  
CC antisense oligonucleotides can be used to suppress translation of  
CC endogenous fsh16 mRNAs, and hence to ameliorate a fsh16 disorder or a  
CC neuropsychiatric disorder such as schizophrenia, attention deficit  
CC disorder, a schizoaffective disorder, unipolar disorders, or bipolar  
CC affective disorders, e.g. severe bipolar affective (mood) disorder,  
CC bipolar affective (mood) disorder with hypomania and major depression, or  
CC schizoaffective disorder manic type

XX Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 2 GAGGG 6

RESULT 31  
AAV81846/c  
ID AAV81846 standard; DNA; 10 BP.

XX AAV81846;  
AC  
XX  
DT 11-MAR-1999 (first entry)  
XX  
DE Human interleukin-1 forward primer OPG20.  
XX  
KW Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;  
KW primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5849578-A.  
XX  
PD 15-DEC-1998.  
XX  
PF 15-MAR-1996; 96US-00616844.  
XX  
PR 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00458873.  
PR 09-FEB-1996; 96US-00599654.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Falb DA;  
XX  
DR WPI; 1999-069743/06.  
XX  
PT DNA encoding rchd528 polypeptide - associated with cardiovascular  
PT disease.  
XX  
PS Example; Col 99; 122pp; English.  
XX  
CC The present invention describes rchd528 protein. A method has been  
CC developed for producing the rchd528 gene product. The present invention  
CC also describes methods and compositions for the treatment and diagnosis  
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
CC present sequence represents a primer used in an example from the present  
CC invention  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
8 GAGGG 4  
  
RESULT 32  
AAX53570  
ID AAX53570 standard; DNA; 10 BP.  
XX  
AC AAX53570;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9913886-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 17-SEP-1998; 98WO-US019419.  
XX  
PR 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1999-229400/19.  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
XX  
PS Disclosure; Page 38; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
CC end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX5272-74. These multiple target oligonucleotides  
CC (specifically AAX5180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
4 GAGGG 8  
  
RESULT 33  
AAX53547  
ID AAX53547 standard; DNA; 10 BP.  
XX  
AC AAX53547;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;



KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX Synthetic.  
OS WO9913886-A1.  
XX  
XX  
PN 25-MAR-1999.  
XX  
XX  
PD 17-SEP-1998; 98WO-US019419.  
XX  
XX  
PF 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX  
PI Nyce JW;  
XX  
XX  
DR WPI; 1999-229400/19.  
XX  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
XX  
XX  
PS Disclosure; Page 37; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
CC -end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 5 GAGGG 9  
RESULT 34  
AAX53633  
ID AAX53633 standard; DNA; 10 BP.  
XX  
AC AAX53633;  
XX  
XX  
DT 05-JUL-1999 (first entry)  
XX  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;

KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX Synthetic.  
OS WO9913886-A1.  
XX  
XX  
PN 25-MAR-1999.  
XX  
XX  
PD 17-SEP-1998; 98WO-US019419.  
XX  
XX  
PF 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX  
PI Nyce JW;  
XX  
XX  
DR WPI; 1999-229400/19.  
XX  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
XX  
XX  
PS Disclosure; Page 39; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
CC -end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 1 GAGGG 5  
RESULT 35  
AAX53592  
ID AAX53592 standard; DNA; 10 BP.  
XX  
AC AAX53592;  
XX  
XX  
DT 05-JUL-1999 (first entry)  
XX  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;



KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9913886-A1.  
PN  
XX 25-MAR-1999.  
PD  
XX  
XX 17-SEP-1998; 98WO-US019419.  
PF  
XX 17-SEP-1997; 97US-0059160P.  
PR  
XX 09-JUN-1998; 98US-00093972.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX  
PI Nyce JW;  
XX  
XX WPI; 1999-229400/19.  
DR  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
PT  
XX Disclosure; Page 38; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
CC -end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
3 GAGGG 7  
  
RESULT 36  
AAX53613  
ID AAX53613 standard; DNA; 10 BP.  
XX  
AC AAX53613;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;

KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9913886-A1.  
PN  
XX 25-MAR-1999.  
PD  
XX  
XX 17-SEP-1998; 98WO-US019419.  
PF  
XX 17-SEP-1997; 97US-0059160P.  
PR  
XX 09-JUN-1998; 98US-00093972.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX  
PI Nyce JW;  
XX  
XX WPI; 1999-229400/19.  
DR  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
PT  
XX Disclosure; Page 39; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
CC -end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
2 GAGGG 6  
  
RESULT 37  
AAX53523  
ID AAX53523 standard; DNA; 10 BP.  
XX  
AC AAX53523;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9913886-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 17-SEP-1998; 98WO-US019419.  
XX  
PR 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1999-229400/19.  
XX  
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
XX  
PS Disclosure; Page 37; 120pp; English.  
XX  
CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
CC end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GAGGG 5  
Db |||||  
6 GAGGG 10  
RESULT 38  
AAX14783/c  
ID AAX14783 standard; DNA; 10 BP.  
XX  
AC AAX14783;  
XX  
DT 24-MAR-1999 (first entry)

XX Triple helix third strand of Hepatitis B virus nucleotides 3071-3080.  
DE  
XX  
KW Triplex formation; DNA detection; triple helix; identification; bacteria;  
KW oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Hepatitis B virus.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
DR WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 19-20; 168pp; English.  
XX  
CC The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GAGGG 5  
Db |||||  
7 GAGGG 3  
RESULT 39  
AAX14812/c  
ID AAX14812 standard; DNA; 10 BP.  
XX  
AC AAX14812;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix forming nucleotides 427-436 of Hepatitis B virus.  
XX  
KW Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
XX  
OS Hepatitis B virus.  
XX  
PN US5861244-A.

XX 19-JAN-1999.  
PT  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
XX 29-OCT-1992; 92US-00968436.  
PR  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
PA  
XX Hepburn AG, Wang C;  
PI  
XX WPI; 1999-130384/11.  
DR  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 19-20; 168pp; English.  
XX The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
8 GAGGG 4  
  
RESULT 40  
AAX14901/C  
ID AAX14901 standard; DNA; 10 BP.  
XX  
AC AAX14901;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix third strand of 23S rRNA gene nucleotides 149-158.  
XX  
KW Triplex formation; DNA detection; triple helix; identification; bacteria;  
KW oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Clostridium pasteurianum.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
XX Hepburn AG, Wang C;  
PI  
XX WPI; 1999-130384/11.  
DR

XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 23-24; 168pp; English.  
XX The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 0 A; 5 C; 0 G; 5 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db |||||  
9 GAGGG 5  
  
RESULT 41  
AAX19477  
ID AAX19477 standard; DNA; 10 BP.  
XX  
AC AAX19477;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Human senescence factor p23 primer SEQ ID NO:19.  
XX  
KW Human; senescence factor; p23; cancer; persistent inflammation;  
KW proliferative disorder; degenerative disorder; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9907893-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 05-AUG-1998; 98WO-US016343.  
XX  
PR 08-AUG-1997; 97US-00908873.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Swisshelm K, Hosier S, Kubbies M;  
XX  
DR WPI; 1999-167454/14.  
XX  
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23  
PT polypeptide - useful for inducing a senescence phenotype in a cell.  
XX  
PS Example 1; Page 19; 44pp; English.  
XX  
CC The present invention describes human senescence factor p23. An  
CC expression vector for p23 is useful for inducing a senescent phenotype in  
CC a cell (preferably eukaryotic). This may help in regulating diseases,

CC including cancer, persistent inflammation, and various proliferative and  
CC degenerative disorders. These transgenic cells are useful in gene therapy  
CC for treating cancer, particularly where antisense oligonucleotides are  
CC useful for blocking normal or mutant p23 expression in cancer cells or  
CC other proliferating cells. Transgenic cells are also useful for producing  
CC the p23 polypeptide in large quantities. The antibodies are useful for  
CC raising antiserum against p23, and for identifying senescent cells in  
CC culture and tissue biopsies. The p23 polynucleotides are useful for  
CC modulating or altering p23 activity in a cell, and for identifying and  
CC isolating the whole gene encoding p23, and variants of p23. Assays based  
CC on p23 elements, which detect p23 levels and activity are useful as  
CC diagnostic markers for staging tumours, determining prognosis, and/or  
CC predicting therapeutic success. These elements also provide an assay for  
CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The  
CC isolation of the p23 polynucleotide permits the manipulation of malignant  
CC growth in cancer. The present sequence represents a primer used in an  
CC example from the present invention

XX  
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db |||||  
2 GAGGG 6

RESULT 42  
AAX26259/c  
ID AAX26259 standard; DNA; 10 BP.  
XX  
AC AAX26259;  
XX  
DT 24-MAY-1999 (first entry)  
XX  
DE Forward primer OPG20.  
XX  
KW Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5882925-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 09-FEB-1996; 96US-00599654.  
XX  
PR 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00485573.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Falb DA;  
XX  
DR WPI; 1999-214071/18.  
XX  
PT New polynucleotides consisting of residues 1-1929 of the rchd502 gene -  
PT are differentially expressed in cardiovascular disease states, and can  
PT therefore be used to treat and diagnose cardiovascular diseases.  
XX  
PS Disclosure; Col 10; 121pp; English.  
XX  
CC The invention relates to a rchd502 target/fingerprint gene encoding a  
CC transmembrane protein. The invention provides cDNAs contained in plasmids  
CC pFCHD502SF (ATCC 69981) and pFCHD502SJ (ATCC 69982) that encode the  
CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
CC disease states. Cultured genetically engineered host cell containing the

CC rchd502 polynucleotides in operative association with a nucleotide  
CC regulatory element are used for producing a polypeptide rchd502 gene  
CC product. Identifying that the fingerprint/target gene rchd502 is  
CC differentially expressed (up-regulated) by endothelial cells subjected to  
CC shear-stress, provides a tool for the diagnosis and treatment of  
CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
CC hypertension, restenosis. The fingerprint gene is useful for testing the  
CC efficacy of candidate drugs in basic research and in clinical trials and  
CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
CC in screening for ligands of target gene product receptor domains, as well  
CC as antagonists of the ligand-receptor interaction

XX  
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db |||||  
8 GAGGG 4

RESULT 43  
AAX86215/c  
ID AAX86215 standard; DNA; 10 BP.  
XX  
AC AAX86215;  
XX  
DT 22-SEP-1999 (first entry)  
XX  
DE SAGE tag used to identify transcripts which are enhanced by p53.  
XX  
KW p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;  
KW neoplastic; p53 binding site; FIG-3 promoter; SAGE tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9914356-A2.  
XX  
PD 25-MAR-1999.  
XX  
PF 17-SEP-1998; 98WO-US019300.  
XX  
PR 17-SEP-1997; 97US-0059153P.  
PR 30-MAR-1998; 98US-0079817P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW, Polyak K;  
XX  
DR WPI; 1999-443793/37.  
XX  
PT Use of p53 transcription tags to determine p53 status in, e.g. cancer  
PT diagnosis.  
XX  
PS Claim 1; Page 26; 73pp; English.  
XX  
CC The specification describes the use of p53 transcription tags for  
CC developing products to determine p53 status, to diagnose cancer and to  
CC evaluate cytotoxicity or carcinogenicity of a test agent. A method for  
CC diagnosing cancer or determining p53 status in a sample suspected for  
CC being neoplastic comprises comparing the level of transcription of an RNA  
CC transcript in a first sample (s1) of a first tissue (t1) to the level of  
CC transcription of the transcript in a second sample (s2) of a second  
CC tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal  
CC human tissue (of the same type) and the transcript is identified by a tag  
CC ; and categorizing s1 as neoplastic or as having a mutant p53 when  
CC transcription is found to be the same or lower in the first, than in s2.  
CC The methods and products can be used to determine p53 status, to diagnose  
CC cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.  
CC AAX86201-33 represent SAGE tags used to identify transcripts which are  
CC enhanced by p53



KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200009525-A2.  
PN  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PS New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 359; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db 2 GAGGG 6  
  
RESULT 47  
ID AAA33076 standard; DNA; 10 BP.  
XX

AC AAA33076;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:765.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PS New antisense oligonucleotides useful for treating e.g. pulmonary  
XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 362; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
Db 1 GAGGG 5



RESULT 48		Best Local Similarity 100.0%; Pred. No. 1.8e+06;			
AAA32966		Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
ID	AAA32966 standard; DNA; 10 BP.				
XX	AC	1 GAGGG 5			
AC	AAA32966;				
XX	DT	6 GAGGG 10			
DT	28-JUL-2000 (first entry)				
XX	DE	RESULT 49			
DE	Low adenosine antisense oligonucleotide SEQ ID NO:655.	AAA33035			
XX	KW	Human; adenosine receptor; low adenosine antisense oligonucleotide;			
KW	phosphorothioate; impaired respiration; inflammation; allergy;	AC			
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;	XX			
KW	antiallergic; antiasthmatic; cytotstatic; analgesic; impaired airway;	DT			
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;	XX			
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;	DE			
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;	XX			
KW	cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.	KW			
OS	Homo sapiens.	KW			
XX	WO200009525-A2.	KW			
XX	24-FEB-2000.	KW			
PF	03-AUG-1999; 99WO-US017712.	KW			
XX	03-AUG-1998; 98US-0095212P.	KW			
PR	(UYEC-) UNIV EAST CAROLINA.	KW			
PA	Nyce JW;	KW			
XX	WPI; 2000-205971/18.	KW			
PI	New antisense oligonucleotides useful for treating e.g. pulmonary	KW			
XX	vasoconstriction, inflammation, allergies, asthma, hypertension,	KW			
DR	bronchitis, emphysema, respiratory distress syndrome, ischemia or	KW			
XX	cancers.	KW			
PS	Claim 18; Page 349; 1343pp; English.	KW			
XX	The present invention describes a new composition comprising an antisense	KW			
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets	KW			
CC	nucleic acids involved in bronchoconstriction, allergies, and/or	KW			
CC	inflammation. The ON can have antiinflammatory, antiallergic,	KW			
CC	antiasthmatic, cytotstatic and analgesic activities. The compositions are	KW			
CC	useful for the treatment of diseases associated with inflammation,	KW			
CC	impaired airways, including lung disease and diseases whose secondary	KW			
CC	effects afflict the lungs of a subject. They can be used for treating	KW			
CC	e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,	KW			
CC	impeded respiration, respiratory distress syndrome, pain, cystic	KW			
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive	KW			
CC	pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,	KW			
CC	carcinomas, and cancers which may metastasise to the lungs, including	KW			
CC	breast and prostate cancer. The reduction of the adenosine content of the	KW			
CC	ONs reduces side effects. The A-containing ONs break down with the	KW			
CC	release of deoxyadenosine which activates adenosine receptors causing	KW			
CC	bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the	KW			
CC	nucleotide sequences given in the sequence listing from the present	KW			
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185	KW			
CC	sequences are also called SEQ ID NO:1 to 185, but the sequences differ	KW			
CC	from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to	KW			
CC	AAA33992) are specifically claimed ONs from the present invention. N.B.	KW			
CC	sequences given in the disclosure of the present invention do not match	KW			
CC	up with their corresponding SEQ ID NO: sequences given in the sequence	KW			
CC	listing	KW			
XX	Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;	KW			
SQ	Query Match 100.0%; Score 5; DB 3; Length 10;	KW			



CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 3 GAGGG 7  
RESULT 50  
AAA33013  
ID AAA33013 standard; DNA; 10 BP.  
XX  
AC AAA33013;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:702.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 354; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 4 GAGGG 8  
Search completed: January 7, 2005, 07:11:56  
Job time : 262.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GAGGG  
Perfect score: 5  
Sequence: 1 gaggg 5

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues  
Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	10	6	CF305881
2	5	100.0	10	6	CF323895
3	5	100.0	10	6	CF325441
4	5	100.0	11	1	AJ657108
5	5	100.0	11	4	BM395228
6	5	100.0	11	6	CF304450
7	5	100.0	11	6	CF322692
8	5	100.0	11	6	CF323154
9	5	100.0	11	8	BH129987
10	5	100.0	11	9	AJ589163
11	5	100.0	11	9	CL437735
12	5	100.0	11	9	CL657848
13	5	100.0	12	4	BG925521
14	5	100.0	12	6	CF306837
15	5	100.0	12	8	BH129328
16	5	100.0	12	9	AJ587286
17	5	100.0	12	9	AJ600549
18	5	100.0	13	1	AJ647701
19	5	100.0	13	1	AJ667961
20	5	100.0	13	5	BQ589768
21	5	100.0	13	6	CF306647
22	5	100.0	14	5	BQ588202
23	5	100.0	14	5	BQ590450
24	5	100.0	14	5	BQ593808

C	25	5	100.0	14	5	BQ605961
C	26	5	100.0	14	9	AJ588060
C	27	5	100.0	15	6	CF303956
C	28	5	100.0	15	6	CF304766
C	29	5	100.0	15	9	AJ599339
C	30	5	100.0	16	1	AA968729
C	31	5	100.0	16	1	AI075064
C	32	5	100.0	16	1	AI094839
C	33	5	100.0	16	1	AI560058
C	34	5	100.0	16	1	AI564678
C	35	5	100.0	16	1	AI569544
C	36	5	100.0	16	4	BM394080
C	37	5	100.0	16	6	CF303743
C	38	5	100.0	16	6	CF305660
C	39	5	100.0	16	6	CF323664
C	40	5	100.0	16	9	AJ587352
C	41	5	100.0	16	9	AJ595160
C	42	5	100.0	17	1	AJ666397
C	43	5	100.0	17	2	AW246940
C	44	5	100.0	17	4	BG896889
C	45	5	100.0	17	4	BG926068
C	46	5	100.0	17	5	BQ789989
C	47	5	100.0	17	9	AJ587432
C	48	5	100.0	17	9	AJ595555
C	49	5	100.0	17	9	AJ599163
C	50	5	100.0	17	9	CL436788
C	51	5	100.0	18	1	AJ648240
C	52	5	100.0	18	2	AW250267
C	53	5	100.0	18	4	BG896958
C	54	5	100.0	18	4	BG925569
C	55	5	100.0	18	4	BM397132
C	56	5	100.0	18	6	CA850820
C	57	5	100.0	18	6	CD530428
C	58	5	100.0	18	6	CF323060
C	59	5	100.0	19	1	AA934650
C	60	5	100.0	19	1	AI187072
C	61	5	100.0	19	1	AI251781
C	62	5	100.0	19	1	AJ360784
C	63	5	100.0	19	1	AJ570374
C	64	5	100.0	19	1	AI648553
C	65	5	100.0	19	1	AI696833
C	66	5	100.0	19	1	AJ649246
C	67	5	100.0	19	1	AJ679811
C	68	5	100.0	19	4	BG896949
C	69	5	100.0	19	5	BQ593604
C	70	5	100.0	19	6	C00981
C	71	5	100.0	19	6	CF322872
C	72	5	100.0	19	7	CO578459
C	73	5	100.0	19	8	AZ307462
C	74	5	100.0	19	8	AZ307686
C	75	5	100.0	19	8	AZ323931
C	76	5	100.0	19	8	AZ324165
C	77	5	100.0	19	8	AZ324945
C	78	5	100.0	19	8	AZ345792
C	79	5	100.0	19	8	AZ400662
C	80	5	100.0	19	8	AZ412553
C	81	5	100.0	19	8	AZ418201
C	82	5	100.0	19	8	AZ420252
C	83	5	100.0	19	8	AZ432757
C	84	5	100.0	19	8	AZ447248
C	85	5	100.0	19	8	AZ447414
C	86	5	100.0	19	8	AZ471573
C	87	5	100.0	19	8	AZ480415
C	88	5	100.0	19	8	AZ494890
C	89	5	100.0	19	8	AZ505490
C	90	5	100.0	19	8	AZ508355
C	91	5	100.0	19	8	AZ510143
C	92	5	100.0	19	8	AZ512762
C	93	5	100.0	19	8	AZ579189
C	94	5	100.0	19	8	AZ595016
C	95	5	100.0	19	8	AZ597219
C	96	5	100.0	19	8	AZ608537
C	97	5	100.0	19	8	AZ636812

c 98	5	100.0	19	8	AZ654214	1M0528H13	AZ654214	1M0528H13	c 171	5	100.0	20	8	AZ869047	AZ869047	2M0181E06
c 99	5	100.0	19	8	AZ664265	1M0544A19	AZ664265	1M0544A19	172	5	100.0	20	8	AZ938686	AZ938686	2M0197B22
c 100	5	100.0	19	8	AZ760597	1M0554N21	AZ760597	1M0554N21	173	5	100.0	20	8	AZ938721	AZ938721	2M0197H21
101	5	100.0	19	8	AZ775865	2M0009P05	AZ775865	2M0009P05	c 174	5	100.0	20	8	AZ969440	AZ969440	2M0242O12
c 102	5	100.0	19	8	AZ778302	2M0013C02	AZ778302	2M0013C02	175	5	100.0	20	8	BH000596	BH000596	2M0288N06
c 103	5	100.0	19	8	AZ783420	2M0025D07	AZ783420	2M0025D07	c 176	5	100.0	20	9	TA18A08P	AL451952 T. brucei	AL451952 T. brucei
104	5	100.0	19	8	AZ789827	2M0038C02	AZ789827	2M0038C02	177	5	100.0	20	9	CL660020	PRI0135d	CL660020 PRI0135d
105	5	100.0	19	8	AZ794440	2M0048A15	AZ794440	2M0048A15	178	5	100.0	20	9	CL661389	PRI0139c	CL661389 PRI0139c
106	5	100.0	19	8	AZ809734	2M0073D19	AZ809734	2M0073D19	179	5	100.0	20	9	CL661719	PRI013c_E	CL661719 PRI013c_E
107	5	100.0	19	8	AZ827092	2M0103M18	AZ827092	2M0103M18	180	5	100.0	20	9	CL670850	PRI0163a	CL670850 PRI0163a
c 108	5	100.0	19	8	AZ842379	2M0140N17	AZ842379	2M0140N17	c 181	5	100.0	20	9	CL687844	PRI0147d	CL687844 PRI0147d
c 109	5	100.0	19	8	AZ854718	2M0158N23	AZ854718	2M0158N23	182	5	100.0	20	9	AG189827	Pan trogl	AG189827 Pan trogl
c 110	5	100.0	19	8	AZ977338	2M0253P10	AZ977338	2M0253P10	183	5	100.0	20	9	AG197313	Pan trogl	AG197313 Pan trogl
c 111	5	100.0	19	9	AJ587161	Arabidops	AJ587161	Arabidops	c 184	5	100.0	20	9	AG203409	Pan trogl	AG203409 Pan trogl
c 112	5	100.0	19	9	AJ587166	Arabidops	AJ587166	Arabidops	c 185	5	100.0	20	9	AG203984	Pan trogl	AG203984 Pan trogl
c 113	5	100.0	19	9	AJ587167	Arabidops	AJ587167	Arabidops	c 186	5	100.0	21	1	AJ646946	Pan trogl	AJ646946 Pan trogl
c 114	5	100.0	19	9	AJ592567	Arabidops	AJ592567	Arabidops	187	5	100.0	21	1	AU254493	AJ646946	AJ646946 AJ646946
c 115	5	100.0	19	9	AJ592764	Arabidops	AJ592764	Arabidops	188	5	100.0	21	1	AU254493	AU254493	AU254493 AU254493
c 116	5	100.0	19	9	CL657666	PRI012a_H	CL657666	PRI012a_H	c 189	5	100.0	21	5	BQ121116	EST606692	BQ121116 EST606692
c 117	5	100.0	19	9	CL657902	PRI012d_D	CL657902	PRI012d_D	c 190	5	100.0	21	6	CB174486	hage002aB	BQ789783 hage002aB
c 118	5	100.0	20	1	AJ675323	AJ675323	AJ675323	AJ675323	c 191	5	100.0	21	6	CD531370	OR 2oE2C1	CB174486 OR 2oE2C1
c 119	5	100.0	20	1	AJ696560	AJ696560	AJ696560	AJ696560	c 192	5	100.0	21	6	CF276280	14ETL--01	CD531370 10I03 Ara
c 120	5	100.0	20	1	AJ798166	AJ798166	AJ798166	AJ798166	193	5	100.0	21	6	CF324789	JMT1--01-	CF276280 14ETL--01
121	5	100.0	20	1	AJ798166	AJ798166	AJ798166	AJ798166	194	5	100.0	21	6	CF324789	JMT1--03-	CF324789 JMT1--01-
122	5	100.0	20	2	AW250737	2822626.5	AW250737	2822626.5	c 195	5	100.0	21	8	AZ307929	1M0010F24	CF325365 JMT1--03-
c 123	5	100.0	20	5	BQ789787	hage002aB	BQ789787	hage002aB	c 196	5	100.0	21	8	AZ319778	1M0039G02	AZ307929 1M0010F24
c 124	5	100.0	20	6	C211208	HUMGS00223	C21208 HUMGS00223	C21208 HUMGS00223	c 197	5	100.0	21	8	AZ320581	1M0040P08	AZ319778 1M0039G02
c 125	5	100.0	20	6	CF293092	30DGS--02	CF293092 30DGS--02	CF293092 30DGS--02	c 198	5	100.0	21	8	AZ325878	1M0048D18	AZ320581 1M0040P08
c 126	5	100.0	20	6	CF293747	30DGS--03	CF293747 30DGS--03	CF293747 30DGS--03	c 199	5	100.0	21	8	AZ341689	1M0074A16	AZ325878 1M0048D18
127	5	100.0	20	6	CF306120	HDA1--02-	CF306120 HDA1--02-	CF306120 HDA1--02-	c 200	5	100.0	21	8	AZ345472	1M0080O11	AZ341689 1M0074A16
128	5	100.0	20	6	CF306620	HDA1--04-	CF306620 HDA1--04-	CF306620 HDA1--04-	c 201	5	100.0	21	8	AZ394677	1M0158A24	AZ345472 1M0080O11
129	5	100.0	20	6	CF327699	NACL--02-	CF327699 NACL--02-	CF327699 NACL--02-	c 202	5	100.0	21	8	AZ405188	1M0173G15	AZ394677 1M0158A24
c 130	5	100.0	20	7	CF921149	gmhrRw3--	CF921149 gmhrRw3--	CF921149 gmhrRw3--	c 203	5	100.0	21	8	AZ405406	1M0174P08	AZ405188 1M0173G15
c 131	5	100.0	20	7	CF932153	SP1-A4 (P6	CF932153 SP1-A4 (P6	CF932153 SP1-A4 (P6	c 204	5	100.0	21	8	AZ440229	1M0231N10	AZ405406 1M0174P08
c 132	5	100.0	20	7	CF752083	ApHL3SD-X	CN752083 ApHL3SD-X	CN752083 ApHL3SD-X	c 205	5	100.0	21	8	AZ443457	1M0238F08	AZ440229 1M0231N10
c 133	5	100.0	20	7	CO785157	BL282C_H0	CO785157 BL282C_H0	CO785157 BL282C_H0	c 206	5	100.0	21	8	AZ462622	1M0269C08	AZ443457 1M0238F08
c 134	5	100.0	20	8	AZ308143	1M0010A21	AZ308143 1M0010A21	AZ308143 1M0010A21	207	5	100.0	21	8	AZ466689	1M0277L03	AZ462622 1M0269C08
c 135	5	100.0	20	8	AZ308291	1M0011E10	AZ308291 1M0011E10	AZ308291 1M0011E10	c 208	5	100.0	21	8	AZ472401	1M0287C07	AZ466689 1M0277L03
c 136	5	100.0	20	8	AZ328822	1M0052I13	AZ328822 1M0052I13	AZ328822 1M0052I13	c 209	5	100.0	21	8	AZ476392	1M0295F12	AZ472401 1M0287C07
c 137	5	100.0	20	8	AZ339930	1M0071E07	AZ339930 1M0071E07	AZ339930 1M0071E07	c 210	5	100.0	21	8	AZ480208	1M0301J03	AZ476392 1M0295F12
138	5	100.0	20	8	AZ338212	1M0148A10	AZ338212 1M0148A10	AZ338212 1M0148A10	c 211	5	100.0	21	8	AZ482019	1M0306I17	AZ480208 1M0301J03
139	5	100.0	20	8	AZ389565	1M0150C24	AZ389565 1M0150C24	AZ389565 1M0150C24	c 212	5	100.0	21	8	AZ486694	1M0314F22	AZ482019 1M0306I17
c 140	5	100.0	20	8	AZ405596	1M0174B06	AZ405596 1M0174B06	AZ405596 1M0174B06	c 213	5	100.0	21	8	AZ499793	1M0337K15	AZ486694 1M0314F22
c 141	5	100.0	20	8	AZ417235	1M0192N15	AZ417235 1M0192N15	AZ417235 1M0192N15	c 214	5	100.0	21	8	AZ583408	1M0378N23	AZ499793 1M0337K15
c 142	5	100.0	20	8	AZ417738	1M0193J01	AZ417738 1M0193J01	AZ417738 1M0193J01	c 215	5	100.0	21	8	AZ596349	1M0409K03	AZ583408 1M0378N23
c 143	5	100.0	20	8	AZ427740	1M0209J23	AZ427740 1M0209J23	AZ427740 1M0209J23	c 216	5	100.0	21	8	AZ653464	1M0527G11	AZ596349 1M0409K03
c 144	5	100.0	20	8	AZ447706	1M0245C06	AZ447706 1M0245C06	AZ447706 1M0245C06	c 217	5	100.0	21	8	AZ653464	1M0527G11	AZ653464 1M0527G11
c 145	5	100.0	20	8	AZ486007	1M0313E17	AZ486007 1M0313E17	AZ486007 1M0313E17	c 218	5	100.0	21	8	AZ654883	1M0529O19	AZ653464 1M0527G11
c 146	5	100.0	20	8	AZ489135	1M0319H15	AZ489135 1M0319H15	AZ489135 1M0319H15	c 219	5	100.0	21	8	AZ662168	1M0541B12	AZ654883 1M0529O19
c 147	5	100.0	20	8	AZ512326	1M0357I18	AZ512326 1M0357I18	AZ512326 1M0357I18	c 220	5	100.0	21	8	AZ769086	1M0569G22	AZ662168 1M0541B12
148	5	100.0	20	8	AZ579495	1M0367C13	AZ579495 1M0367C13	AZ579495 1M0367C13	c 221	5	100.0	21	8	AZ770188	1M0571A12	AZ769086 1M0569G22
149	5	100.0	20	8	AZ626183	1M0466K15	AZ626183 1M0466K15	AZ626183 1M0466K15	c 222	5	100.0	21	8	AZ780316	2M0017L02	AZ770188 1M0571A12
c 150	5	100.0	20	8	AZ626505	1M0466K15	AZ626505 1M0466K15	AZ626505 1M0466K15	c 223	5	100.0	21	8	AZ781467	2M0019F23	AZ780316 2M0017L02
c 151	5	100.0	20	8	AZ627859	1M0476E04	AZ627859 1M0476E04	AZ627859 1M0476E04	c 224	5	100.0	21	8	AZ781467	2M0019F23	AZ781467 2M0019F23
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ALIGNMENTS

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Oryza sativa (japonica cultivar-group)  
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDA1)"  
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 5 GAGGG 9

## RESULT 2

CF323895 10 bp mRNA linear EST 18-AUG-2003  
 LOCUS HDN--05-A22.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
 DEFINITION clone HDN--05-A22, mRNA sequence.

ACCESSION CF323895  
 VERSION CF323895.1 GI:33796055  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 10)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

## AUTHORS

Large-scale Sequencing Analysis of Rice ESTs

## TITLE

## JOURNAL

## COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

1. .10  
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HDN--05-A22"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library II (HDN)"  
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 5 GAGGG 9

## RESULT 3

## CF325441

## LOCUS

## DEFINITION

CF325441 10 bp mRNA linear EST 18-AUG-2003  
 JMT1--03-D24.g1 AtJMT-overexpressing transgenic rice lambda phage CDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA  
 clone JMT1--03-D24, mRNA sequence.

## ACCESSION

## CF325441

## VERSION

## CF325441.1 GI:33799167

## KEYWORDS

## EST.

## SOURCE

## ORGANISM

## Oryza sativa (japonica cultivar-group)

## Oryza sativa (japonica cultivar-group)

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

## 1 (bases 1 to 10)

## Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

## Large-scale Sequencing Analysis of Rice ESTs

## Unpublished (2003)

## CONTACT

## Nahm B.H.

## Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

## Yongin, Kyeonggi, Korea

## Tel: 82 31 330 6193

## Fax: 82 31 321 6355

## Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

## 1. .10

## Location/Qualifiers

## /organism="Oryza sativa (japonica cultivar-group)"

## /mol\_type="mRNA"

## /cultivar="Nackdong"

## /db\_xref="taxon:39947"

## /clone="JMT1--03-D24"

## /tissue\_type="leaf"

## /dev\_stage="14 days after germination"

## /lab\_host="E.coli SOLR"

## /clone\_lib="AtJMT-overexpressing transgenic rice lambda phage CDNA library (JMT1)"

## /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## 5; Conservative

## 0; Mismatches

## 0; Indels

## 0; Gaps

## 0;

## QY

## 1 GAGGG 5

## |||||

## Db

## 5 GAGGG 9

## RESULT 4

## AJ657108

## LOCUS

## DEFINITION

## AJ657108 KN277 Sus scrofa CDNA clone C0005196\_K06, mRNA sequence.

## ACCESSION

## AJ657108

## VERSION

## AJ657108.1 GI:49341140

## KEYWORDS

## EST.

## SOURCE

## Sus scrofa (pig)

## ORGANISM

## Sus scrofa

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

## REFERENCE

## 1 (bases 1 to 11)

## AUTHORS

## Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

## TITLE

## Development of cDNA and EST resources for studying reproduction and



embryo development in pigs and cattle  
Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled early embryos, from 8- cell stage to blastocysts.  
Clones available from UK Centre for Functional Genomics in Farm  
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
www.arkgenomics.org.

Query Match 100.0%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 11 GAGGG 7

RESULT 6

CF304450

LOCUS  
DEFINITION  
ABF1--05-A03.g1 ABF3-overexpressing transgenic rice lambda phage  
cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--05-A03, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..11  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--05-A03"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda  
phage CDNA library (ABF1)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

RESULT 7

CF322692

LOCUS

DEFINITION

HDN--01-M19.g1 OsHDAC1-overexpressing transgenic rice lambda phage  
cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
clone HDN--01-M19, mRNA sequence.

ACCESSION

VERSION

CF322692.1 GI:33793616

embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled early embryos, from 8- cell stage to blastocysts.  
Clones available from UK Centre for Functional Genomics in Farm  
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
www.arkgenomics.org.

FEATURES

source

1..11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005196 K06"  
/tissue\_type="embryo"  
/clone\_lib="KN277"

/note="Vector: pBluescriptII(SK+); Site\_1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pooled early embryos, from 8-cell stage  
to blastocysts."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

|||||

Db 5 GAGGG 9

RESULT 5

BM395228/c

LOCUS

DEFINITION

50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 11)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..11  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

KEYWORDS  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..11  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN--01-M19"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda  
phage CDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

RESULT 8  
CF323154  
LOCUS HDN--03-B04.g1 OshDAC1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) CDNA  
clone HDN--03-B04, mRNA sequence.  
ACCESSION CF323154  
VERSION CF323154.1 GI:33794534  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

1..11  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN--03-B04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDAC1-overexpressing transgenic rice lambda  
phage CDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

RESULT 9  
BH129987/c  
LOCUS BH129987  
DEFINITION G-6e3.f Maize Random Small-insert Genomic Library Zea mays genomic  
clone G-6e3 both, genomic survey sequence.  
ACCESSION BH129987  
VERSION BH129987.1 GI:14998894  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Meyers, B.C., Tingey, S.V. and Morgante, M.  
TITLE Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome  
JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
MEDLINE 21475670  
PUBMED 11591643  
COMMENT Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M13univ  
Class: shotgun.  
Location/Qualifiers

FEATURES  
source  
1..11  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="G-6e3"  
/sex="hermaphrodite"  
/tissue\_type="leaf"  
/cell\_type="young leaf"  
/dev\_stage="seedling"  
/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: pCR-Script; Total genomic DNA was  
nebulized; ends were polished with Pfu polymerase and the

ORIGIN		fragments cloned into pCR-Script."									
Query Match		100.0%;		Score 5;		DB 8;		Length 11;			
Best Local Similarity		100.0%;		Pred. No. 1.2e+07;							
Matches		5;		Conservative		0;		Mismatches		0;	
										Indels	
										0;	
										Gaps	
										0;	
QY		1 GAGGG 5									
Db		7 GAGGG 3									
RESULT 10		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
FEATURES		Location/Qualifiers									
source		1..11									
		/organism="Arabidopsis thaliana"									
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		/cultivar="Wassillewskija"									
		/db_xref="taxon:3702"									
		/clone="545D12"									
		/clone_lib="Arabidopsis thaliana T-DNA insertion lines"									
misc_feature		1..11									
		/note="T-DNA flanking sequence left border"									
ORIGIN		Query Match									
Best Local Similarity		100.0%;		Score 5;		DB 9;		Length 11;			
Matches		5;		Conservative		0;		Mismatches		0;	
										Indels	
										0;	
										Gaps	
										0;	
Qy		1 GAGGG 5									
Db		7 GAGGG 3									
RESULT 11		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
FEATURES		Location/Qualifiers									
source		1..11									
		/organism="Arabidopsis thaliana"									
		/mol_type="genomic DNA"									
		/cultivar="Wassillewskija"									
		/db_xref="taxon:3702"									
		/clone="545D12"									
		/clone_lib="Arabidopsis thaliana T-DNA insertion lines"									
misc_feature		1..11									
		/note="T-DNA flanking sequence left border"									
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										Gaps	
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Qy		1 GAGGG 5									
Db		7 GAGGG 3									
RESULT 11		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
FEATURES		Location/Qualifiers									
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										Gaps	
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Db		7 GAGGG 3									
RESULT 11		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
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										Gaps	
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Qy		1 GAGGG 5									
Db		7 GAGGG 3									
RESULT 11		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
FEATURES		Location/Qualifiers									
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ORIGIN		Query Match									
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										Gaps	
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Qy		1 GAGGG 5									
Db		7 GAGGG 3									
RESULT 11		AJ589163									
AJ589163/c											
LOCUS											
DEFINITION		Arabidopsis thaliana T-DNA flanking sequence, left border, clone		S45D12, genomic survey sequence.							
ACCESSION		AJ589163									
VERSION		AJ589163.1		GI:37938787							
KEYWORDS		GSS; left border; T-DNA flanking sequence.									
SOURCE		Arabidopsis thaliana (thale cress)									
ORGANISM		Arabidopsis thaliana									
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.									
AUTHORS		1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.									
TITLE		T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites									
JOURNAL		EMBO Rep. 3 (12), 1152-1157 (2002)									
MEDLINE		22363535									
PUBMED		12446565									
REFERENCE		2 (bases 1 to 11)									
AUTHORS		Balzergue, S.									
TITLE		Direct Submission									
JOURNAL		Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE									
COMMENT		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbsgap.versailles.inra.fr/publiclines/">http://dbsgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).									
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REFERENCE 1 (bases 1 to 12)  
AUTHORS Meyers,B.C., Tingey,S.V. and Morgante,M.  
TITLE Abundance, distribution and transcriptional activity of repetitive elements in the maize genome  
JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
MEDLINE 21475670  
PUBMED 11591643  
COMMENT Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.  
Seq primer: M1juniv  
Class: shotgun.  
FEATURES  
source  
1. .12  
/organism="Zea mays"  
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/sex="hermaphrodite"  
/tissue\_type="leaf"  
/cell\_type="Young leaf"  
/dev\_stage="seedling"  
/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: PCR-Script; Total genomic DNA was nebulized; ends were polished with Pfu polymerase and the fragments cloned into pCR-Script."  
ORIGIN  
Query Match 100.0%; Score 5; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
|||||  
Db 4 GAGGG 8  
RESULT 16  
AJ587286/c  
LOCUS  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 258G07, genomic survey sequence.  
ACCESSION AJ587286  
VERSION AJ587286.1 GI:37936875  
KEYWORDS GSS; left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 12)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
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/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="258G07"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="T-DNA flanking sequence  
left border"

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and [http://www.genoplante-info.infobiogen.fr](http://genoplante-info.infobiogen.fr)).  
FEATURES  
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1. .12  
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/db\_xref="taxon:3702"  
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/note="T-DNA flanking sequence  
left border"  
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Query Match 100.0%; Score 5; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
|||||  
Db 8 GAGGG 4  
RESULT 17  
AJ600549  
LOCUS  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 508F08, genomic survey sequence.  
ACCESSION AJ600549  
VERSION AJ600549.1 GI:37950177  
KEYWORDS GSS; right border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 12)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
source  
1. .12  
/organism="Arabidopsis thaliana"

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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
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misc_feature
1..12
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right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 3 GAGGG 7

RESULT 18
AJ647701/c      13 bp mRNA linear EST 07-JUL-2004
LOCUS
DEFINITION
AJ647701 CSEQRAN19 Sus scrofa cDNA clone C0003260_G16, mRNA
sequence.
ACCESSION
AJ647701
VERSION
AJ647701.1 GI:49324546
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 13)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
Location/Qualifiers
1..13
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/db_xref="taxon:9823"
/clone="C0000044_G09"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled ovaries."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 8 GAGGG 12

RESULT 20
BQ589768/c
LOCUS
DEFINITION
BQ589768 024-020-D03-SP6 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
ACCESSION
BQ589768
VERSION
BQ589768.1 GI:26119351
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 11 GAGGG 7

RESULT 19
AJ667961
LOCUS
DEFINITION
AJ667961 CSEQRAN09 Sus scrofa cDNA clone C0000044_G09, mRNA
sequence.
ACCESSION
AJ667961
VERSION
AJ667961.1 GI:49352412
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 13)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..13
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000044_G09"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 8 GAGGG 12

RESULT 20
BQ589768/c
LOCUS
DEFINITION
BQ589768 024-020-D03-SP6 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
ACCESSION
BQ589768
VERSION
BQ589768.1 GI:26119351
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
```



FEATURES  
source

Email: weisshaa@mpiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 5 GAGGG 1  
  
RESULT 21  
CF306647  
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ACCESSION  
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VERSION  
CF306647.1  
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Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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FEATURES  
source

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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

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Db 5 GAGGG 9  
  
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VERSION  
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1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
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12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"



Query Match 100.0%; Score 5; DB 5; Length 14;  
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QY 1 GAGGG 5  
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RESULT 23  
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DEFINITION cDNA clone 024-019-A07 5-PRIME, mRNA sequence.

ACCESSION BQ590450  
VERSION BQ590450.1 GI:26120033  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

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Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 14;  
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DEFINITION cDNA clone 024-026-007 5-PRIME, mRNA sequence.

ACCESSION BQ593808  
VERSION BQ593808.1 GI:26123391  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
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Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 14;  
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Db 14 GAGGG 10

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DEFINITION mRNA sequence.  
ACCESSION BQ605961  
VERSION BQ605961.1 GI:21555112  
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SOURCE Triticum aestivum (bread wheat)

ORGANISM   Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE   1 (bases 1 to 14)  
AUTHORS    Clarke,B., Lambrecht,M. and Rhee,S.Y.  
TITLE       Arabidopsis genomic information for interpreting wheat EST  
            sequences  
JOURNAL     Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
MEDLINE     22478026  
PUBMED      12590341  
COMMENT     Contact: Lambrecht M  
            The Arabidopsis Information Resource  
            Carnegie Institution of Washington, Dept. of Plant Biology  
            260 Panama Street, Stanford, CA 94305, USA  
            Tel: 1 650 325 1521 x 251  
            Fax: 1 650 325 3748  
            Email: rhee@acom.stanford.edu.  
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DB           10 GAGGG 6  
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DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
526B05, genomic survey sequence.  
ACCESSION    AJ588060  
VERSION       AJ588060.1 GI:37937684  
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ORGANISM     Arabidopsis thaliana  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE    1  
AUTHORS      Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
            Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences  
            of pre-insertion sites  
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE      22363535  
PUBMED       12446565  
REFERENCE    2 (bases 1 to 14)  
AUTHORS      Balzergue,S.  
TITLE        Direct Submission  
JOURNAL      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
            Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana  
            plants from INRA (Versailles). The DNA fragment(s) resulting from  
            the PCR were directly sequenced from the left or the right border  
            to determine the genomic sequence flanking the insertion. T-DNA  
            derived sequences were removed. Information to order the  
            corresponding mutant line and a link to a database providing a  
            graphical display of the insertion site are available at

http://dbgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).  
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LOCUS       CF303956           15 bp   mRNA   linear   EST 15-AUG-2003  
DEFINITION   ABF1--03-K24.g1 ABF3-overexpressing transgenic rice lambda phage  
cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--03-K24, mRNA sequence.  
ACCESSION    CF303956  
VERSION       CF303956.1 GI:33675717  
KEYWORDS     EST.  
SOURCE       Oryza sativa (japonica cultivar-group)  
ORGANISM     Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Ehrhartioideae; Oryzaceae; Oryza.  
REFERENCE    1 (bases 1 to 15)  
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE        Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL      Unpublished (2003)  
COMMENT      Contact: Nahm B.H.  
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
            of Bioscience and Bioinformatics, Myongji University  
            Yongin, Kyeonggi, Korea  
            Tel: 82 31 330 6193  
            Fax: 82 31 321 6355  
            Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.  
FEATURES    source  
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ORIGIN  
Query Match           100.0%;   Score 5;   DB 6;   Length 15;

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5 GAGGG 9

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DEFINITION CDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--05-O06, mRNA sequence.
ACCESSION CF304766
VERSION CF304766.1 GI:33676527
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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XhoI; Leaf was dried for 2hrs. cDNA was inserted into
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with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
4 GAGGG 8

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DEFINITION 485B10, genomic survey sequence.
ACCESSION AJ599339
VERSION AJ599339.1 GI:37948967
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

1
REFERENCE
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 15)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES
source
Location/Qualifiers
1. .15
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="485B10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1. .15
/note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
5 GAGGG 1

RESULT 30
AA968729 16 bp mRNA linear EST 27-AUG-1998
LOCUS or69h11.s1 NCI CGAP GC3 Homo sapiens CDNA clone IMAGE:1601157 3,
DEFINITION similar to SW:PRPE_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
;contains element MSRI repetitive element ;, mRNA sequence.
ACCESSION AA968729
VERSION AA968729.1 GI:3143909
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
```

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 514 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:1601157"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP GC3"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. Library is not normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

Db |||||  
10 GAGGG 14

RESULT 31

AI075064/c

LOCUS

DEFINITION ou61g11.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632356 3'  
similar to TR:Q24348 Q24348 FIBRILLARIN ;, mRNA sequence.

ACCESSION

AI075064 1 GI:3399844

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 712 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="IMAGE:1632356"  
/sex="female, pooled"  
/tissue\_type="breast"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Br2"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from pooled bulk  
breast tumor tissue, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. This library is the normalized version of  
NCI\_CGAP\_Brl.1. Library was constructed by Bento Soares  
and M. Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

Db |||||  
12 GAGGG 8

RESULT 32

AI094839/c

LOCUS

DEFINITION

qa22c08.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'  
similar to TR:O00599 O00599 CON1.; contains element MSRI repetitive  
element ;, mRNA sequence.

ACCESSION

AI094839

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1687502"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Brn23"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCCGCATATCTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 8 GAGGG 4

RESULT 33

AI560058

LOCUS

DEFINITION AI560058 16 bp mRNA linear EST 13-MAY-1999  
tq38h11.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2211141 3',  
similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15  
PRECUSOR. ;contains MSRI.t2 MSRI repetitive element ;, mRNA  
sequence.

ACCESSION

VERSION AI560058.1 GI:4510263

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 2104 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2211141"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

|||||

Db 10 GAGGG 14

RESULT 34

AI564678/c

LOCUS

DEFINITION

AI564678 16 bp mRNA linear EST 14-MAY-1999  
tq78g03.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2214964 3',  
similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1  
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION

VERSION AI564678.1 GI:4523135

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1719 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2214964"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

|||||

Db 11 GAGGG 7

RESULT 35

AI569544/c

LOCUS

DEFINITION

AI569544 16 bp mRNA linear EST 12-MAY-1999  
t028d10.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2180371 3',  
similar to TR:Q18444 Q18444 COSMID C34D4. ;contains MSRI.b2 MSRI  
repetitive element ;, mRNA sequence.

ACCESSION

VERSION AI569544.1 GI:4532918

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1683 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2180371"  
/tissue type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 6 GAGGG 2

RESULT 36  
BM394080/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM394080 16 bp mRNA linear EST 17-JAN-2002  
50072-2-12-H02.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
BM394080  
BM394080.1 GI:18194133  
EST.  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 16)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,I.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: [apturkew@midway.uchicago.edu](mailto:apturkew@midway.uchicago.edu)  
Seq primer: T3.  
Location/Qualifiers

FEATURES

Location/Qualifiers

source  
1. .16  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

RESULT 37  
CF303743  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF303743 16 bp mRNA linear EST 15-AUG-2003  
ABF1--03-B14.g1 ABF3-overexpressing transgenic rice lambda phage  
cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--03-B14, mRNA sequence.  
CF303743  
CF303743.1 GI:33675504  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bhnaahm@gbio.com](mailto:bhnaahm@gbio.com), [bhnaahm@bio.myongji.ac.kr](mailto:bhnaahm@bio.myongji.ac.kr).

FEATURES  
source  
Location/Qualifiers

1. .16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--03-B14"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 9



```

RESULT 38
CF305660
LOCUS
DEFINITION
HDAL--01-F18.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--01-F18, mRNA sequence.
ACCESSION
CF305660
VERSION
CF305660.1 GI:33677421
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--01-F18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
|||||
Db 11 GAGGG 15

RESULT 39
CF323664
LOCUS
DEFINITION
HDN--04-H04.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
clone HDN--04-H04, mRNA sequence.
ACCESSION
CF323664
VERSION
CF323664.1 GI:33795589
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--04-H04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
|||||
Db 5 GAGGG 9

RESULT 40
AJ587352/c
LOCUS
DEFINITION
AJ587352 16 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
266H05, genomic survey sequence.
ACCESSION
AJ587352
VERSION
AJ587352.1 GI:37936976
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 16)
AUTHORS
Balzerque,S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics

```

```

program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1. .16
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="266H05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .16_
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
| | | | |
Db 11 GAGGG 7

RESULT 41
AJ595160
LOCUS
DEFINITION
AJ595160 16 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
412D05, genomic survey sequence.
ACCESSION
AJ595160
VERSION
AJ595160.1 GI:37944784
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
12446565
PUBMED
REFERENCE
2 (bases 1 to 16)
Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1. .16
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="412D05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .16_
/notes="T-DNA flanking sequence
left border"

FEATURES
source
Query Match 100.0%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
| | | | |
Db 10 GAGGG 6

RESULT 43
AW246940
LOCUS
DEFINITION
AW246940 17 bp mRNA linear EST 07-JAN-2000
2822481.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822481 5',
mRNA sequence.
ACCESSION
AW246940
VERSION
AW246940.1 GI:6589933
KEYWORDS
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
| | | | |
Db 4 GAGGG 8

RESULT 42
AJ666397/c
LOCUS
DEFINITION
AJ666397 CSEQRAN09 Sus scrofa cDNA clone C0000033_K10, mRNA
sequence.
ACCESSION
AJ666397
VERSION
AJ666397.1 GI:49350848
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 17)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1. .17
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_K10"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

FEATURES
source
Query Match 100.0%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
| | | | |
Db 10 GAGGG 6

RESULT 43
AW246940
LOCUS
DEFINITION
AW246940 17 bp mRNA linear EST 07-JAN-2000
2822481.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822481 5',
mRNA sequence.
ACCESSION
AW246940
VERSION
AW246940.1 GI:6589933
KEYWORDS
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 17)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2822481.3prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence.  
Plate: LLCM9 row: I column: 10.

FEATURES  
source  
1. .17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822481"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 5; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 6 GAGGG 10  
RESULT 44  
BG896889/c  
LOCUS BG896889  
DEFINITION HOA58-1-G10.R HOA (Human Osteoarthritic Cartilage) Homo sapiens  
cDNA, mRNA sequence.  
ACCESSION BG896889  
VERSION BG896889.1 GI:14307130  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177

REFERENCE 44  
BG896889/c  
LOCUS BG896889  
DEFINITION HOA58-1-G10.R HOA (Human Osteoarthritic Cartilage) Homo sapiens  
cDNA, mRNA sequence.  
ACCESSION BG896889  
VERSION BG896889.1 GI:14307130  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177

COMMENT Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: [sanjay.kumar-l@gsk.com](mailto:sanjay.kumar-l@gsk.com)  
Seq primer: T7.  
FEATURES  
source  
1. .17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 17 GAGGG 13  
RESULT 45  
BG926068/c  
LOCUS BG926068  
DEFINITION HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BG926068  
VERSION BG926068.1 GI:14320591  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177

COMMENT Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: [sanjay.kumar-l@gsk.com](mailto:sanjay.kumar-l@gsk.com)  
Seq primer: T7.  
FEATURES  
source  
1. .17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI;  
Directional"

REFERENCE 44  
BG926068/c  
LOCUS BG926068  
DEFINITION HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BG926068  
VERSION BG926068.1 GI:14320591  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
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Db 7 GAGGG 3

RESULT 46  
BQ789989/c  
LOCUS  
DEFINITION BQ789989 17 bp mRNA linear EST 30-JUL-2002  
hage005aB12 Heterobasidion annosum - Scots pine infection stage  
(HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion  
annosum mixed EST library cDNA clone hage005aB12, mRNA sequence.

ACCESSION BQ789989  
VERSION BQ789989.1 GI:22004951  
KEYWORDS EST.

SOURCE Pinus sylvestris/Heterobasidion annosum mixed EST library  
ORGANISM Pinus sylvestris/Heterobasidion annosum mixed EST library  
Eukaryota; mixed EST libraries.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Asiegbu,F.O., Nahalkova,J. and Dean,R.A.  
TITLE Selected Expressed sequence tags of cDNA clones from the  
interaction of the root rot fungus (Heterobasidion annosum) with  
seedling roots of Scots pine (Pinus sylvestris)

JOURNAL Unpublished (2001)  
COMMENT Contact: Fred O. Asiegbu  
Dept. of Forest Mycology & Pathology  
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,  
Sweden  
Tel: +46 18 67 15 98  
Fax: +46 18 30 92 45  
Email: Fred.Asiegbu@mykopat.slu.se  
Seq primer: T7 primer.

FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Pinus sylvestris/Heterobasidion annosum mixed  
EST library"  
/mol\_type="mRNA"  
/db\_xref="taxon:169015"  
/clone="hage005aB12"  
/dev\_stage="Seedling roots of scots pine were infected for  
6 days with H. annosum"  
/clone\_lib="Heterobasidion annosum - Scots pine infection  
stage (HAGE) subtraction cDNA library"  
/notes="Vector: pT-Adv; Site 1: EcoRI; The subtractive  
hybridization cDNA library was constructed from scots pine  
roots infected for 6-days with mycelia of Heterobasidion  
annosum (FP5)."

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||

Db 12 GAGGG 8

RESULT 47  
AJ587432/c  
LOCUS  
DEFINITION AJ587432 17 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
277All, genomic survey sequence.

ACCESSION AJ587432  
VERSION AJ587432.1 GI:37937056  
KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565

REFERENCE 2 (bases 1 to 17)  
AUTHORS Balzergue,S.  
TITLE Direct Submision  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).

FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Massillewskija"  
/db\_xref="taxon:3702"  
/clone="277All"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

misc\_feature 1. .17  
/note="T-DNA flanking sequence  
left border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||

Db 7 GAGGG 3

RESULT 48  
AJ595555  
LOCUS  
DEFINITION AJ595555 17 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
419A03, genomic survey sequence.

ACCESSION AJ595555  
VERSION AJ595555.1 GI:37945183  
KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565

REFERENCE 2 (bases 1 to 17)  
AUTHORS Balzergue,S.  
TITLE Direct Submision  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES source

1. .17  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="419A03"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1. .17  
/note="T-DNA flanking sequence  
left border"

ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 7 GAGGG 11

RESULT 49

AJ599163

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 481F12, genomic survey sequence.

ACCESSION

VERSION AJ599163.1 GI:37948791

KEYWORDS

GSS; left border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.

TITLE

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL

MEDLINE EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED

22363535

AUTHORS

12446565

TITLE

Balzergue,S.

JOURNAL

Direct Submission

COMMENT

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES source

1. .17

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QY 1 GAGGG 5

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Db 5 GAGGG 9

RESULT 50

CL436788

LOCUS

DEFINITION CL436788 17 bp DNA linear GSS 18-MAR-2004 PST3832-NL.Seq MICB1 Mus musculus genomic clone PST3832-NL.Seq, genomic survey sequence.

ACCESSION

VERSION CL436788

KEYWORDS CL436788.1 GI:45571937

SOURCE

GSS.  
Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 17)

AUTHORS

Hicks,G.G.

TITLE

www.EScells.ca

JOURNAL

Unpublished (2002)

COMMENT

Contact: Hicks GG

Mammalian Functional Genomics Centre

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ONS029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicksgg@cc.umanitoba.ca

U3NeoSv1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from [http://140.193.242.7/esdb/public\\_search\\_frame.php?PST=PST3832-NL.Se](http://140.193.242.7/esdb/public_search_frame.php?PST=PST3832-NL.Se)

FEATURES

source

1. .17

Location/Qualifiers

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ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5

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Db 11 GAGGG 15

Search completed: January 7, 2005, 11:00:56  
Job time : 2250.4 secs

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C 345 5 100.0 14 2 US-08-173-489C-336 Sequence 336, Appl  
C 346 5 100.0 14 2 US-08-364-246-4 Sequence 4, Appl  
C 347 5 100.0 14 2 US-08-866-958-21 Sequence 21, Appl  
C 348 5 100.0 14 2 US-08-866-958-68 Sequence 68, Appl  
C 349 5 100.0 14 2 US-08-856-141-14 Sequence 14, Appl  
C 350 5 100.0 14 2 US-08-856-141-18 Sequence 18, Appl  
C 351 5 100.0 14 2 US-08-485-133-79 Sequence 79, Appl  
C 352 5 100.0 14 2 US-08-810-599-15 Sequence 15, Appl  
C 353 5 100.0 14 3 US-08-671-824-15 Sequence 15, Appl  
C 354 5 100.0 14 3 US-08-757-024-499 Sequence 499, Appl  
C 355 5 100.0 14 3 US-08-757-024-527 Sequence 527, Appl  
C 356 5 100.0 14 3 US-08-757-024-554 Sequence 554, Appl  
C 357 5 100.0 14 3 US-08-757-024-580 Sequence 580, Appl  
C 358 5 100.0 14 3 US-08-757-024-605 Sequence 605, Appl  
C 359 5 100.0 14 3 US-08-757-024-629 Sequence 629, Appl  
C 360 5 100.0 14 3 US-08-757-024-652 Sequence 652, Appl  
C 361 5 100.0 14 3 US-08-757-024-674 Sequence 674, Appl  
C 362 5 100.0 14 3 US-08-757-024-695 Sequence 695, Appl  
C 363 5 100.0 14 3 US-08-757-024-715 Sequence 715, Appl  
C 364 5 100.0 14 3 US-08-544-381B-237 Sequence 237, Appl  
C 365 5 100.0 14 3 US-08-985-162-1829 Sequence 1829, Appl  
C 366 5 100.0 14 3 US-08-797-722-2 Sequence 2, Appl  
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C 369 5 100.0 14 3 US-08-998-099-341 Sequence 341, Appl  
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C 371 5 100.0 14 3 US-09-006-597-26 Sequence 26, Appl  
C 372 5 100.0 14 3 US-08-765-340-118 Sequence 118, Appl  
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C 378 5 100.0 14 3 US-08-192-946-28 Sequence 28, Appl  
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C 392 5 100.0 14 4 US-09-230-652-21 Sequence 21, Appl

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C 395 5 100.0 14 4 US-09-230-652-64 Sequence 64, Appl  
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399 5 100.0 14 4 US-09-904-420A-5 Sequence 5, Appli  
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C 410 5 100.0 14 6 5486603-1 Patent No. 5486603  
411 5 100.0 14 6 5486603-2 Patent No. 5486603  
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413 5 100.0 15 1 US-08-156-020-13 Sequence 13, Appl  
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415 5 100.0 15 1 US-07-909-383-5 Sequence 5, Appli  
C 416 5 100.0 15 1 US-08-170-095B-13 Sequence 13, Appl  
417 5 100.0 15 1 US-08-170-095B-14 Sequence 14, Appl  
C 418 5 100.0 15 1 US-08-050-073-264 Sequence 264, App  
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C 420 5 100.0 15 1 US-08-452-196A-8 Sequence 8, Appli  
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C 422 5 100.0 15 1 US-08-182-968A-3 Sequence 3, Appli  
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C 442 5 100.0 15 1 US-08-319-492B-435 Sequence 435, App  
C 443 5 100.0 15 1 US-08-319-492B-436 Sequence 436, App  
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445 5 100.0 15 1 US-08-434-503-50 Sequence 50, Appl  
446 5 100.0 15 1 US-08-241-372-8 Sequence 8, Appli  
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C 449 5 100.0 15 1 US-08-373-124A-87 Sequence 87, Appl  
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C 451 5 100.0 15 1 US-08-291-932A-11 Sequence 11, Appl  
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C 453 5 100.0 15 1 US-08-291-932A-13 Sequence 13, Appl  
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C 466 5 100.0 15 1 US-08-291-932A-221 Sequence 221, App  
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C 468 5 100.0 15 1 US-08-291-932A-242 Sequence 242, App  
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477 5 100.0 15 1 US-08-580-242-5 Sequence 5, Appli  
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C 482 5 100.0 15 1 US-08-363-240A-19 Sequence 19, Appl  
C 483 5 100.0 15 1 US-08-363-240A-117 Sequence 117, App  
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C 487 5 100.0 15 1 US-08-363-240A-644 Sequence 644, App  
C 488 5 100.0 15 1 US-08-363-240A-645 Sequence 645, App  
C 489 5 100.0 15 1 US-08-363-240A-646 Sequence 646, App  
C 490 5 100.0 15 1 US-08-363-240A-736 Sequence 736, App  
C 491 5 100.0 15 1 US-08-651-835A-2 Sequence 2, Appli  
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494 5 100.0 15 1 US-08-686-116A-23 Sequence 23, Appl  
495 5 100.0 15 1 US-08-686-116A-24 Sequence 24, Appl  
496 5 100.0 15 1 US-08-685-484-19 Sequence 19, Appl  
497 5 100.0 15 1 US-08-685-484-20 Sequence 20, Appl  
498 5 100.0 15 1 US-08-685-484-23 Sequence 23, Appl  
499 5 100.0 15 1 US-08-685-484-24 Sequence 24, Appl  
500 5 100.0 15 1 US-08-847-108-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-09-263-790-24  
; Sequence 24, Application US/09263790  
; Patent No. Pp12997  
; GENERAL INFORMATION:  
; APPLICANT: Nirmal Kumar PATRA et al.  
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS  
; FILE REFERENCE: 2761-0120P  
; CURRENT APPLICATION NUMBER: US/09/263,790  
; CURRENT FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: OPT 04 Primer - Used to develop the unique RAPD profiles of the  
; OTHER INFORMATION: plant Jal Pallavi  
US-09-263-790-24

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||  
Db 5 GAGGG 9

RESULT 2  
US-09-721-777-4  
; Sequence 4, Application US/09721777

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; Patent No. PP13279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
;
US-09-721-777-4

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
Db      5 GAGGG 9

RESULT 3
US-07-704-288C-5/c
; Sequence 5, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
;
US-07-704-288C-5

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
Db      5 GAGGG 1

RESULT 4
US-07-963-723A-3/c
; Sequence 3, Application US/07963723A
; Patent No. 5494794
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; TITLE OF INVENTION: Detection of Mitochondrial DNA Mutations
; TITLE OF INVENTION: Associated with Alzheimer's Disease and Parkinson's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 133 Carnegie Way, N.W., Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,723A
; FILING DATE: 19921020
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 0510.027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-07-963-723A-3

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
Db      7 GAGGG 3

RESULT 5
US-08-049-283A-28/c
; Sequence 28, Application US/08049283A
; Patent No. 5502176
; GENERAL INFORMATION:
; APPLICANT: Tenen, Daniel G.
; APPLICANT: Pahl, Heike L.
```

APPLICANT: Burn, Timothy C.  
TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/049,283A  
FILING DATE: 14-APR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/020,465  
FILING DATE: 19-FEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/837,776  
FILING DATE: 13-FEB-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: BIH91-03'A  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-049-283A-28

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||  
Db 9 GAGGG 5

RESULT 6  
US-08-308-894-6/c  
Sequence 6, Application US/08308894  
Patent No. 5571672  
GENERAL INFORMATION:  
APPLICANT: Slavicek, James M.  
APPLICANT: Garner, Karen J.  
APPLICANT: Schreiber, David E.  
TITLE OF INVENTION: GYPSY MOTH GENOTYPE ASSAY  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: USDA - Forest Products Laboratory  
STREET: One Gifford Pinchot Drive  
CITY: Madison  
STATE: WI  
COUNTRY: U.S.A.  
ZIP: 53705-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,894  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stockhausen, Janet I.  
REGISTRATION NUMBER: 34,256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 231-9502  
TELEFAX: (608) 231-9508  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
US-08-308-894-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||  
Db 8 GAGGG 4

RESULT 7  
US-08-330-123A-11/c  
Sequence 11, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA



US-08-330-123A-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 8

US-08-233-608-43/c

; Sequence 43, Application US/08233608  
; Patent No. 5585238  
; GENERAL INFORMATION:  
; APPLICANT: Ligon, James M  
; APPLICANT: Beck, James J  
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/233,608  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: CGC 1739  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8615  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: Oligonucleotide primer OPE-6  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

US-08-233-608-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 10 GAGGG 6

RESULT 9

US-08-210-222-34/c

; Sequence 34, Application US/08210222  
; Patent No. 5599917  
; GENERAL INFORMATION:  
; APPLICANT: Coppola, George R.  
; APPLICANT: Beutel, Bruce A.  
; APPLICANT: Bertelsen, Arthur H.

; TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
; ADDRESSEE: Cecchi, Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/210,222  
; FILING DATE: Unassigned  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Herron, Charles J.  
; REGISTRATION NUMBER: 28,019  
; REFERENCE/DOCKET NUMBER: 23550-114  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 BASES  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; HYPOTHETICAL: NO

US-08-210-222-34

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 10

US-07-971-978-18/c

; Sequence 18, Application US/07971978  
; Patent No. 5614617  
; GENERAL INFORMATION:  
; APPLICANT: Cook and Sanghvi  
; TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
; TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
; TITLE OF INVENTION: Gene Expression  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5614617is  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/971,978  
; FILING DATE: February 18, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/558,806

US-07-971-978-18/c

US-07-971-978-18/c

```
; FILING DATE: July 27, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: 6-aza-thymidine substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: 6-aza-thymidine substitution
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: 6-aza-thymidine substitution
; US-07-971-978-18
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 GAGGG 5
Db 10 GAGGG 6
;
; RESULT 11
; US-08-379-259-5/c
; Sequence 5, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-379-259-5
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 2.6e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 GAGGG 5
Db 5 GAGGG 1
;
; RESULT 12
; US-08-171-718-38/c
; Sequence 38, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-171-718-38
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
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Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 6 GAGGG 2

## RESULT 13

US-08-171-718-40/c  
; Sequence 40, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:

; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/171,718  
; FILING DATE: 22-DEC-1993  
; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463

; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-171-718-40

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

## RESULT 14

US-08-171-718-41  
; Sequence 41, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:

; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/171,718  
; FILING DATE: 22-DEC-1993  
; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463

; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-171-718-41

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 3 GAGGG 7

## RESULT 15

US-08-482-115B-11/c  
; Sequence 11, Application US/08482115B  
; Patent No. 5776679  
; GENERAL INFORMATION:

; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter

; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Assays for the RNA Component of Human  
; TITLE OF INVENTION: Telomerase

; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA

; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,115B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000830US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-482-115B-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 16  
US-08-887-480-43/c  
; Sequence 43, Application US/08887480  
; Patent No. 5814453  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James J  
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5814453artis Corporation  
; STREET: 520 White Plains Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,480  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/722,187  
; FILING DATE: 15-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: Oligonucleotide primer OPE-6  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-887-480-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 10 GAGGG 6

RESULT 17  
US-08-465-590-35  
; Sequence 35, Application US/08465590  
; Patent No. 5824770  
; GENERAL INFORMATION:  
; APPLICANT: Georgopoulos, Katia A.  
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
; NUMBER OF SEQUENCES: 164  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, Suite 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,590  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/238,212  
; FILING DATE: 02-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/121,438  
; FILING DATE: 14-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/946,233  
; FILING DATE: 14-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Paul L.  
; REGISTRATION NUMBER: 35,695  
; REFERENCE/DOCKET NUMBER: MFG-006C2DV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-465-590-35

Query Match 100.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 1 GAGGG 5

RESULT 18  
US-08-480-994-20/c  
; Sequence 20, Application US/08480994  
; Patent No. 5834248  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,994  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
US-08-480-994-20  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
|||||  
Db 8 GAGGG 4  
  
RESULT 19  
US-08-660-678A-11/c  
; Sequence 11, Application US/08660678A  
; Patent No. 5837857  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli

; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,678A  
; FILING DATE: 05-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000811US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-660-678A-11  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAGGG 5  
|||||  
Db 9 GAGGG 5  
  
RESULT 20  
US-08-616-844-20/c  
; Sequence 20, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/616,844  
; FILING DATE: 15-MAR-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"  
; HYPOTHETICAL: NO  
US-08-616-844-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 8 GAGGG 4

RESULT 21  
US-08-173-489C-170/c  
; Sequence 170, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 199:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; DESCRIPTION: hepatitis B virus adr isolate,  
; DESCRIPTION: nucleotides 427 to 436  
; HYPOTHETICAL: no

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 170:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: third strand derived from Hepatitis B  
; DESCRIPTION: isolate ayw sequence region in Seq ID No. 5861244169  
; HYPOTHETICAL: yes  
; ANTI-SENSE: no  
; PUBLICATION INFORMATION:  
; RELEVANT RESIDUES IN SEQ ID NO: 170 :FROM 1 TO 10  
US-08-173-489C-170

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

RESULT 22  
US-08-173-489C-199/c  
; Sequence 199, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 199:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; DESCRIPTION: hepatitis B virus adr isolate,  
; DESCRIPTION: nucleotides 427 to 436  
; HYPOTHETICAL: no



```
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adr
; PUBLICATION INFORMATION:
; AUTHORS: Toneyama, A., Miyanochara, A, No. 5861244aki, C,
; AUTHORS: Fujiyama, A., Ohromo, N, Matsubara, K.
; TITLE: Cloning and structural
; TITLE: analysis of Hepatitis B virus DNAs subtype adr
; JOURNAL: Nucleic Acids Research
; VOLUME: 11
; PAGES: 4601-4610
; DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 199 :FROM 1 TO 10
US-08-173-489C-199

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      8 GAGGG 4

RESULT 23
US-08-173-489C-288/c
; Sequence 288, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from C.
; DESCRIPTION: pasteurianum 16s region in Seq ID No. 5861244287
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
```

```
; RELEVANT RESIDUES IN SEQ ID NO: 288 :FROM 1 TO 10
US-08-173-489C-288

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      9 GAGGG 5

RESULT 24
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-29

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      5 GAGGG 9

RESULT 25
US-08-485-778-42/c
; Sequence 42, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
```

;; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
;; NUMBER OF SEQUENCES: 45  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/485,778  
;; FILING DATE: 07-JE-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/387,524  
;; FILING DATE: 13-FEB-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/272,102  
;; FILING DATE: 07-JUL-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: CSHL94-05A4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-861-6240  
;; TELEFAX: 617-861-9540  
;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-485-778-42

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||  
Db 9 GAGGG 5

RESULT 26  
US-08-599-654-20/c  
; Sequence 20, Application US/08599654  
; Patent No. 5882925  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/599,654  
;; FILING DATE: 09-FEB-1996  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/485,573  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/386,844  
;; FILING DATE: 10-FEB-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CORUZZI, LAURA A  
;; REGISTRATION NUMBER: 30,742  
;; REFERENCE/DOCKET NUMBER: 7853-041  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; DESCRIPTION: /desc = "synthetic oligonucleotide"  
;; HYPOTHETICAL: NO  
US-08-599-654-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||  
Db 8 GAGGG 4

RESULT 27  
US-08-828-009-4  
; Sequence 4, Application US/08828009  
; Patent No. 5914394  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Hong  
; APPLICANT: Friemer, Nelson, B.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,009  
; FILING DATE: 27-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-070  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090

```
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Antisense oligonucleotide
; LOCATION: 1...10
; OTHER INFORMATION:
US-08-828-009-4

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 2 GAGGG 6

RESULT 28
US-08-722-187-43/c
; Sequence 43, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-6
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-187-43

Query Match 100.0%; Score 5; DB 2; Length 10;
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```
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Antisense oligonucleotide
; LOCATION: 1...10
; OTHER INFORMATION:
US-08-828-009-4

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 2 GAGGG 6

RESULT 29
US-08-472-802C-12/c
; Sequence 12, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-472-802C-12

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 9 GAGGG 5

RESULT 30
US-08-485-573-20/c
; Sequence 20, Application US/08485573
; Patent No. 5968770
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
```

; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,573  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
US-08-485-573-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 8 GAGGG 4

RESULT 31  
US-08-899-786-9  
; Sequence 9, Application US/08899786  
; Patent No. 6001572  
; GENERAL INFORMATION:  
; APPLICANT: Toothman, Penelope  
; TITLE OF INVENTION: Method of Identifying Aloe Using  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
; COMPUTER: IBM pc compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 8.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,786  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/022,611

; FILING DATE: 26-JULY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: UNI.07  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
US-08-899-786-9

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 2 GAGGG 6

RESULT 32  
US-08-520-550A-42/c  
; Sequence 42, Application US/08520550A  
; Patent No. 6013468  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avillion, Ariel A.  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol  
; APPLICANT: Marhuenda, Maria A. B.  
; APPLICANT: Villeponteau, Bryant  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,550A  
; FILING DATE: 29-AUG-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/387,524  
; FILING DATE: 13-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 42:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-520-550A-42
Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 9 GAGGG 5

RESULT 33
US-08-944-868A-20/c
; Sequence 20, Application US/08944868A
; Patent No. 6018025
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,868A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,654
; FILING DATE:
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
US-08-944-868A-20
Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4

US-08-944-868A-20
Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4
```

```
RESULT 34
US-08-944-423A-20/c
; Sequence 20, Application US/08944423A
; Patent No. 6020463
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,423A
; FILING DATE: 06-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: JUN-07-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
US-08-944-423A-20
Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4

RESULT 35
US-08-757-024-609
; Sequence 609, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
```

;; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
;; STREET: P.O. Drawer 34009  
;; CITY: Charlotte  
;; STATE: No. 6025339th Carolina  
;; COUNTRY: USA  
;; ZIP: 28234  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/757,024  
;; FILING DATE: 26-NOV-1996  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5218-41  
;; TELEPHONE: 919-881-3140  
;; TELEFAX: 919-881-3175  
;; TELEX: 575102  
;; INFORMATION FOR SEQ ID NO: 609:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-609

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 6 GAGGG 10

RESULT 36  
US-08-757-024-633  
; Sequence 633, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102

;; INFORMATION FOR SEQ ID NO: 633:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-633

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

RESULT 37  
US-08-757-024-656  
; Sequence 656, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 656:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-656

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 4 GAGGG 8

RESULT 38  
US-08-757-024-678  
; Sequence 678, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:



```
/ APPLICANT: Nyce, Jonathan W.
/ TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
/ NUMBER OF SEQUENCES: 952
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BELL, SELTZER, PARK & GIBSON
/ STREET: P.O. Drawer 34009
/ CITY: Charlotte
/ STATE: No. 6025339th Carolina
/ COUNTRY: USA
/ ZIP: 28234
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/757,024
/ FILING DATE: 26-NOV-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sibley, Kenneth D.
/ REGISTRATION NUMBER: 31,665
/ REFERENCE/DOCKET NUMBER: 5218-41
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-881-3140
/ TELEFAX: 919-881-3175
/ TELEX: 575102
/ INFORMATION FOR SEQ ID NO: 678:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-757-024-678

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 3 GAGGG 7

RESULT 39
US-08-757-024-699
/ Sequence 699, Application US/08757024
/ Patent No. 6025339
/ GENERAL INFORMATION:
/ APPLICANT: Nyce, Jonathan W.
/ TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
/ NUMBER OF SEQUENCES: 952
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BELL, SELTZER, PARK & GIBSON
/ STREET: P.O. Drawer 34009
/ CITY: Charlotte
/ STATE: No. 6025339th Carolina
/ COUNTRY: USA
/ ZIP: 28234
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/757,024
/ FILING DATE: 26-NOV-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sibley, Kenneth D.
/ REGISTRATION NUMBER: 31,665
/ REFERENCE/DOCKET NUMBER: 5218-41
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-881-3140
/ TELEFAX: 919-881-3175
/ TELEX: 575102
/ INFORMATION FOR SEQ ID NO: 719:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-757-024-719

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 3 GAGGG 7
```

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-881-3140
/ TELEFAX: 919-881-3175
/ TELEX: 575102
/ INFORMATION FOR SEQ ID NO: 699:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-757-024-699

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 2 GAGGG 6

RESULT 40
US-08-757-024-719
/ Sequence 719, Application US/08757024
/ Patent No. 6025339
/ GENERAL INFORMATION:
/ APPLICANT: Nyce, Jonathan W.
/ TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
/ NUMBER OF SEQUENCES: 952
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BELL, SELTZER, PARK & GIBSON
/ STREET: P.O. Drawer 34009
/ CITY: Charlotte
/ STATE: No. 6025339th Carolina
/ COUNTRY: USA
/ ZIP: 28234
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/757,024
/ FILING DATE: 26-NOV-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sibley, Kenneth D.
/ REGISTRATION NUMBER: 31,665
/ REFERENCE/DOCKET NUMBER: 5218-41
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-881-3140
/ TELEFAX: 919-881-3175
/ TELEX: 575102
/ INFORMATION FOR SEQ ID NO: 719:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-757-024-719

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 1 GAGGG 5

RESULT 41
```

```
US-08-925-743-20/c
; Sequence 20, Application US/08925743
; Patent No. 6054558
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,573
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-925-743-20

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4

RESULT 42
US-09-075-215A-1
; Sequence 1, Application US/09075215A
; Patent No. 6054571
; GENERAL INFORMATION:
; APPLICANT: JOLICOEUR, Paul
; APPLICANT: BALSALOBRE, Aurelio
; TITLE OF INVENTION: dft-A GENE, DIAGNOSTIC AND
; THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swabey Ogilvy Renault
; STREET: Suite 1600, 1981 McGill College
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,215A
FILING DATE: 11-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ctt, France
REGISTRATION NUMBER: 37,037
REFERENCE/DOCKET NUMBER: 13497-4"US" FC/ld
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514-845-7126
TELEFAX: 514-288-8389
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-075-215A-1

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 3 GAGGG 7

RESULT 43
US-08-998-443-11/c
; Sequence 11, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
```

```
;
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-0008111US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-998-443-11

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 9 GAGGG 5

RESULT 44
US-08-906-691-19
; Sequence 19, Application US/08906691
; Patent No. 6066452
; GENERAL INFORMATION:
; APPLICANT: Weissman, Sherman M.
; APPLICANT: Nallur, Girish N.
; APPLICANT: Kulkarni, Prakash
; TITLE OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR
; TITLE OF INVENTION: IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 981094
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906.691
; FILING DATE: 31-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066452tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 390036.403C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-906-691-19

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 5 GAGGG 9
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RESULT 45
US-08-478-087-38/c
; Sequence 38, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-087-38

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 6 GAGGG 2

RESULT 46
US-08-478-087-40/c
; Sequence 40, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
```

```
;
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-087-40

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db |||||
7 GAGGG 3

RESULT 47
US-08-478-087-41
; Sequence 41, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-087-41

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
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3 GAGGG 7

RESULT 48
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; Sequence 20, Application US/08944496
; Patent No. 6124433
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,496
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-944-496-20

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4

RESULT 49
US-08-991-789A-102
; Sequence 102, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; Smith, John M.
; Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-08-991-789A-102
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Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 3 GAGGG 7

RESULT 50
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; Sequence 20, Application US/08925767
; Patent No. 6225084
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,767
; FILING DATE: 09-SEPT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-925-767-20

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 8 GAGGG 4
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
(without alignments)  
106.177 Million cell updates/sec

Title: GAGGG  
Perfect score: 5  
Sequence: 1 gaggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

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Maximum Match 100%  
Listing first 500 summaries

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	5	100.0	10 9	US-09-811-286-18
	3	5	100.0	10 9	US-09-796-138-15
	4	5	100.0	10 9	US-09-909-903-15
C	5	5	100.0	10 9	US-09-154-750A-18
	6	5	100.0	10 9	US-09-154-750A-49
	7	5	100.0	10 9	US-09-154-750A-58
	8	5	100.0	10 9	US-09-989-789-92
	9	5	100.0	10 9	US-09-989-789-93
	10	5	100.0	10 9	US-09-989-789-626
	11	5	100.0	10 9	US-09-989-789-1630
	12	5	100.0	10 9	US-09-989-789-1631

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c 87	10	13	US-10-033-145-1426	Sequence 1426, Ap	c 160	5	100.0	10	15	US-10-330-627-1340	Sequence 1340, Ap
c 88	10	13	US-10-033-145-1457	Sequence 1457, Ap	c 161	5	100.0	10	15	US-10-330-627-1414	Sequence 1414, Ap
c 89	10	13	US-10-033-145-1481	Sequence 1481, Ap	162	5	100.0	10	15	US-10-330-627-1461	Sequence 1461, Ap
c 90	10	13	US-10-033-145-1482	Sequence 1482, Ap	163	5	100.0	10	15	US-10-330-627-1548	Sequence 1548, Ap
c 91	10	13	US-10-033-145-1495	Sequence 1495, Ap	c 164	5	100.0	10	15	US-10-186-950-20	Sequence 20, Appl
c 92	10	13	US-10-033-145-1686	Sequence 1686, Ap	c 165	5	100.0	10	15	US-10-328-194A-23	Sequence 23, Appl
c 93	10	13	US-10-033-145-1755	Sequence 1755, Ap	166	5	100.0	10	15	US-10-160-358-114	Sequence 114, App
c 94	10	13	US-10-033-145-1832	Sequence 1832, Ap	c 167	5	100.0	10	15	US-10-160-358-115	Sequence 115, App
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c 96	10	13	US-10-033-145-2081	Sequence 2081, Ap	169	5	100.0	10	15	US-10-160-358-122	Sequence 122, App
c 97	10	13	US-10-033-145-2094	Sequence 2094, Ap	170	5	100.0	10	15	US-10-197-019-90	Sequence 90, Appl
c 98	10	13	US-10-033-145-2126	Sequence 2126, Ap	171	5	100.0	10	15	US-10-257-021-111	Sequence 111, App
c 99	10	14	US-10-055-713-63	Sequence 63, Appl	c 172	5	100.0	10	15	US-10-401-194-80	Sequence 80, Appl
c 100	10	14	US-10-010-802-249	Sequence 249, App	c 173	5	100.0	10	15	US-10-401-194-84	Sequence 84, Appl
c 101	10	14	US-10-010-802-266	Sequence 266, App	174	5	100.0	10	15	US-10-418-552-49	Sequence 49, Appl
102	10	15	US-10-142-111-20	Sequence 20, Appl	175	5	100.0	10	16	US-10-193-507-79	Sequence 79, Appl
103	10	15	US-10-142-111-41	Sequence 41, Appl	176	5	100.0	10	16	US-10-293-222-58	Sequence 58, Appl
c 104	10	15	US-10-140-763A-7	Sequence 7, Appl	177	5	100.0	10	16	US-10-293-222-135	Sequence 135, App
c 105	10	15	US-10-055-711-67	Sequence 67, Appl	178	5	100.0	10	16	US-10-293-222-197	Sequence 197, App
106	10	15	US-10-053-883-69	Sequence 69, Appl	c 179	5	100.0	10	16	US-10-293-222-202	Sequence 202, App
107	10	15	US-10-212-679-102	Sequence 102, App	c 180	5	100.0	10	16	US-10-293-222-212	Sequence 212, App
c 108	10	15	US-10-008-960-8	Sequence 8, Appl	c 181	5	100.0	10	16	US-10-293-222-216	Sequence 216, App
c 109	10	15	US-10-008-960-8	Sequence 8, Appl	183	5	100.0	10	16	US-10-293-222-217	Sequence 217, App
c 110	10	15	US-10-105-101A-8	Sequence 11, Appl	c 184	5	100.0	10	16	US-10-293-222-248	Sequence 248, App
c 111	10	15	US-10-359-935-11	Sequence 51, Appl	c 185	5	100.0	10	16	US-10-293-222-295	Sequence 295, App
c 112	10	15	US-10-176-464A-51	Sequence 12, Appl	c 186	5	100.0	10	16	US-10-293-222-436	Sequence 436, App
c 113	10	15	US-10-195-383-12	Sequence 21, Appl	187	5	100.0	10	16	US-10-079-137B-102	Sequence 68, Appl
c 114	10	15	US-10-195-383-21	Sequence 18, Appl	188	5	100.0	10	17	US-10-470-180-63	Sequence 63, Appl
115	10	15	US-10-329-465-18	Sequence 100, App	189	5	100.0	10	18	US-10-670-011-391	Sequence 391, App
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c 119	10	15	US-10-329-465-184	Sequence 193, App	c 193	5	100.0	10	18	US-10-487-934-185	Sequence 185, App
c 120	10	15	US-10-329-465-193	Sequence 199, App	c 194	5	100.0	10	18	US-10-487-934-186	Sequence 186, App
121	10	15	US-10-223-765-211	Sequence 211, App	c 195	5	100.0	10	18	US-10-487-934-187	Sequence 187, App
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125	10	15	US-10-223-765-231	Sequence 254, App	c 199	5	100.0	11	8	US-08-944-410-79	Sequence 79, Appl
126	10	15	US-10-223-765-254	Sequence 259, App	c 200	5	100.0	11	9	US-09-320-337-33	Sequence 33, Appl
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129	10	15	US-10-196-677-11	Sequence 61, Appl	203	5	100.0	11	9	US-09-263-959-684	Sequence 684, App
130	10	15	US-10-044-674-61	Sequence 16, Appl	204	5	100.0	11	9	US-09-263-959-707	Sequence 707, App
c 131	10	15	US-10-330-627-16	Sequence 19, Appl	c 205	5	100.0	11	9	US-09-263-959-737	Sequence 737, App
c 132	10	15	US-10-330-627-19	Sequence 23, Appl	206	5	100.0	11	9	US-09-263-959-906	Sequence 906, App
c 133	10	15	US-10-330-627-23	Sequence 51, Appl	207	5	100.0	11	10	US-09-918-715-30	Sequence 30, Appl
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144	10	15	US-10-330-627-493	Sequence 529, App	218	5	100.0	11	10	US-09-967-237-81	Sequence 81, Appl
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-057-351-11

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; Patent No. US20010051712A1  
; GENERAL INFORMATION:  
; APPLICANT: Drysdale, Connie M  
; APPLICANT: Judson, Richard S  
; APPLICANT: Liggett, Stephen B  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Stack, Catherine B.  
; APPLICANT: Stephens, J. Claiborne  
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes  
; FILE REFERENCE: with drug response  
; FILE REFERENCE: MWH-0303US1  
; CURRENT APPLICATION NUMBER: US/09/811,286  
; CURRENT FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-811-286-18

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 15, Application US/09796138  
; Patent No. US20020031782A1  
; GENERAL INFORMATION:  
; APPLICANT: Waterman, Michael R.  
; APPLICANT: Bellamine, Aouatef  
; APPLICANT: Podust, Larissa M.  
; TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 HIGH RESOLUTION STRUCTURE, POLYPEPTIDES AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: RELATING TO SAME  
; FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2  
; CURRENT APPLICATION NUMBER: US/09/796,138  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 09/345,218  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 21  
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; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
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RESULT 4  
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; Patent No. US20020052031A1  
; GENERAL INFORMATION:  
; APPLICANT: Waterman, Michael R.  
; APPLICANT: Bellamine, Aouatef  
; TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 POLYPEPTIDES AND  
; TITLE OF INVENTION: NUCLEIC ACIDS AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: RELATING TO SAME  
; FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17  
; CURRENT APPLICATION NUMBER: US/09/909,903  
; CURRENT FILING DATE: 2001-07-20  
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; Sequence 18, Application US/09154750A  
; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert

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; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
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US-09-154-750A-18

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; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1997-09-17
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US-09-154-750A-49

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; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153

; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-58

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 8
US-09-989-789-92
; Sequence 92, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-92

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 9
US-09-989-789-93
; Sequence 93, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-93
```



Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 1 GAGGG 5

## RESULT 10

US-09-989-789-626  
; Sequence 626, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 626  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-626

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 1 GAGGG 5

## RESULT 11

US-09-989-789-1630  
; Sequence 1630, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1630  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1630

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 1 GAGGG 5

## RESULT 12

US-09-989-789-1631

; Sequence 1631, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1631  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1631

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 1 GAGGG 5

## RESULT 13

US-09-989-789-1666  
; Sequence 1666, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1666  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1666

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 2 GAGGG 6

## RESULT 14

US-09-989-789-1674  
; Sequence 1674, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1674

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
      |||||
Db      2 GAGGG 6

RESULT 15
US-09-989-789-1685
; Sequence 1685, Application US/099889789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1685
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1685

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 16
US-09-989-789-1703
; Sequence 1703, Application US/099889789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1703
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1703

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
```

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 17
US-09-989-789-1704
; Sequence 1704, Application US/099889789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1704

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 18
US-09-810-936-102
; Sequence 102, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA
US-09-810-936-102

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
```





```
; Sequence 92, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-92

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 26
US-09-990-186-93
; Sequence 93, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-93

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 27
US-09-990-186-626
; Sequence 626, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-626

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 28
US-09-990-186-1630
; Sequence 1630, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1630

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 29
US-09-990-186-1631
; Sequence 1631, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1631

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5
```

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
   |||||
Db 1 GAGGG 5

RESULT 30
US-09-990-186-1666
; Sequence 1666, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1666

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
   |||||
Db 2 GAGGG 6

RESULT 31
US-09-990-186-1674
; Sequence 1674, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1674

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
   |||||
Db 2 GAGGG 6

RESULT 32
US-09-990-186-1685
; Sequence 1685, Application US/09990186
; Publication No. US20030068675A1
```

```
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1685
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1685

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
   |||||
Db 1 GAGGG 5

RESULT 33
US-09-990-186-1703
; Sequence 1703, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1703
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1703

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
   |||||
Db 1 GAGGG 5

RESULT 34
US-09-990-186-1704
; Sequence 1704, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 10
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1704

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 35
US-09-979-593-41/c
; Sequence 41, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MWH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-41

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 36
US-09-979-593-47
; Sequence 47, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MWH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-41

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      7 GAGGG 3

RESULT 37
US-09-979-593-609
; Sequence 609, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 609:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 609:
US-09-093-972C-609

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-47

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      5 GAGGG 9

RESULT 37
US-09-979-593-609
; Sequence 609, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 609:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 609:
US-09-093-972C-609

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAGGG 5  
|||||  
Db 6 GAGGG 10

## RESULT 38

US-09-093-972C-633  
; Sequence 633, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:

; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998

; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 633:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 633:  
US-09-093-972C-633

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

## RESULT 39

US-09-093-972C-656  
; Sequence 656, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:

; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998

; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 656:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 656:  
US-09-093-972C-656

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 4 GAGGG 8

## RESULT 40

US-09-093-972C-678  
; Sequence 678, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:

; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA

ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 678:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 678:  
US-09-093-972C-678

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 41  
US-09-093-972C-699  
Sequence 699, Application US/09093972C  
Publication No. US20030087845A1  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 699:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 699:  
US-09-093-972C-699  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
Db 2 GAGGG 6

RESULT 42  
US-09-093-972C-719  
Sequence 719, Application US/09093972C  
Publication No. US20030087845A1  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930

```
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 719:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 719:
US-09-093-972C-719

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 43
US-09-811-285-18
; Sequence 18, Application US/09811285
; Publication No. US20030091998A1
; GENERAL INFORMATION:
; APPLICANT: Drysdale, Connie M
; APPLICANT: Judson, Richard S
; APPLICANT: Liggett, Stephen B
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
; FILE REFERENCE: MWH-0303US2
; CURRENT APPLICATION NUMBER: US/09/811,285
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-285-18

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      5 GAGGG 9

RESULT 44
US-09-989-994-92
; Sequence 92, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-92

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 45
US-09-989-994-93
; Sequence 93, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-93

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 46
US-09-989-994-626
; Sequence 626, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-626

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5
```

```
Db      1 GAGGG 5

RESULT 47
US-09-989-994-1630
; Sequence 1630, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 48
US-09-989-994-1631
; Sequence 1631, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1631

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
      |||||
Db      1 GAGGG 5

RESULT 49
US-09-989-994-1666
; Sequence 1666, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1666

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
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Db      2 GAGGG 6

RESULT 50
US-09-989-994-1674
; Sequence 1674, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1674

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
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Db      2 GAGGG 6

Search completed: January 7, 2005, 11:31:21
Job time : 274.2 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGGAG  
Perfect score: 5  
Sequence: 1 gggag 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

- GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	5	100.0	10	6	A08947 Nucleotide
C 3	5	100.0	10	6	AR029980 Sequence
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C 476	5	100.0	11	6	AR301611	AR301611 Sequence
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LOCUS	A08937					
DEFINITION	A08937					
ACCESSION	A08937					
VERSION	A08937.1	GI:411846				
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
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		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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REFERENCE		Taniguchi,T.				
AUTHORS		Improvements in and relating to the regulation of gene expression				
TITLE		Patent: EP 0374503-A 4 27-JUN-1990;				
JOURNAL		Taniguchi, Tadatsugu, Prof. Dr				
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QY 1 GGGAG 5  
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Db 10 GGGAG 6

RESULT 2  
A08947/c  
LOCUS A08947 10 bp DNA linear PAT 27-AUG-1993  
DEFINITION Nucleotide sequence 16 from patent number EP0374503.  
ACCESSION A08947  
VERSION A08947.1 GI:411856  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Taniguchi,T.  
TITLE Improvements in and relating to the regulation of gene expression  
JOURNAL Patent: EP 0374503-A 16 27-JUN-1990;  
Taniguchi, Tadatsugu, Prof. Dr  
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Db 10 GGGAG 6

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AR029980  
LOCUS AR029980 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 169 from patent US 5861244.  
ACCESSION AR029980  
VERSION AR029980.1 GI:5943194  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 169 19-JAN-1999;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GGGAG 7

RESULT 4  
AR030011/c  
LOCUS AR030011 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 200 from patent US 5861244.  
ACCESSION AR030011  
VERSION AR030011.1 GI:5943225

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 200 19-JAN-1999;  
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Db 7 GGGAG 3

RESULT 5  
AR030098  
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DEFINITION Sequence 287 from patent US 5861244.  
ACCESSION AR030098  
VERSION AR030098.1 GI:5943312  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 287 19-JAN-1999;  
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QY 1 GGGAG 5  
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Db 5 GGGAG 9

RESULT 6  
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DEFINITION Sequence 19 from patent US 5861246.  
ACCESSION AR030208  
VERSION AR030208.1 GI:5943422  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 19 19-JAN-1999;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9 GGGAG 5

RESULT 7  
AR030218  
LOCUS AR030218 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 29 from patent US 5861246.  
ACCESSION AR030218  
VERSION AR030218.1 GI:5943432  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 29 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 3 GGGAG 7

RESULT 8  
AR030220/c  
LOCUS AR030220 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 31 from patent US 5861246.  
ACCESSION AR030220  
VERSION AR030220.1 GI:5943434  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 31 19-JAN-1999;  
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Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
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Db 9 GGGAG 5

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LOCUS AR030221 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 32 from patent US 5861246.

ACCESSION AR030221  
VERSION AR030221.1 GI:5943435  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 32 19-JAN-1999;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GGGAG 10

RESULT 10  
AR053555/c  
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DEFINITION Sequence 20 from patent US 5834248.  
ACCESSION AR053555  
VERSION AR053555.1 GI:5978417  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchd534, a gene uregulated by shear stress  
JOURNAL Patent: US 5834248-A 20 10-NOV-1998;  
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Db 6 GGGAG 2

RESULT 11  
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DEFINITION Sequence 30 from patent US 5834248.  
ACCESSION AR053565  
VERSION AR053565.1 GI:5978427  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchd534, a gene uregulated by shear stress  
JOURNAL Patent: US 5834248-A 30 10-NOV-1998;  
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QY      1 GGGAG 5
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RESULT 12
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DEFINITION      Sequence 40 from patent US 5837832.
ACCESSION      AR058463
VERSION      AR058463.1 GI:5984040
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE      Arrays of nucleic acid probes on biological chips
JOURNAL      Patent: US 5837832-A 40 17-NOV-1998;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      6 GGGAG 10

RESULT 13
AR058519
LOCUS      AR058519      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 96 from patent US 5837832.
ACCESSION      AR058519
VERSION      AR058519.1 GI:5984096
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE      Arrays of nucleic acid probes on biological chips
JOURNAL      Patent: US 5837832-A 96 17-NOV-1998;
FEATURES
      source
      1..10
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
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Db      5 GGGAG 9
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RESULT 14
AR058771/c
LOCUS      AR058771      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 348 from patent US 5837832.
ACCESSION      AR058771
VERSION      AR058771.1 GI:5984348
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE      Arrays of nucleic acid probes on biological chips
JOURNAL      Patent: US 5837832-A 348 17-NOV-1998;
FEATURES
      source
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      /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      7 GGGAG 3

RESULT 15
AR058772/c
LOCUS      AR058772      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 349 from patent US 5837832.
ACCESSION      AR058772
VERSION      AR058772.1 GI:5984349
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE      Arrays of nucleic acid probes on biological chips
JOURNAL      Patent: US 5837832-A 349 17-NOV-1998;
FEATURES
      source
      1..10
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      8 GGGAG 4

RESULT 16
AR058773/c
LOCUS      AR058773      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 350 from patent US 5837832.
ACCESSION      AR058773
VERSION      AR058773.1 GI:5984350
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
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TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 5837832-A 350 17-NOV-1998;  
FEATURES  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db  
RESULT 17  
AR058774/c  
LOCUS AR058774 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 351 from patent US 5837832.  
ACCESSION AR058774  
VERSION AR058774.1 GI:5984351  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,  
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 5837832-A 351 17-NOV-1998;  
FEATURES  
source 1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
RESULT 18  
AR065882/c  
LOCUS AR065882 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5849578.  
ACCESSION AR065882  
VERSION AR065882.1 GI:5996098  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of  
cardiovascular using RCHD528 as a target  
JOURNAL Patent: US 5849578-A 20 15-DEC-1998;  
FEATURES  
source 1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5

Db 6 GGGAG 2  
RESULT 19  
AR065892  
LOCUS AR065892 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 30 from patent US 5849578.  
ACCESSION AR065892  
VERSION AR065892.1 GI:5996108  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of  
cardiovascular using RCHD528 as a target  
JOURNAL Patent: US 5849578-A 30 15-DEC-1998;  
FEATURES  
source 1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db 6 GGGAG 10  
RESULT 20  
AR070981/c  
LOCUS AR070981 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 15 from patent US 5908978.  
ACCESSION AR070981  
VERSION AR070981.1 GI:7221869  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Amerson,H.V., Wilcox,P., Sederoff,R.R., Kuhlman,E.George.,  
O'Malley,D.M. and Grattapaglia,D.  
TITLE Methods for within family selection of disease resistance in woody  
perennials using genetic markers  
JOURNAL Patent: US 5908978-A 15 01-JUN-1999;  
FEATURES  
source 1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
RESULT 21  
AR080364/c  
LOCUS AR080364 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 20 from patent US 5968770.  
ACCESSION AR080364  
VERSION AR080364.1 GI:10007099  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd523 as a target  
JOURNAL Patent: US 5968770-A 20 19-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 2

RESULT 22  
AR080374  
LOCUS AR080374 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 30 from patent US 5968770.  
ACCESSION AR080374  
VERSION AR080374.1 GI:10007109  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd523 as a target  
JOURNAL Patent: US 5968770-A 30 19-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 10

RESULT 23  
AR092689/c  
LOCUS AR092689 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 1 from patent US 5998193.  
ACCESSION AR092689  
VERSION AR092689.1 GI:10019441  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 1 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 6 GGGAG 10

RESULT 24  
AR092690  
LOCUS AR092690 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 2 from patent US 5998193.  
ACCESSION AR092690  
VERSION AR092690.1 GI:10019442  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 2 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 10 GGGAG 6

RESULT 25  
AR092692  
LOCUS AR092692 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 4 from patent US 5998193.  
ACCESSION AR092692  
VERSION AR092692.1 GI:10019444  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 4 07-DEC-1999;  
FEATURES Location/Qualifiers  
source 1..10  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 1 GGGAG 5

RESULT 26  
AR092697  
LOCUS AR092697 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 9 from patent US 5998193.



ACCESSION AR092697  
VERSION AR092697.1 GI:10019449  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 9 07-DEC-1999;  
Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 1 GGGAG 5

RESULT 27  
AR092698  
LOCUS AR092698 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 10 from patent US 5998193.  
ACCESSION AR092698  
VERSION AR092698.1 GI:10019450  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 10 07-DEC-1999;  
Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 1 GGGAG 5

RESULT 28  
AR092715/c  
LOCUS AR092715 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 27 from patent US 5998193.  
ACCESSION AR092715  
VERSION AR092715.1 GI:10019467  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 27 07-DEC-1999;  
Location/Qualifiers  
source 1..10

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 10 GGGAG 6

RESULT 29  
AR098894/c  
LOCUS AR098894 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 30 from patent US 6077685.  
ACCESSION AR098894  
VERSION AR098894.1 GI:12808660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.  
TITLE Tumor suppressor merlin and antibodies thereof  
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 5 GGGAG 1

RESULT 30  
AR099558/c  
LOCUS AR099558 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 85 from patent US 6077833.  
ACCESSION AR099558  
VERSION AR099558.1 GI:12809324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the  
JOURNAL expression of B7 protein  
FEATURES Patent: US 6077833-A 85 20-JUN-2000;  
Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 5 GGGAG 1

RESULT 31  
AR099558/c  
LOCUS AR099558 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 85 from patent US 6077833.  
ACCESSION AR099558  
VERSION AR099558.1 GI:12809324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the  
JOURNAL expression of B7 protein  
FEATURES Patent: US 6077833-A 85 20-JUN-2000;  
Location/Qualifiers  
source 1..10  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 5 GGGAG 1

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AR106673/C
LOCUS AR106673 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6107078.
ACCESSION AR106673
VERSION AR106673.1 GI:12821203
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 1 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
|||||
Db 10 GGGAG 6

RESULT 32
AR106674
LOCUS AR106674 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6107078.
ACCESSION AR106674
VERSION AR106674.1 GI:12821204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 2 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
|||||
Db 10 GGGAG 6

RESULT 33
AR106676
LOCUS AR106676 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6107078.
ACCESSION AR106676
VERSION AR106676.1 GI:12821206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof

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JOURNAL Patent: US 6107078-A 4 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
|||||
Db 1 GGGAG 5

RESULT 34
AR106681
LOCUS AR106681 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107078.
ACCESSION AR106681
VERSION AR106681.1 GI:12821211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
|||||
Db 1 GGGAG 5

RESULT 35
AR106682
LOCUS AR106682 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6107078.
ACCESSION AR106682
VERSION AR106682.1 GI:12821212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 10 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
|||||
Db 1 GGGAG 5

RESULT 35
AR106682
LOCUS AR106682 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6107078.
ACCESSION AR106682
VERSION AR106682.1 GI:12821212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 10 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 5 GGGAG 1

RESULT 41  
BD225310  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for the diagnosis and treatment of lung cancer.  
ACCESSION BD225310  
VERSION BD225310.1 GI:33035080  
KEYWORDS JP 2002509706-A/9.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Jen, J., Beaudry, G.A., Madden, S.L. and Bertelsen, A.H.  
TITLE Methods for the diagnosis and treatment of lung cancer  
JOURNAL Patent: JP 2002509706-A 9 02-APR-2002;  
GENZYME CORP, JOHN HOPKINS UNIVERSITY  
COMMENT OS Artificial Sequence  
PN JP 2002509706-A/9  
PD 02-APR-2002  
PF 30-MAR-1999 JP 2000540746  
PR 31-MAR-1998 US 60/080044  
PI JIN JEN, GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC  
C12N15/09, A61K45/00, A61K48/00, A61P35/00, C12Q1/68, G01N33/50, PC  
G01N33/574,  
PC C12N15/00  
CC Description of Artificial Sequence: SAGE tags FH Key  
LOCUS Location/Qualifiers  
FT source 1..10  
FT /organism='Artificial Sequence'.  
FEATURES  
source 1..10  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 42  
BD225330  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Compositions and methods for the identification of lung tumor cells.  
ACCESSION BD225330  
VERSION BD225330.1 GI:33035100  
KEYWORDS JP 2002509707-A/12.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Beaudry, G.A., Madden, S.L. and Bertelsen, A.H.  
TITLE Compositions and methods for the identification of lung tumor cells  
JOURNAL Patent: JP 2002509707-A 12 02-APR-2002;  
GENZYME CORP  
COMMENT OS Artificial Sequence  
PN JP 2002509707-A/12  
PD 02-APR-2002  
PF 30-MAR-1999 JP 2000541180

PR 31-MAR-1998 US 60/080037  
PI GARY A BEAUDRY, STEPHEN L MADDEN, ARTHUR H BERTELSEN PC  
C12N15/09, A01K67/027, C07H21/04, C07K14/47, C07K16/18, C12N1/15, PC  
C12N1/19.  
PC C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/15, G01N33/53, PC  
G01N33/566//  
PC A61K45/00, A61P9/00, A61P35/00, C12N15/00, C12N5/00 CC  
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RESULT 43  
BD238630/c  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238630  
VERSION BD238630.1 GI:33048400  
KEYWORDS JP 2002534056-A/48.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts, B.L. and Shankara, S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 48 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/48  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR  
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08-DEC-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR  
PI BRUCE L ROBERTS, SRINIVAS SHANKARA  
PC C12N15/09, C12N15/10, G01N33/15, G01N33/50, A61P35/00, A61P37/04, C12N1/15, PC  
C12N1/19, G01N37/00,  
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR  
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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RESULT 49  
BD238903

LOCUS BD238903 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238903  
VERSION BD238903.1 GI:33048673  
KEYWORDS JP 2002534056-A/321.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
Roberts,B.L. and Shankara,S.  
AUTHORS Preparation and use of superior vaccines  
TITLE Patent: JP 2002534056-A 321 15-OCT-2002;  
JOURNAL GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/321  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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RESULT 50  
BD239031

LOCUS BD239031 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239031  
VERSION BD239031.1 GI:33048801  
KEYWORDS JP 2002534056-A/449.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
Roberts,B.L. and Shankara,S.  
AUTHORS Preparation and use of superior vaccines  
TITLE Patent: JP 2002534056-A 449 15-OCT-2002;  
JOURNAL GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/449  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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Db 1 GGGAG 5

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GenCore version 5.1.6  
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Listing first 500 summaries

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7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
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10: geneseqn2003cs: \*  
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12: geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 28	5	100.0	10	2	AAT98839	Aat98839 Binding s
29	5	100.0	10	2	AAT98848	Aat98848 Binding s
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c 141	5	100.0	10	3	AAZ86265	Aaz86265	Metastati
c 142	5	100.0	10	3	AAZ82355	Aaz82355	Metastati
143	5	100.0	10	3	AAZ84360	Aaz84360	Metastati
144	5	100.0	10	3	AAZ85013	Aaz85013	Metastati
145	5	100.0	10	3	AAZ85076	Aaz85076	Metastati
c 146	5	100.0	10	3	AAZ81368	Aaz81368	Metastati
c 147	5	100.0	10	3	AAZ82432	Aaz82432	Metastati
c 148	5	100.0	10	3	AAZ83915	Aaz83915	Metastati
c 149	5	100.0	10	3	AAZ86194	Aaz86194	Metastati
150	5	100.0	10	3	AAZ81290	Aaz81290	Metastati
c 151	5	100.0	10	3	AAZ81470	Aaz81470	Metastati
152	5	100.0	10	3	AAZ81590	Aaz81590	Metastati
c 153	5	100.0	10	3	AAZ81619	Aaz81619	Metastati
154	5	100.0	10	3	AAZ81785	Aaz81785	Metastati
c 155	5	100.0	10	3	AAZ83166	Aaz83166	Metastati
156	5	100.0	10	3	AAZ83318	Aaz83318	Metastati
157	5	100.0	10	3	AAZ83603	Aaz83603	Metastati
158	5	100.0	10	3	AAZ84320	Aaz84320	Metastati
159	5	100.0	10	3	AAZ84852	Aaz84852	Metastati
160	5	100.0	10	3	AAZ85025	Aaz85025	Metastati
c 161	5	100.0	10	3	AAZ85581	Aaz85581	Metastati
162	5	100.0	10	3	AAZ85849	Aaz85849	Metastati
163	5	100.0	10	3	AAZ86025	Aaz86025	Metastati
c 164	5	100.0	10	3	AAZ80768	Aaz80768	Metastati
165	5	100.0	10	3	AAZ82496	Aaz82496	Metastati
166	5	100.0	10	3	AAZ84027	Aaz84027	Metastati
167	5	100.0	10	3	AAZ85543	Aaz85543	Metastati

168	5	100.0	10	3	AAZ85550	Aaz85550	Metastati
c 169	5	100.0	10	3	AAZ85614	Aaz85614	Metastati
170	5	100.0	10	3	AAZ81401	Aaz81401	Metastati
171	5	100.0	10	3	AAZ81631	Aaz81631	Metastati
c 172	5	100.0	10	3	AAZ81824	Aaz81824	Metastati
c 173	5	100.0	10	3	AAZ82340	Aaz82340	Metastati
174	5	100.0	10	3	AAZ82499	Aaz82499	Metastati
c 175	5	100.0	10	3	AAZ82606	Aaz82606	Metastati
176	5	100.0	10	3	AAZ84445	Aaz84445	Metastati
177	5	100.0	10	3	AAZ84590	Aaz84590	Metastati
178	5	100.0	10	3	AAZ84874	Aaz84874	Metastati
179	5	100.0	10	3	AAZ86305	Aaz86305	Metastati
180	5	100.0	10	3	AAZ80964	Aaz80964	Metastati
c 181	5	100.0	10	3	AAZ81390	Aaz81390	Metastati
182	5	100.0	10	3	AAZ82079	Aaz82079	Metastati
183	5	100.0	10	3	AAZ83640	Aaz83640	Metastati
c 184	5	100.0	10	3	AAZ83853	Aaz83853	Metastati
185	5	100.0	10	3	AAZ84372	Aaz84372	Metastati
186	5	100.0	10	3	AAZ84779	Aaz84779	Metastati
187	5	100.0	10	3	AAZ85006	Aaz85006	Metastati
188	5	100.0	10	3	AAZ85749	Aaz85749	Metastati
c 189	5	100.0	10	3	AAZ85837	Aaz85837	Metastati
c 190	5	100.0	10	3	AAZ86005	Aaz86005	Metastati
c 191	5	100.0	10	3	AAZ80804	Aaz80804	Metastati
192	5	100.0	10	3	AAZ80816	Aaz80816	Metastati
c 193	5	100.0	10	3	AAZ82698	Aaz82698	Metastati
c 194	5	100.0	10	3	AAZ82799	Aaz82799	Metastati
c 195	5	100.0	10	3	AAZ83863	Aaz83863	Metastati
c 196	5	100.0	10	3	AAZ84156	Aaz84156	Metastati
197	5	100.0	10	3	AAZ84316	Aaz84316	Metastati
198	5	100.0	10	3	AAZ84659	Aaz84659	Metastati
c 199	5	100.0	10	3	AAZ82099	Aaz82099	Metastati
200	5	100.0	10	3	AAZ85403	Aaz85403	Metastati
201	5	100.0	10	3	AAZ85959	Aaz85959	Metastati
c 202	5	100.0	10	3	AAZ86193	Aaz86193	Metastati
c 203	5	100.0	10	3	AAZ86415	Aaz86415	Metastati
c 204	5	100.0	10	3	AAZ86488	Aaz86488	Metastati
c 205	5	100.0	10	3	AAZ80779	Aaz80779	Metastati
c 206	5	100.0	10	3	AAZ81719	Aaz81719	Metastati
c 207	5	100.0	10	3	AAZ82165	Aaz82165	Metastati
c 208	5	100.0	10	3	AAZ83174	Aaz83174	Metastati
209	5	100.0	10	3	AAZ83271	Aaz83271	Metastati
210	5	100.0	10	3	AAZ83458	Aaz83458	Metastati
211	5	100.0	10	3	AAZ83757	Aaz83757	Metastati
c 212	5	100.0	10	3	AAZ84610	Aaz84610	Metastati
c 213	5	100.0	10	3	AAZ82131	Aaz82131	Metastati
c 214	5	100.0	10	3	AAZ82415	Aaz82415	Metastati
c 215	5	100.0	10	3	AAZ83469	Aaz83469	Metastati
c 216	5	100.0	10	3	AAZ83494	Aaz83494	Metastati
217	5	100.0	10	3	AAZ84149	Aaz84149	Metastati
c 218	5	100.0	10	3	AAZ84857	Aaz84857	Metastati
219	5	100.0	10	3	AAZ85139	Aaz85139	Metastati
c 220	5	100.0	10	3	AAZ85251	Aaz85251	Metastati
c 221	5	100.0	10	3	AAZ85599	Aaz85599	Metastati
222	5	100.0	10	3	AAZ85646	Aaz85646	Metastati
c 223	5	100.0	10	3	AAZ86386	Aaz86386	Metastati
c 224	5	100.0	10	3	AAZ80853	Aaz80853	Metastati
c 225	5	100.0	10	3	AAZ83295	Aaz83295	Metastati
226	5	100.0	10	3	AAZ84362	Aaz84362	Metastati
227	5	100.0	10	3	AAZ85960	Aaz85960	Metastati
228	5	100.0	10	3	AAZ86365	Aaz86365	Metastati
c 229	5	100.0	10	3	AAZ86444	Aaz86444	Metastati
230	5	100.0	10	3	AAC74009	Aac74009	Human den
c 231	5	100.0	10	3	AAC74186	Aac74186	Human den
c 232	5	100.0	10	3	AAC74010	Aac74010	Human den
233	5	100.0	10	3	AAC73959	Aac73959	Human den
c 234	5	100.0	10	3	AAA56548	Aaa56548	Human mac
c 235	5	100.0	10	3	AAA56236	Aaa56236	Human mac
236	5	100.0	10	3	AAA56427	Aaa56427	Human mac
237	5	100.0	10	3	AAA56133	Aaa56133	Human mon
c 238	5	100.0	10	3	AAA56327	Aaa56327	Human mac
239	5	100.0	10	3	AAA56547	Aaa56547	Human mac
240	5	100.0	10	3	AAA56520	Aaa56520	Human mac

241	5	100.0	10	3	AAA56395	Aaa56395	Human mac	314	5	100.0	10	4	AAH64621	Aah64621	Human col
C 242	5	100.0	10	3	AAA56165	Aaa56165	Human mon	315	5	100.0	10	4	AAH63466	Aah63466	Human ubi
243	5	100.0	10	3	AAA56189	Aaa56189	Human mon	316	5	100.0	10	4	AAH64499	Aah64499	Human ubi
244	5	100.0	10	3	AAA56564	Aaa56564	Human mac	317	5	100.0	10	4	AAH63757	Aah63757	Human ubi
245	5	100.0	10	3	AAA56297	Aaa56297	Human mac	318	5	100.0	10	4	AAH63841	Aah63841	Human ubi
246	5	100.0	10	3	AAA56422	Aaa56422	Human mac	C 319	5	100.0	10	4	AAH64663	Aah64663	Human col
C 247	5	100.0	10	3	AAA06056	Aaa06056	CFTR gene	C 320	5	100.0	10	4	AAH63736	Aah63736	Human ubi
248	5	100.0	10	3	AAA06049	Aaa06049	CFTR gene	C 321	5	100.0	10	4	AAH64015	Aah64015	Human ubi
C 249	5	100.0	10	3	AAZ79748	Aaz79748	Human col	C 322	5	100.0	10	4	AAH64021	Aah64021	Human ubi
250	5	100.0	10	3	AAZ79784	Aaz79784	Human col	323	5	100.0	10	4	AAH63171	Aah63171	Human col
251	5	100.0	10	3	AAZ79801	Aaz79801	Human cys	324	5	100.0	10	4	AAH63839	Aah63839	Human ubi
252	5	100.0	10	3	AAZ79784	Aaz79784	Human bil	325	5	100.0	10	4	AAH64479	Aah64479	Human ubi
253	5	100.0	10	3	AAZ60708	Aac60708	Polynucle	C 326	5	100.0	10	4	AAH63542	Aah63542	Human ubi
C 254	5	100.0	10	3	AAZ89808	Aaz89808	Different	C 327	5	100.0	10	4	AAH63435	Aah63435	Human ubi
255	5	100.0	10	3	AAZ89818	Aaz89818	Different	328	5	100.0	10	4	AAS57302	Aas57302	Human CHR
C 256	5	100.0	10	3	AAZ88020	Aaz88020	Human umb	C 329	5	100.0	10	4	AAS57284	Aas57284	Human CHR
257	5	100.0	10	3	AAZ88030	Aaz88030	Human umb	330	5	100.0	10	4	AAS57307	Aas57307	Human CHR
C 258	5	100.0	10	3	AAA61015	Aaa61015	Protein b	331	5	100.0	10	4	AAS57290	Aas57290	Human CHR
C 259	5	100.0	10	3	AAA61004	Aaa61004	Protein b	C 332	5	100.0	10	4	AAS57286	Aas57286	Human CHR
260	5	100.0	10	3	AAA61013	Aaa61013	Protein b	333	5	100.0	10	4	AAS57281	Aas57281	Human CHR
261	5	100.0	10	3	AAZ68262	Aac68262	Lama2/APP	334	5	100.0	10	4	AAS57292	Aas57292	Human CHR
C 262	5	100.0	10	3	AAA73654	Aaa73654	Probe #23	C 335	5	100.0	10	4	AAF70107	Aaf70107	Human TNF
C 263	5	100.0	10	3	AAA73657	Aaa73657	Probe #26	C 336	5	100.0	10	4	AAF70101	Aaf70101	Human TNF
C 264	5	100.0	10	3	AAA73655	Aaa73655	Probe #24	C 337	5	100.0	10	4	AAD20713	Aad20713	Primer #5
C 265	5	100.0	10	3	AAA73656	Aaa73656	Probe #25	338	5	100.0	10	4	AAF98106	Aaf98106	Human IGE
C 266	5	100.0	10	3	AAA73652	Aaa73652	Probe #21	339	5	100.0	10	4	AAF98100	Aaf98100	Human IGE
C 267	5	100.0	10	3	AAA73653	Aaa73653	Probe #22	340	5	100.0	10	4	AAH32933	Aah32933	LPS activ
268	5	100.0	10	3	AAZ83350	Aac83350	Sequencin	341	5	100.0	10	4	AAH32791	Aah32791	LPS activ
C 269	5	100.0	10	3	AAA74368	Aaa74368	Mouse tra	342	5	100.0	10	4	AAH32698	Aah32698	LPS activ
C 270	5	100.0	10	4	AAZ32888	Aaf32888	Human B7-	C 343	5	100.0	10	4	ABA81635	Aba81635	Human pho
271	5	100.0	10	4	AAH18983	Aah18983	UCP3 poly	344	5	100.0	10	5	AAF75023	Aaf75023	HTR1A gen
272	5	100.0	10	4	AAH18998	Aah18998	UCP3 poly	345	5	100.0	10	5	ABA06179	Aba06179	Human nor
C 273	5	100.0	10	4	AAH18980	Aah18980	UCP3 poly	346	5	100.0	10	5	ABA06157	Aba06157	Human nor
274	5	100.0	10	4	AAH18967	Aah18967	UCP3 poly	C 347	5	100.0	10	5	ABA06027	Aba06027	Human nor
C 275	5	100.0	10	4	AAH18990	Aah18990	UCP3 poly	C 348	5	100.0	10	5	ABA06072	Aba06072	Human nor
C 276	5	100.0	10	4	AAF97341	Aaf97341	Human gen	C 349	5	100.0	10	5	AAF81043	Aaf81043	Primer fo
277	5	100.0	10	4	AAI67380	Aai67380	Human FKB	C 350	5	100.0	10	5	AAF81030	Aaf81030	Primer fo
C 278	5	100.0	10	4	AAF60257	Aaf60257	DNA linke	351	5	100.0	10	5	AAF70431	Aaf70431	Human DRD
279	5	100.0	10	4	AAZ04443	Aas04443	Human DAX	C 352	5	100.0	10	5	AAF70444	Aaf70444	Human DRD
280	5	100.0	10	4	AAH63496	Aah63496	Human ubi	353	5	100.0	10	5	AAF27934	Aaf27934	Interleuk
C 281	5	100.0	10	4	AAH63970	Aah63970	Human ubi	C 354	5	100.0	10	5	AAF69608	Aaf69608	Human IL4
282	5	100.0	10	4	AAH64426	Aah64426	Human ubi	C 355	5	100.0	10	5	AAF69609	Aaf69609	Human IL4
283	5	100.0	10	4	AAH64108	Aah64108	Human ubi	C 356	5	100.0	10	5	AAF69623	Aaf69623	Human IL4
284	5	100.0	10	4	AAH64109	Aah64109	Human ubi	357	5	100.0	10	5	AAF69635	Aaf69635	Human IL4
285	5	100.0	10	4	AAH63682	Aah63682	Human ubi	C 358	5	100.0	10	5	AAF74061	Aaf74061	Human SLC
286	5	100.0	10	4	AAH63951	Aah63951	Human ubi	359	5	100.0	10	5	AAF74059	Aaf74059	Human SLC
C 287	5	100.0	10	4	AAH64235	Aah64235	Human ubi	360	5	100.0	10	5	AAF74011	Aaf74011	Human SLC
288	5	100.0	10	4	AAH63996	Aah63996	Human ubi	361	5	100.0	10	5	AAF82517	Aaf82517	HIV-1 pro
C 289	5	100.0	10	4	AAH64557	Aah64557	Human ubi	362	5	100.0	10	5	AAF82518	Aaf82518	HIV-1 pro
C 290	5	100.0	10	4	AAH64559	Aah64559	Human ubi	C 363	5	100.0	10	5	ABA83129	Aba83129	HDGF ovar
C 291	5	100.0	10	4	AAH64560	Aah64560	Human ubi	364	5	100.0	10	5	ABA83131	Aba83131	CD63 anti
C 292	5	100.0	10	4	AAH64121	Aah64121	Human ubi	365	5	100.0	10	5	ABA83151	Aba83151	Glutathio
293	5	100.0	10	4	AAH64153	Aah64153	Human ubi	C 366	5	100.0	10	5	AAF33839	Aaf33839	Yeast NOR
294	5	100.0	10	4	AAH63579	Aah63579	Human ubi	C 367	5	100.0	10	5	AAF33845	Aaf33845	Yeast NOR
295	5	100.0	10	4	AAH63939	Aah63939	Human ubi	C 368	5	100.0	10	5	AAF35149	Aaf35149	Yeast NOR
C 296	5	100.0	10	4	AAH64229	Aah64229	Human ubi	369	5	100.0	10	5	AAF35167	Aaf35167	Yeast NOR
C 297	5	100.0	10	4	AAH64501	Aah64501	Human ubi	370	5	100.0	10	5	AAF37976	Aaf37976	Yeast NOR
C 298	5	100.0	10	4	AAH64558	Aah64558	Human ubi	371	5	100.0	10	5	AAF38235	Aaf38235	Yeast NOR
C 299	5	100.0	10	4	AAH63211	Aah63211	Human col	C 372	5	100.0	10	5	AAF42993	Aaf42993	Yeast NOR
C 300	5	100.0	10	4	AAH64264	Aah64264	Human ubi	373	5	100.0	10	5	AAF41193	Aaf41193	Yeast NOR
C 301	5	100.0	10	4	AAH63258	Aah63258	Human col	C 374	5	100.0	10	5	AAF42869	Aaf42869	Yeast NOR
C 302	5	100.0	10	4	AAH63822	Aah63822	Human ubi	C 375	5	100.0	10	5	AAF43899	Aaf43899	Yeast NOR
303	5	100.0	10	4	AAH63840	Aah63840	Human ubi	C 376	5	100.0	10	5	AAF33815	Aaf33815	Yeast NOR
304	5	100.0	10	4	AAH63950	Aah63950	Human ubi	C 377	5	100.0	10	5	AAF33846	Aaf33846	Yeast NOR
305	5	100.0	10	4	AAH63971	Aah63971	Human ubi	C 378	5	100.0	10	5	AAF35078	Aaf35078	Yeast NOR
C 306	5	100.0	10	4	AAH64170	Aah64170	Human ubi	C 379	5	100.0	10	5	AAF37508	Aaf37508	Yeast NOR
307	5	100.0	10	4	AAH64270	Aah64270	Human ubi	380	5	100.0	10	5	AAF38182	Aaf38182	Yeast NOR
308	5	100.0	10	4	AAH64708	Aah64708	Human hig	381	5	100.0	10	5	AAF38517	Aaf38517	Yeast NOR
C 309	5	100.0	10	4	AAH63321	Aah63321	Human lun	C 382	5	100.0	10	5	AAF40953	Aaf40953	Yeast NOR
C 310	5	100.0	10	4	AAH63801	Aah63801	Human ubi	383	5	100.0	10	5	AAF41192	Aaf41192	Yeast NOR
311	5	100.0	10	4	AAH63940	Aah63940	Human ubi	384	5	100.0	10	5	AAF34480	Aaf34480	Yeast NOR
312	5	100.0	10	4	AAH63952	Aah63952	Human ubi	C 385	5	100.0	10	5	AAF36234	Aaf36234	Yeast NOR
C 313	5	100.0	10	4	AAH64042	Aah64042	Human ubi	C 386	5	100.0	10	5	AAF41098	Aaf41098	Yeast NOR

C 387	5	100.0	10	5	AAF33285	Aaf33285	Yeast	hig
C 388	5	100.0	10	5	AAF37110	Aaf37110	Yeast	NOR
C 389	5	100.0	10	5	AAF37595	Aaf37595	Yeast	NOR
C 390	5	100.0	10	5	AAF37818	Aaf37818	Yeast	NOR
C 391	5	100.0	10	5	AAF38175	Aaf38175	Yeast	NOR
C 392	5	100.0	10	5	AAF33329	Aaf33329	Yeast	NOR
C 393	5	100.0	10	5	AAF33517	Aaf33517	Yeast	NOR
C 394	5	100.0	10	5	AAF40094	Aaf40094	Yeast	NOR
C 395	5	100.0	10	5	AAF43676	Aaf43676	Yeast	NOR
C 396	5	100.0	10	5	AAF37161	Aaf37161	Yeast	NOR
C 397	5	100.0	10	5	AAF37827	Aaf37827	Yeast	NOR
C 398	5	100.0	10	5	AAF41372	Aaf41372	Yeast	NOR
C 399	5	100.0	10	5	AAF37825	Aaf37825	Yeast	NOR
C 400	5	100.0	10	5	AAF40219	Aaf40219	Yeast	NOR
C 401	5	100.0	10	5	AAF40871	Aaf40871	Yeast	NOR
C 402	5	100.0	10	5	AAF41373	Aaf41373	Yeast	NOR
C 403	5	100.0	10	5	AAF37826	Aaf37826	Yeast	NOR
C 404	5	100.0	10	5	AAF39835	Aaf39835	Yeast	NOR
C 405	5	100.0	10	5	AAF35782	Aaf35782	Yeast	NOR
C 406	5	100.0	10	5	AAF36321	Aaf36321	Yeast	NOR
C 407	5	100.0	10	5	AAF36854	Aaf36854	Yeast	NOR
C 408	5	100.0	10	5	AAF33847	Aaf33847	Yeast	NOR
C 409	5	100.0	10	5	AAF33850	Aaf33850	Yeast	NOR
C 410	5	100.0	10	5	AAF40348	Aaf40348	Yeast	NOR
C 411	5	100.0	10	5	AAF43264	Aaf43264	Yeast	NOR
C 412	5	100.0	10	5	AAF43265	Aaf43265	Yeast	NOR
C 413	5	100.0	10	5	AAF34444	Aaf34444	Yeast	NOR
C 414	5	100.0	10	5	AAF37747	Aaf37747	Yeast	NOR
C 415	5	100.0	10	5	AAF40677	Aaf40677	Yeast	NOR
C 416	5	100.0	10	5	AAF33811	Aaf33811	Yeast	NOR
C 417	5	100.0	10	5	AAF35340	Aaf35340	Yeast	NOR
C 418	5	100.0	10	5	AAF42421	Aaf42421	Yeast	NOR
C 419	5	100.0	10	5	AAF42643	Aaf42643	Yeast	NOR
C 420	5	100.0	10	5	AAF34090	Aaf34090	Yeast	NOR
C 421	5	100.0	10	5	AAF34956	Aaf34956	Yeast	NOR
C 422	5	100.0	10	5	AAF35366	Aaf35366	Yeast	NOR
C 423	5	100.0	10	5	AAF42398	Aaf42398	Yeast	NOR
C 424	5	100.0	10	5	AAF42994	Aaf42994	Yeast	NOR
C 425	5	100.0	10	5	AAF34867	Aaf34867	Yeast	NOR
C 426	5	100.0	10	5	AAF38240	Aaf38240	Yeast	NOR
C 427	5	100.0	10	6	AAS19577	Aas19577	Primer-ex	
C 428	5	100.0	10	6	AAS19589	Aas19589	Primer-ex	
C 429	5	100.0	10	6	ABK90355	Abk90355	Bcl-2-tar	
C 430	5	100.0	10	6	AAS18741	Aas18741	Primer-ex	
C 431	5	100.0	10	6	AAD25080	Aad25080	Primer #7	
C 432	5	100.0	10	6	AAD25092	Aad25092	Primer #1	
C 433	5	100.0	10	6	AAS98374	Aas98374	Galanin r	
C 434	5	100.0	10	6	AAS98387	Aas98387	Galanin r	
C 435	5	100.0	10	6	AAS98380	Aas98380	Galanin r	
C 436	5	100.0	10	6	AAS98370	Aas98370	Galanin r	
C 437	5	100.0	10	6	AAS98378	Aas98378	Galanin r	
C 438	5	100.0	10	6	AAS98382	Aas98382	Galanin r	
C 439	5	100.0	10	6	AAS98399	Aas98399	Galanin r	
C 440	5	100.0	10	6	AAS98372	Aas98372	Galanin r	
C 441	5	100.0	10	6	AAS98376	Aas98376	Galanin r	
C 442	5	100.0	10	6	AAS98384	Aas98384	Galanin r	
C 443	5	100.0	10	6	AAD25297	Aad25297	Human HSD	
C 444	5	100.0	10	6	ABK24243	Abk24243	Retinalde	
C 445	5	100.0	10	6	AAL45322	Aal45322	Human KCN	
C 446	5	100.0	10	6	AAL45320	Aal45320	Human KCN	
C 447	5	100.0	10	6	ABK97526	Abk97526	Human LCA	
C 448	5	100.0	10	6	AAS18304	Aas18304	Primer-ex	
C 449	5	100.0	10	6	AAS18299	Aas18299	Primer-ex	
C 450	5	100.0	10	6	AAD25445	Aad25445	Human GNR	
C 451	5	100.0	10	6	AAD25432	Aad25432	Human GNR	
C 452	5	100.0	10	6	AAS18502	Aas18502	Vector pH	
C 453	5	100.0	10	6	AAD26032	Aad26032	Primer #3	
C 454	5	100.0	10	6	AAS99283	Aas99283	Human F12	
C 455	5	100.0	10	6	ABL88338	Ab188338	Human CHR	
C 456	5	100.0	10	6	ABL88325	Ab188325	Human CHR	
C 457	5	100.0	10	6	ABK55538	Abk55538	Selectin	
C 458	5	100.0	10	6	ABL52211	Ab152211	Human PER	
C 459	5	100.0	10	6	ABL52165	Ab152165	Human PER	

C 460	5	100.0	10	6	ABL52210	Ab152210	Human PER	
C 461	5	100.0	10	6	ABK81932	Abk81932	Human CYP	
C 462	5	100.0	10	6	ABK95830	Abk95830	Solute Ca	
C 463	5	100.0	10	6	ABK95857	Abk95857	Solute Ca	
C 464	5	100.0	10	6	ABK95831	Abk95831	Solute Ca	
C 465	5	100.0	10	6	ABK95832	Abk95832	Solute Ca	
C 466	5	100.0	10	6	AAS98896	Aas98896	Colony st	
C 467	5	100.0	10	6	AAS98818	Aas98818	Colony st	
C 468	5	100.0	10	6	AAS98902	Aas98902	Colony st	
C 469	5	100.0	10	6	AAS98828	Aas98828	Colony st	
C 470	5	100.0	10	6	AAS98907	Aas98907	Colony st	
C 471	5	100.0	10	6	AAS98843	Aas98843	Colony st	
C 472	5	100.0	10	6	AAS98829	Aas98829	Colony st	
C 473	5	100.0	10	6	AAS98841	Aas98841	Colony st	
C 474	5	100.0	10	6	ABL01316	Ab101316	Human MMP	
C 475	5	100.0	10	6	ABL01319	Ab101319	Human MMP	
C 476	5	100.0	10	6	AAD25885	Aad25885	Primer #7	
C 477	5	100.0	10	6	ABL42696	Ab142696	Human mat	
C 478	5	100.0	10	6	ABL42710	Ab142710	Human mat	
C 479	5	100.0	10	6	ABL42711	Ab142711	Human mat	
C 480	5	100.0	10	6	ABL42738	Ab142738	Human mat	
C 481	5	100.0	10	6	ABL42665	Ab142665	Human mat	
C 482	5	100.0	10	6	ABL42716	Ab142716	Human mat	
C 483	5	100.0	10	6	ABL42734	Ab142734	Human mat	
C 484	5	100.0	10	6	ABL42791	Ab142791	Human mat	
C 485	5	100.0	10	6	ABL42743	Ab142743	Human mat	
C 486	5	100.0	10	6	ABL99039	Ab199039	Mouse neu	
C 487	5	100.0	10	6	ABL99037	Ab199037	Mouse neu	
C 488	5	100.0	10	6	ABL60194	Ab160194	Human MUC	
C 489	5	100.0	10	6	ABK89140	Abk89140	RNA seque	
C 490	5	100.0	10	6	ABS51933	Abs51933	Human FMO	
C 491	5	100.0	10	6	AAD45291	Aad45291	Human PON	
C 492	5	100.0	10	6	ABN81468	Abn81468	Human HTA	
C 493	5	100.0	10	6	ABN81469	Abn81469	Human HTA	
C 494	5	100.0	10	6	ABK96056	Abk96056	Human LIP	
C 495	5	100.0	10	6	ABK96057	Abk96057	Human LIP	
C 496	5	100.0	10	6	AAD26171	Aad26171	Human end	
C 497	5	100.0	10	6	AAD26176	Aad26176	Human end	
C 498	5	100.0	10	6	AAD26167	Aad26167	Human end	
C 499	5	100.0	10	6	AAD26169	Aad26169	Human end	
C 500	5	100.0	10	12	ADI13733	Adi13733	Cytoplasm	

ALIGNMENTS

RESULT 1	
AAQ25520	
ID	AAQ25520 standard; DNA; 10 BP.
XX	AAQ25520;
AC	AAQ25520;
XX	
DT	25-MAR-2003 (revised)
DT	01-DEC-1992 (first entry)
XX	
DE	Antisense nucleic acid derivative 19.
XX	
KW	HIV; ras; c-myb; AIDS-related complex; ss.
XX	
OS	Synthetic.
XX	
PN	WO9208729-A1.
XX	
PD	29-MAY-1992.
XX	
PF	18-NOV-1991; 91WO-JP001572.
XX	
PR	20-NOV-1990; 90JP-00315007.
XX	
PA	(SANY ) SANKYO CO LTD.
XX	
PI	Furukawa H, Momota K, Takiguchi Y, Hotoda H, Kaneko M;
XX	

DR WPI; 1992-200131/24.  
XX  
PT New antiviral and antitumoural antisense nucleic acid derivs. - useful  
PT for treating AIDS and AIDS-related complex.  
PS  
XX Claim 78; Page 200; 235pp; Japanese.  
XX  
CC The sequences given in AAQ25502-21 are nucleic acid derivatives which are  
CC complementary to either a viral or a tumor gene ie. the sequence is  
CC complementary to the HIV gene at 7947-7975 on the viral genome or to the  
CC ras or c-myb oncogenes. These derivatives are useful as anticancer and  
CC antiviral agents, esp. for the treatment of AIDS and AIDS-related  
CC complex. They may be given orally or parenterally. The derivatives were  
CC tritiated so that they could be monitored easily. (Updated on 25-MAR-2003  
CC to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 2 GGGAG 6  
|||||  
AAQ79358 standard; DNA; 10 BP.  
  
RESULT 2  
ID AAQ79358 standard; DNA; 10 BP.  
XX  
AC AAQ79358;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Sequence of AP2 regulatory sequence located at posn. 896 in hEpsLH.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UJNY ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table I, p. 12; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
CC 5' flanking region and includes all the 5' regulatory elements. This  
CC region, consisting of the first 3892 of AAQ79353, was not found in the  
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
CC show several of these elements and their positions. The nucleotide  
CC position of these elements is measured from the BamHI site at the 5' end

CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
|||||  
AAQ71089/c  
ID AAQ71089 standard; cDNA; 10 BP.  
XX  
AC AAQ71089;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 7 splice acceptor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX  
PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Trofatter JA, Maccollin MM, Gusella JF;  
XX  
DR WPI; 1994-272992/34.  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
PT tumours and neurofibromatosis (NF2).  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance  
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
XX



SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 5 GGGAG 1

RESULT 4  
AAQ64610/c  
ID AAQ64610 standard; cDNA; 10 BP.  
XX  
AC AAQ64610;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-DEC-1994 (first entry)  
XX  
DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.  
XX  
KW Mitochondrial DNA mutation; associated with Alzheimer's;  
KW Parkinson's disease; mismatch primers; PCR; amplification;  
KW polymerase chain reaction; ss.  
XX Homo sapiens.  
OS  
XX WO9409162-A1.  
PN  
XX 28-APR-1994.  
PD  
XX 20-OCT-1993; 93WO-US010072.  
PF  
XX 20-OCT-1992; 92US-00963723.  
PR  
XX (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
PA  
XX Wallace DC;  
PI  
XX WPI; 1994-151346/18.  
DR  
XX  
XX Detection of mitochondrial DNA mutation associated with Alzheimer's  
PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-  
PT disposition to Alzheimer's disease and/or Parkinson's disease in a  
PT patient.  
XX  
XX Disclosure; Page 36; 83pp; English.  
PS  
XX A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene  
CC insertion. Direct sequence analysis revealed that the insertion consisted  
CC of approximately five cytosines within AAQ64610. This mitochondrial DNA  
CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The  
CC detection of the mutations is useful for diagnosing or predicting a pre-  
CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 9 GGGAG 5

RESULT 5  
AAX32614  
ID AAX32614 standard; DNA; 10 BP.  
XX  
AC AAX32614;

XX 23-JUN-1999 (first entry)  
DT  
XX Anticancer duplex forming oligonucleotide SEQ ID #14.  
DE  
XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
KW  
XX Synthetic.  
OS  
XX WO9523162-A1.  
PN  
XX 31-AUG-1995.  
PD  
XX 27-FEB-1995; 95WO-US002419.  
PF  
XX 28-FEB-1994; 94US-00202927.  
PR  
XX (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
DR  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 50; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl-pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 10

RESULT 6  
AAQ96493  
ID AAQ96493 standard; DNA; 10 BP.  
XX  
AC AAQ96493;  
XX  
XX 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
DT  
XX HIV-1 NL4-3 nef gene nucleotide deletion 88.  
DE  
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW  
XX Human immunodeficiency virus 1.  
OS  
XX WO9521912-A1.  
PN  
XX 17-AUG-1995.  
PD  
XX 14-FEB-1995; 95WO-AU0000063.  
PF  
XX

PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
DB |||||  
3 GGGAG 7  
RESULT 7  
AAQ96710/c  
ID AAQ96710 standard; DNA; 10 BP.  
XX  
AC AAQ96710;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 305.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX

PS Claim 13; Page 192; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
DB |||||  
6 GGGAG 2  
RESULT 8  
AAQ97063  
ID AAQ97063 standard; DNA; 10 BP.  
XX  
AC AAQ97063;  
XX  
DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 LTR nucleotide deletion 45.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 14; Page 196; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy		1 GGGAG 5							
Db		4 GGGAG 8							
RESULT 9									
AAQ97065									
ID	AAQ97065 standard; DNA; 10 BP.								
XX									
AC	AAQ97065;								
XX									
DT	16-OCT-2003 (revised)								
DT	27-MAR-1996 (first entry)								
XX									
DE	HIV-1 NL4-3 LTR nucleotide deletion 47.								
XX									
KW	HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.								
XX	Human immunodeficiency virus 1.								
OS									
XX									
PN	WO9521912-A1.								
XX									
PD	17-AUG-1995.								
XX									
PF	14-FEB-1995; 95WO-AU0000063.								
XX									
PR	14-FEB-1994; 94AU-000003864.								
PR	21-FEB-1994; 94AU-00004002.								
PR	23-DEC-1994; 94AU-00000284.								
XX									
PA	(MACF-) MACFARLANE BURNET CENT MEDICAL.								
PA	(AURE-) AUSTRALIAN RED CROSS SOC.								
XX									
PI	Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;								
XX									
DR	WPI; 1995-293115/38.								
XX									
PT	New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or								
PT	LTR region - can be used in a vaccine to inhibit/reduce productive								
PT	infection in an individual by a pathogenic strain.								
XX									
PS	Claim 14; Page 196; 301pp; English.								
XX									
CC	Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or								
CC	more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more								
CC	decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of								
CC	AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The								
CC	resulting avirulent HIV strains are still capable of inducing an immune								
CC	response in humans, and enable the generation of therapeutic, diagnostic								
CC	and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to								
CC	standardise OS field)								
XX									
SQ	Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;								
Query Match 100.0%; Score 5; DB 2; Length 10;									
Best Local Similarity 100.0%; Pred. No. 1.9e+06;									
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy		1 GGGAG 5							
Db		2 GGGAG 6							
RESULT 10									
AAQ96707/c									
ID	AAQ96707 standard; DNA; 10 BP.								
XX									
AC	AAQ96707;								
XX									
DT	16-OCT-2003 (revised)								
DT	22-MAR-1996 (first entry)								

PR 23-DEC-1994; 94AU-00000284.  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
4 GGGAG 8  
  
RESULT 12  
AAQ97062  
ID AAQ97062 standard; DNA; 10 BP.  
XX  
AC AAQ97062;  
XX  
DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 LTR nucleotide deletion 44.  
DE  
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW  
XX Human immunodeficiency virus 1.  
OS  
XX WO9521912-A1.  
PN  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 14; Page 196; 301pp; English.  
XX

CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
5 GGGAG 9  
  
RESULT 13  
AAQ96495  
ID AAQ96495 standard; DNA; 10 BP.  
XX  
AC AAQ96495;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 90.  
DE  
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW  
XX Human immunodeficiency virus 1.  
OS  
XX WO9521912-A1.  
PN  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 1 GGGAG 5

RESULT 14  
AAQ96706/c  
ID AAQ96706 standard; DNA; 10 BP.  
XX  
AC AAQ96706;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 301.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 192; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 10 GGGAG 6

RESULT 15  
AAQ96491  
ID AAQ96491 standard; DNA; 10 BP.  
XX  
AC AAQ96491;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 86.

XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW Human immunodeficiency virus 1.  
OS  
XX WO9521912-A1.  
PN  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 16  
AAQ96711/c  
ID AAQ96711 standard; DNA; 10 BP.  
XX  
AC AAQ96711;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 306.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 192; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||  
5 GGGAG 1  
RESULT 17  
AAQ96494  
ID AAQ96494 standard; DNA; 10 BP.  
XX  
AC AAQ96494;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 89.  
DE  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
ID AAQ96494 standard; DNA; 10 BP.  
XX  
AC AAQ96494;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 89.  
DE  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more

CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||  
2 GGGAG 6  
RESULT 18  
AAQ96490  
ID AAQ96490 standard; DNA; 10 BP.  
XX  
AC AAQ96490;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 85.  
DE  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||

Db 6 GGGAG 10

RESULT 19  
AAQ97066  
ID AAQ97066 standard; DNA; 10 BP.  
XX  
AC AAQ97066;  
XX  
DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 LTR nucleotide deletion 48.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.  
PT  
XX  
PS Claim 14; Page 196; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
1 GGGAG 5  
  
RESULT 20  
AAQ96709/c  
ID AAQ96709 standard; DNA; 10 BP.  
XX  
AC AAQ96709;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 304.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.  
PT  
XX  
PS Claim 13; Page 192; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 4 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
7 GGGAG 3  
  
RESULT 21  
AAQ96708/c  
ID AAQ96708 standard; DNA; 10 BP.  
XX  
AC AAQ96708;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 303.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.



XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 13; Page 192; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db |||||  
 8 GGGAG 4  
 RESULT 22  
 ID AAQ97061 standard; DNA; 10 BP.  
 XX  
 AC AAQ97061;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HIV-1 NL4-3 LTR nucleotide deletion 43.  
 XX  
 KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 OS  
 PN WO9521912-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX  
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 14; Page 196; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db |||||  
 6 GGGAG 10  
 RESULT 23  
 ID AAQ97064 standard; DNA; 10 BP.  
 XX  
 AC AAQ97064;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HIV-1 NL4-3 LTR nucleotide deletion 46.  
 XX  
 KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 OS  
 PN WO9521912-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX  
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 14; Page 196; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db |||||  
 3 GGGAG 7

RESULT 24  
AAQ88437  
ID AAQ88437 standard; DNA; 10 BP.  
XX  
AC AAQ88437;  
XX  
DT 19-DEC-1995 (first entry)  
XX  
DE Human mitochondrial D-loop region DNA probe 16-0.  
XX  
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
KW D-loop region; biological chip; hybridisation fingerprint;  
KW interrogation position; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 10  
FT /\*tag= a  
FT /note= "3'-end of probe is covalently attached to chip  
FT surface"  
XX  
PN WO9511995-A1.  
XX  
PD 04-MAY-1995.  
XX  
PF 26-OCT-1994; 94WO-US012305.  
XX  
PR 26-OCT-1993; 93US-00143312.  
PR 02-AUG-1994; 94US-00284064.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;  
PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;  
XX  
DR WPI; 1995-178887/23.  
XX  
PT New arrays of oligo:nucleotide probes - used for comparing known  
PT sequences with variants for detection of mutation(s) and sequencing.  
XX  
PS Disclosure; Page 106; 223pp; English.  
XX  
CC A DNA chip was prepared for analysing sequences contained in a 1.3kb  
CC fragment of human mitochondrial DNA from the D-loop region, the most  
CC polymorphic region of human mitochondrial DNA. The chip comprised a set  
CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of  
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm  
CC x 1cm array. Each position in the sequence was represented by at least  
CC one probe (usually 2 or more). DNA was amplified from six human donors  
CC and then transcribed to give the 1.3kb RNA transcripts which were  
CC fragmented and hybridised to the chip. For each individual, a unique  
CC hybridisation fingerprint was produced on the chip; all differences could  
CC be correlated with differences in the cloned genomic DNA sequence  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
6 GGGAG 10  
  
RESULT 25  
AAQ88493  
ID AAQ88493 standard; DNA; 10 BP.  
XX  
AC AAQ88493;  
XX

DT 20-DEC-1995 (first entry)  
XX  
DE Human mitochondrial D-loop region DNA probe 4-4.  
XX  
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
KW D-loop region; biological chip; hybridisation fingerprint;  
KW interrogation position; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 10  
FT /\*tag= a  
FT /note= "3'-end of probe is covalently attached to chip  
FT surface"  
XX  
PN WO9511995-A1.  
XX  
PD 04-MAY-1995.  
XX  
PF 26-OCT-1994; 94WO-US012305.  
XX  
PR 26-OCT-1993; 93US-00143312.  
PR 02-AUG-1994; 94US-00284064.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;  
PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;  
XX  
DR WPI; 1995-178887/23.  
XX  
PT New arrays of oligo:nucleotide probes - used for comparing known  
PT sequences with variants for detection of mutation(s) and sequencing.  
XX  
PS Disclosure; Page 107; 223pp; English.  
XX  
CC A DNA chip was prepared for analysing sequences contained in a 1.3kb  
CC fragment of human mitochondrial DNA from the D-loop region, the most  
CC polymorphic region of human mitochondrial DNA. The chip comprised a set  
CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of  
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm  
CC x 1cm array. Each position in the sequence was represented by at least  
CC one probe (usually 2 or more). DNA was amplified from six human donors  
CC and then transcribed to give the 1.3kb RNA transcripts which were  
CC fragmented and hybridised to the chip. For each individual, a unique  
CC hybridisation fingerprint was produced on the chip; all differences could  
CC be correlated with differences in the cloned genomic DNA sequence  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 8 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
5 GGGAG 9  
  
RESULT 26  
AAQ99831/c  
ID AAQ99831 standard; cDNA; 10 BP.  
XX  
AC AAQ99831;  
XX  
DT 06-MAR-1996 (first entry)  
XX  
DE Eucalyptus grandis coppicing vigour marker primer V2.  
XX  
KW Eucalyptus; urophylla; grandis; coppicing vigour marker;  
KW RAPD genetic marker; random amplified polymorphic DNA analysis;  
KW woody perennial plant; family selection; pedigree; mapping; primer; ss.

XX OS Synthetic.  
XX PN WO9519697-A1.  
XX 27-JUL-1995.  
XX PF 19-JAN-1995; 95WO-US000677.  
XX PR 21-JAN-1994; 94US-00184567.  
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX PI Omalley DM, Sederoff RR, Grattapaglia D;  
XX DR WPI; 1995-269212/35.  
XX PT Determn. of heritable oligogenic traits in woody plants by genomic  
PT mapping of multiple markers in a two generation plant family - used to  
PT select plants with desired characteristics for breeding.  
XX PS Example 6; Page 58; 103pp; English.  
XX CC RAPD analysis was used to determine whether certain quantitative traits  
CC were heritable oligogenic traits in Eucalyptus trees. Sets of  
CC commercially available random 10-mer primers were used to amplify  
CC fragments from the genomic DNA of E.urophylla, E.grandis and F1 progeny  
CC obtained by crossing the two species. Subsequent mapping analysis showed  
CC that the primers in AAO99829-Q99833 are all useful for amplifying markers  
CC of coppicing vigour from E.grandis  
XX SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
  
RESULT 27  
AAT10087/c  
ID AAT10087 standard; DNA; 10 BP.  
XX AC AAT10087;  
XX DT 29-AUG-1996 (first entry)  
XX DE Hammerhead ribozyme RNA complementary oligonucleotide.  
XX KW Hammerhead; ribozyme; enhanced RNA cleavage; cleavage efficiency;  
KW viral inactivation; viral RNA transcript; hybridisation; target RNA;  
KW complementary oligonucleotide; ss.  
XX OS Synthetic.  
XX PN WO9600232-A1.  
XX PD 04-JAN-1996.  
XX PF 21-JUN-1995; 95WO-AU000359.  
XX PR 24-JUN-1994; 94US-00265484.  
XX PA (GENE-) GENE SHEARS PTY LTD.  
XX PI Keese P, Stapper M, Perriman R;  
XX DR WPI; 1996-068825/07.  
XX PT Improved catalytic hammer-head ribozyme(s) and enhanced RNA cleavage -

PT useful in activating target sequences in e.g. infectious viruses.  
XX Example 3; Page 64; 122pp; English.  
XX CC The present oligonucleotide is a complementary oligonucleotide (CO) for  
CC the ribozyme given in AAT10062 or AAT10072, which are specific examples  
CC of a claimed, highly generic, hammerhead ribozyme with enhanced RNA  
CC cleavage. The CO alters the cleavage efficiency of the ribozymes, i.e.  
CC the cleavage efficiency of the CO in combination with a ribozyme as a %  
CC of a control without the CO is 161. The ribozymes of the invention (opt.  
CC in conjunction with a CO) have extensive therapeutic and biological  
CC applications, e.g. disease causing viruses in man, animals and plants may  
CC be inactivated by administering to an infected subject a ribozyme adapted  
CC to hybridise to, and cleave RNA transcripts of the virus  
XX SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
  
RESULT 28  
AAT98839/c  
ID AAT98839 standard; DNA; 10 BP.  
XX AC AAT98839;  
XX DT 20-MAR-1998 (first entry)  
XX DE Binding site BSN12 identified using the method of the invention.  
XX KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.  
XX OS Synthetic.  
XX PN WO9727330-A1.  
XX PD 31-JUL-1997.  
XX PF 24-JAN-1997; 97WO-US001230.  
XX PR 24-JAN-1996; 96US-00590571.  
XX PA (UYYA ) UNIV YALE.  
XX PI Weissman SM, Kulkarni P, Nallur GN;  
XX DR WPI; 1997-393714/36.  
XX PT Identifying protein-binding sites for DNA-binding proteins - using  
PT duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.  
XX PS Example 3; Page 19; 52pp; English.  
XX CC This sequence represents a binding site identified using the method of  
CC the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-

CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
9 GGGAG 5  
  
RESULT 29  
AAT98848  
ID AAT98848 standard; DNA; 10 BP.  
XX  
AC AAT98848;  
XX  
DT 20-MAR-1998 (first entry)  
XX  
DE Binding site BSN6 identified using the method of the invention.  
XX  
KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.  
XX  
OS Synthetic.  
XX  
PN WO9727330-A1.  
XX  
PD 31-JUL-1997.  
XX  
PF 24-JAN-1997; 97WO-US001230.  
XX  
PR 24-JAN-1996; 96US-00590571.  
XX  
PA (UYYA ) UNIV YALE.  
XX  
PI Weissman SM, Kulkarni P, Nallur GN;  
XX  
DR WPI; 1997-393714/36.  
XX  
PT Identifying protein-binding sites for DNA-binding proteins - using  
PT duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.  
XX  
PS Example 3; Page 19; 52pp; English.  
XX  
CC This sequence represents a binding site identified using the method of  
CC the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
3 GGGAG 7  
  
RESULT 30  
AAT98850  
ID AAT98850 standard; DNA; 10 BP.  
XX  
AC AAT98850;  
XX  
DT 20-MAR-1998 (first entry)  
XX  
DE Binding site BSN13 identified using the method of the invention.  
XX  
KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.  
XX  
OS Synthetic.  
XX  
PN WO9727330-A1.  
XX  
PD 31-JUL-1997.  
XX  
PF 24-JAN-1997; 97WO-US001230.  
XX  
PR 24-JAN-1996; 96US-00590571.  
XX  
PA (UYYA ) UNIV YALE.  
XX  
PI Weissman SM, Kulkarni P, Nallur GN;  
XX  
DR WPI; 1997-393714/36.  
XX  
PT Identifying protein-binding sites for DNA-binding proteins - using  
PT duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.  
XX  
PS Example 3; Page 19; 52pp; English.  
XX  
CC This sequence represents a binding site identified using the method of  
CC the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
6 GGGAG 10  
  
RESULT 31

```
AAV48046/c
ID AAV48046 standard; DNA; 10 BP.
XX
AC AAV48046;
XX
DT 19-OCT-1998 (first entry)
XX
DE Human B7-2 targetted oligonucleotide 10991.
XX
KW ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
KW cell proliferation.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /tag= a
FT /note= "Phosphorothioate linkages"
XX
PN WO9829124-A1.
XX
PD 09-JUL-1998.
XX
PF 16-DEC-1997; 97WO-US023270.
XX
PR 31-DEC-1996; 96US-00777266.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Vickers TA;
XX
DR WPI; 1998-387783/33.
XX
PT New oligo:nucleotide(s) that modulate expression of B7 proteins - used
PT for, e.g. controlling activation and proliferation of T cells,
PT particularly for treatment, diagnosis and prevention of inflammation.
XX
PS Example 1; Page 39; 120pp; English.
XX
CC The oligonucleotides which specifically hybridise to B7 modulate its
CC expression (and thus T cell activation and proliferation). This is
CC particularly useful for treatment and prevention of inflammation and
CC autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
CC Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
CC (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
CC rhinitis, allergy, cancer and metastases. The oligonucleotides may also
CC be used to manipulate T cell activation ex vivo; to determine or detect
CC B7 protein expression; for diagnosis; as assay and purification reagents,
CC and to study physiological roles of B7 proteins
XX
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 5 GGGAG 1

RESULT 32
AAZ86960
ID AAZ86960 standard; DNA; 10 BP.
XX
AC AAZ86960;
XX
DT 16-MAY-2000 (first entry)
XX
DE PCR primer for detection of genetic uniformity of a plant clone.
XX
KW PCR primer; genetic uniformity; plant clone body; detection; ss.
```

```
XX Synthetic.
OS
XX JP10262667-A.
PN
XX 06-OCT-1998.
PD
XX 19-MAR-1997; 97JJP-00106563.
PF
XX 19-MAR-1997; 97JJP-00106563.
PR
XX (SAOK ) NIPPON SEISHI KK.
PA
XX WPI; 1998-587287/50.
DR
XX New primer - used for the detection of genetic uniformity of a clone
XX plant body.
XX
PS Example 1; Page 5; 7pp; Japanese.
XX
CC This sequence represents an example of the PCR primer of the invention.
CC The primers of the invention consist of 10 bases and have the formula: 5'
CC -NNNN XY XY XY-3'; where: N, X and Y = optional nucleic acid monomers;
CC and N and X as well as N and Y may be nucleic acids having a same base
CC but X and Y are nucleic acids having different bases. The primers are
CC used to distinguish between plant clone bodies at the DNA level, with
CC high sensitivity
XX
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 3 GGGAG 7

RESULT 33
AAV34986
ID AAV34986 standard; DNA; 10 BP.
XX
AC AAV34986;
XX
DT 13-OCT-1998 (first entry)
XX
DE Synthetic Agaricus bisporus RAPD primer.
XX
KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
XX
OS Synthetic.
XX
PN WO9821975-A1.
XX
PD 28-MAY-1998.
XX
PF 19-NOV-1996; 96WO-US018686.
XX
PR 19-NOV-1996; 96WO-US018686.
XX
PA (AMYC-) AMYCEL INC.
XX
PI Loftus MG, Lodder SC, Legg EJ;
XX
DR WPI; 1998-312054/27.
XX
PT New strains of Agaricus bisporus with improved cap whiteness - compared
PT with the U1 strain but retaining other desirable features of this strain.
XX
PS Disclosure; Page 10; 26pp; English.
XX
CC The sequence is that of an RAPD (random amplified DNA) primer which was
```

CC used in the isolation of an Agaricus bisporus mushroom strain which has  
CC whiter caps, less scaling than known strains, particularly for mushrooms  
CC produced in the first break, so it is more valuable (suitable for  
CC marketing fresh rather than canning). It also retains the desirable  
CC characteristics (good cap shape and shelf life, thick stem and veil) of  
CC the U1 strain  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 1 GGGAG 5  
  
RESULT 34  
AAV50112/c  
ID AAV50112 standard; DNA; 10 BP.  
XX  
AC AAV50112;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for NORF gene locus NORF2.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
PN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-427943/36.  
XX  
PS Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 1; Page 23; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of  
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to

CC AAV50345), or as an array of probes on a solid support  
XX Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
SQ  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 8 GGGAG 4  
  
RESULT 35  
AAV50300/c  
ID AAV50300 standard; DNA; 10 BP.  
XX  
AC AAV50300;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for additional NORF chromosome 11 tag position 93528.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
PN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-427943/36.  
XX  
PT Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 1; Page 27; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of  
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to  
CC AAV50345), or as an array of probes on a solid support  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;



Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
6 GGGAG 2

Db

RESULT 36  
AAV50068/c  
ID AAV50068 standard; DNA; 10 BP.  
XX  
AC AAV50068;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for highly expressed gene locus NORF2.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
PN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX WPI; 1998-427943/36.  
DR  
PT Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 11; Page 21; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of  
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to  
CC AAV50345), or as an array of probes on a solid support  
XX  
SQ Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|

Db 8 GGGAG 4

RESULT 37  
AAV35939/c  
ID AAV35939 standard; DNA; 10 BP.  
XX  
AC AAV35939;  
XX  
DT 26-AUG-1998 (first entry)  
XX  
DE Primer used in RAPD assay of the invention.  
XX  
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX  
OS Synthetic.  
OS Sus sp.  
XX  
PN WO9815837-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 07-OCT-1997; 97WO-GB002741.  
XX  
PR 07-OCT-1996; 96GB-00020904.  
PR 18-FEB-1997; 97GB-00003350.  
PR 20-MAR-1997; 97GB-00005796.  
PR 09-SEP-1997; 97GB-00019002.  
XX  
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX  
PI Maltin CA, Steven J, Warkup CC;  
XX WPI; 1998-240968/21.  
DR  
XX  
PT Assay for alleles or muscle fibre composition characteristic of Duroc  
PT type pigs - comprises determination of genotype or muscle fibre  
PT properties, used to identify animals for breeding programs and to assess  
PT meat quality.  
XX  
PS Example 3; Page 33; 56pp; English.  
XX  
CC PCR primers AAV35877-996 were used in a rapid amplification of  
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
CC is used to determine if an animal has an allele for, or muscle fibre  
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
CC meat of superior quality (particularly tenderness) but are normally less  
CC efficient feed converters and fatter than other types. The assay  
CC comprises analysing a tissue sample to determine if the genotype  
CC comprises the allele, and genetic features typical of animals with Duroc-  
CC type MFC are present. The method is used to select animals that have  
CC Duroc characteristics for use in breeding programmes (to develop the  
CC animals with Duroc pig characteristics), and to assess meat quality  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
7 GGGAG 3

Db

RESULT 38  
AAV35998  
ID AAV35998 standard; DNA; 10 BP.  
XX  
AC AAV35998;  
XX  
DT 26-AUG-1998 (first entry)



XX DE Primer used in to show differences in Large white and Duroc genotypes.  
XX KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
XX KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX OS Synthetic.  
XX OS Sus sp.  
XX PN WO9815837-A1.  
XX PD 16-APR-1998.  
XX PF 07-OCT-1997; 97WO-GB002741.  
XX PR 07-OCT-1996; 96GB-00020904.  
XX PR 18-FEB-1997; 97GB-00003350.  
XX PR 20-MAR-1997; 97GB-00005796.  
XX PR 09-SEP-1997; 97GB-00019002.  
XX PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX PI Maltin CA, Steven J, Warkup CC;  
XX PI WPI; 1998-240968/21.  
XX DR Assay for alleles or muscle fibre composition characteristic of Duroc  
XX PT type pigs - comprises determination of genotype or muscle fibre  
XX PT properties, used to identify animals for breeding programs and to assess  
XX PT meat quality.  
XX PS Example 3; Page 35; 56pp; English.  
XX SS PCR primers AAV35997-6013 were used in a rapid amplification of  
XX CC polymorphic DNA (RAPD) assay to show differences in the Large white and  
XX CC Duroc genotype using the assay of the invention. This assay is used to  
XX CC determine if an animal has an allele for, or muscle fibre composition  
XX CC (MFC) characteristic of, the Duroc pig. Duroc pigs produce meat of  
XX CC superior quality (particularly tenderness) but are normally less  
XX CC efficient feed converters and fatter than other types. The assay  
XX CC comprises analysing a tissue sample to determine if the genotype  
XX CC comprises the allele, and genetic features typical of animals with Duroc-  
XX CC type MFC are present. The method is used to select animals that have  
XX CC Duroc characteristics for use in breeding programmes (to develop the  
XX CC animals with Duroc pig characteristics), and to assess meat quality  
XX SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db 3 GGGAG 7  
RESULT 39  
AAV35963/c  
ID AAV35963 standard; DNA; 10 BP.  
XX AC AAV35963;  
XX DT 26-AUG-1998 (first entry)  
XX DE Primer used in RAPD assay of the invention.  
XX KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
XX KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX OS Synthetic.  
XX OS Sus sp.  
XX XX

PN WO9815837-A1.  
XX PD 16-APR-1998.  
XX PF 07-OCT-1997; 97WO-GB002741.  
XX PR 07-OCT-1996; 96GB-00020904.  
XX PR 18-FEB-1997; 97GB-00003350.  
XX PR 20-MAR-1997; 97GB-00005796.  
XX PR 09-SEP-1997; 97GB-00019002.  
XX PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX PI Maltin CA, Steven J, Warkup CC;  
XX PI WPI; 1998-240968/21.  
XX DR Assay for alleles or muscle fibre composition characteristic of Duroc  
XX PT type pigs - comprises determination of genotype or muscle fibre  
XX PT properties, used to identify animals for breeding programs and to assess  
XX PT meat quality.  
XX PS Example 3; Page 33; 56pp; English.  
XX SS PCR primers AAV35877-996 were used in a rapid amplification of  
XX CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
XX CC is used to determine if an animal has an allele for, or muscle fibre  
XX CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
XX CC meat of superior quality (particularly tenderness) but are normally less  
XX CC efficient feed converters and fatter than other types. The assay  
XX CC comprises analysing a tissue sample to determine if the genotype  
XX CC comprises the allele, and genetic features typical of animals with Duroc-  
XX CC type MFC are present. The method is used to select animals that have  
XX CC Duroc characteristics for use in breeding programmes (to develop the  
XX CC animals with Duroc pig characteristics), and to assess meat quality  
XX SQ Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db 10 GGGAG 6  
RESULT 40  
AAV60193/c  
ID AAX60193 standard; DNA; 10 BP.  
XX AC AAX60193;  
XX DT 10-AUG-1999 (first entry)  
XX DE Pyrimidinone derivative of the invention.  
XX KW Pyrimidinone derivative; labeled binding partner; diagnostic assay;  
XX KW antisense; transfection complex; primer; probe; ss.  
XX OS Synthetic.  
XX PN WO9924452-A2.  
XX PD 20-MAY-1999.  
XX PF 30-OCT-1998; 98WO-US023119.  
XX PR 07-NOV-1997; 97US-00966392.  
XX PR 10-NOV-1997; 97US-00966875.  
XX PA (ISIS-) ISIS PHARM INC.  
XX XX

PI Lin K, Matteucci MD;  
XX WPI; 1999-370671/31.  
DR  
XX Composition comprising pyrimidinone derivatives for diagnostic and  
PT analytical labels.  
XX  
XX Example 4; Page 87; 101pp; English.  
PS  
XX The specification describes pyrimidinone derivatives. These derivatives  
CC are used as labeled binding partners, particularly as labels for  
CC diagnostic, analytical and therapeutic applications. The derivatives are  
CC used as detectable labels for diagnostic assays, to enhance diagnostic  
CC assays that use oligonucleotides and to improve potency of  
CC oligonucleotides as antisense reagents that affect gene expression by  
CC altering intracellular metabolism of complementary RNA sequences encoding  
CC a target gene. They are also used in transfection complexes to deliver  
CC oligonucleotides into cell cytoplasm and in PCR e.g. as primers, and  
CC ligase chain reaction (LCR) e.g. as probes. The derivatives have  
CC increased affinity and specificity for their complementary sequences and  
CC facilitate PCR and LCR processes. The present sequence represents a  
CC pyrimidinone derivative of the invention  
XX  
SQ Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
6 GGGAG 2  
  
RESULT 41  
AAZ07930  
ID AAZ07930 standard; DNA; 10 BP.  
XX  
AC AAZ07930;  
XX  
DT 20-DEC-1999 (first entry)  
XX  
DE Interferon-alpha-inducible gene specific SAGE tag sequence.  
XX  
KW Neoplasia; lung cell; proto-oncogene; b-myb; p67; PGP9.5; 8-oxo-dGTPase;  
KW diagnosis; lung cancer; SAGE; Serial Analysis of Gene Expression; NSCLC;  
KW ss.  
XX  
OS Synthetic.  
XX WO9949774-A2.  
XX  
XX 07-OCT-1999.  
XX  
PF 30-MAR-1999; 99WO-US006947.  
XX  
PR 31-MAR-1998; 98US-0080044P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Jen J, Beaudry GA, Madden SL, Bertelsen AH;  
PI  
XX WPI; 1999-580562/49.  
XX  
PT Diagnosing lung cancer by detecting over-expression of specific proto-  
PT oncogenes, and screening for therapeutic agents that inhibit over-  
PT expression.  
XX  
XX Example; Page 34; 51pp; English.  
PS  
XX The invention relates to the diagnosis of neoplasia of lung cells that  
CC comprises detecting over-expression of one of the proto-oncogenes b-myb,

CC p67, PGP9.5 and 8-oxo-dGTPase. The method is used for diagnosis, and  
CC monitoring, of lung cancer, or predisposition to this disease,  
CC particularly non-small cell lung cancer (NSCLC). Therapeutic agents that  
CC inhibit over-expression of the oncogenes are used to treat lung cancer,  
CC also to prevent progression of pre-neoplastic or non-malignant states.  
CC The specified proto-oncogenes have been found to be expressed in many  
CC primary lung cancers. The method is useful for the early diagnosis and  
CC monitoring of lung cancer. Sequences AAZ07926-938 represents SAGE tag  
CC sequences used in SAGE (Serial Analysis of Gene Expression) analysis of  
CC genes overexpressed NSCLC  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db |||||  
5 GGGAG 9  
  
RESULT 42  
AAV81860  
ID AAV81860 standard; DNA; 10 BP.  
XX  
AC AAV81860;  
XX  
DT 11-MAR-1999 (first entry)  
XX  
DE Human rchd528 forward primer OPI19.  
XX  
KW Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;  
KW primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX US5849578-A.  
XX  
XX 15-DEC-1998.  
XX  
XX 15-MAR-1996; 96US-00616844.  
XX  
XX 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00458873.  
PR 09-FEB-1996; 96US-00599654.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Falb DA;  
PI  
XX WPI; 1999-069743/06.  
XX  
PT DNA encoding rchd528 polypeptide - associated with cardiovascular  
PT disease.  
XX  
XX Example; Col 105; 122pp; English.  
XX  
XX The present invention describes rchd528 protein. A method has been  
CC developed for producing the rchd528 gene product. The present invention  
CC also describes methods and compositions for the treatment and diagnosis  
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
CC present sequence represents a primer used in an example from the present  
CC invention  
XX  
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 43  
AAV81846/C  
ID AAV81846 standard; DNA; 10 BP.  
XX  
AC AAV81846;  
DT 11-MAR-1999 (first entry)  
XX  
DE Human interleukin-1 forward primer OPG20.  
XX  
KW Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;  
KW primer; ss.  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5849578-A.  
XX  
PD 15-DEC-1998.  
XX  
PF 15-MAR-1996; 96US-00616844.  
XX  
PR 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00458873.  
PR 09-FEB-1996; 96US-00599654.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Falb DA;  
XX  
DR WPI; 1999-069743/06.  
XX  
PT DNA encoding rchd528 polypeptide - associated with cardiovascular  
PT disease.  
XX  
PS Example; Col 99; 122pp; English.  
XX  
CC The present invention describes rchd528 protein. A method has been  
CC developed for producing the rchd528 gene product. The present invention  
CC also describes methods and compositions for the treatment and diagnosis  
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
CC present sequence represents a primer used in an example from the present  
CC invention  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 2

RESULT 44  
AAAX14900  
ID AAAX14900 standard; DNA; 10 BP.  
XX  
AC AAAX14900;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix forming nucleotides 149-158 of 23S rRNA gene.  
XX

KW Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
OS Clostridium pasteurianum.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
DR WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 23-24; 168pp; English.  
XX  
CC The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 45  
AAAX14813/C  
ID AAAX14813 standard; DNA; 10 BP.  
XX  
AC AAAX14813;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix third strand of Hepatitis B virus nucleotides 427-436.  
XX  
KW Triplex formation; DNA detection; triple helix; identification; bacteria;  
KW oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Hepatitis B virus.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
PA Hepburn AG, Wang C;  
PI WPI; 1999-130384/11.  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX Disclosure; Col 19-20; 168pp; English.  
PS The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GGGAG 5  
Db 7 GGGAG 3  
  
RESULT 46  
AAX14782  
ID AAX14782 standard; DNA; 10 BP.  
XX  
AC AAX14782;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix forming nucleotides 3071-3080 of Hepatitis B virus.  
XX  
KW Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
XX  
OS Hepatitis B virus.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
DR WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify

PT bacteria.  
XX Disclosure; Col 19-20; 168pp; English.  
XX  
CC The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GGGAG 5  
Db 3 GGGAG 7  
  
RESULT 47  
AAX26269  
ID AAX26269 standard; DNA; 10 BP.  
XX  
AC AAX26269;  
XX  
DT 24-MAY-1999 (first entry)  
XX  
DE Forward primer OPI19.  
XX  
KW Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5882925-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 09-FEB-1996; 96US-00599654.  
XX  
PR 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00485573.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Falb DA;  
XX  
DR WPI; 1999-214071/18.  
XX  
PT New polynucleotides consisting of residues 1-1929 of the rchd502 gene -  
PT are differentially expressed in cardiovascular disease states, and can  
PT therefore be used to treat and diagnose cardiovascular diseases.  
XX  
PS Disclosure; Col 11; 121pp; English.  
XX  
CC The invention relates to a rchd502 target/fingerprint gene encoding a  
CC transmembrane protein. The invention provides cDNAs contained in plasmids  
CC pFCHD502SF (ATCC 69981) and pFCHD502SJ (ATCC 69982) that encode the  
CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
CC disease states. Cultured genetically engineered host cell containing the  
CC rchd502 polynucleotides in operative association with a nucleotide

CC regulatory element are used for producing a polypeptide rchd502 gene  
CC product. Identifying that the fingerprint/target gene rchd502 is  
CC differentially expressed (up-regulated) by endothelial cells subjected to  
CC shear-stress, provides a tool for the diagnosis and treatment of  
CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
CC hypertension, restenosis. The fingerprint gene is useful for testing the  
CC efficacy of candidate drugs in basic research and in clinical trials and  
CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
CC in screening for ligands of target gene product receptor domains, as well  
CC as antagonists of the ligand-receptor interaction

XX  
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 48  
AAX26259/C  
ID AAX26259 standard; DNA; 10 BP.  
XX  
AC AAX26259;  
XX 24-MAY-1999 (first entry)  
XX Forward primer OPG20.  
XX Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX US5882925-A.  
XX 16-MAR-1999.  
XX  
XX 09-FEB-1996; 96US-00599654.  
XX 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00485573.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Falb DA;  
XX  
DR WPI; 1999-214071/18.  
XX  
PT New polynucleotides consisting of residues 1-1929 of the rchd502 gene -  
PT are differentially expressed in cardiovascular disease states, and can  
PT therefore be used to treat and diagnose cardiovascular diseases.  
XX  
PS Disclosure; Col 10; 121pp; English.  
XX  
CC The invention relates to a rchd502 target/fingerprint gene encoding a  
CC transmembrane protein. The invention provides cDNAs contained in plasmids  
CC pFCHD502SF (ATCC 69981) and pFCHD502SJ (ATCC 69982) that encode the  
CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
CC disease states. Cultured genetically engineered host cell containing the  
CC rchd502 polynucleotides in operative association with a nucleotide  
CC regulatory element are used for producing a polypeptide rchd502 gene  
CC product. Identifying that the fingerprint/target gene rchd502 is  
CC differentially expressed (up-regulated) by endothelial cells subjected to  
CC shear-stress, provides a tool for the diagnosis and treatment of  
CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
CC hypertension, restenosis. The fingerprint gene is useful for testing the

CC efficacy of candidate drugs in basic research and in clinical trials and  
CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
CC in screening for ligands of target gene product receptor domains, as well  
CC as antagonists of the ligand-receptor interaction

XX  
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 6 GGGAG 2

RESULT 49  
AAZ28332  
ID AAZ28332 standard; cDNA; 10 BP.  
XX  
AC AAZ28332;  
XX 20-DEC-1999 (first entry)  
XX Lung cancer indicator polynucleotide #12.  
DE  
XX Lung cancer; tumour; primary squamous cell; gene expression pattern; ss;  
KW antibody; detect; diagnosis; transgenic animal; p27 gene.  
XX Homo sapiens.  
XX WO9950278-A1.  
XX 07-OCT-1999.  
XX 30-MAR-1999; 99WO-US006938.  
XX 31-MAR-1998; 98US-0080037P.  
XX (GENZ ) GENZYME CORP.  
XX Beaudry GA, Madden SL, Bertelsen AH;  
DR WPI; 1999-591271/50.  
XX  
PT Polynucleotides which are differentially expressed in lung cancer, used  
PT for diagnosis and screening for therapeutic agents.  
XX  
PS Claim 1; Page 50; 69pp; English.  
XX  
CC Sequences AAZ28321-Z28360 are polynucleotides isolated from primary  
CC squamous cell lung cancers of two patients. These sequences represent a  
CC profile of gene expression patterns in lung cancer. Sequences AAZ28321-  
CC Z28360 correspond to previously characterised genes, this sequence  
CC corresponds to the p27 gene. Sequences AAZ28341-Z28360 do not correspond  
CC to known genes, although some do correspond to reported Expressed  
CC Sequence Tags (ESTs). The presence of these polynucleotide sequences in  
CC lung cells is indicative of lung cancer. The sequences can be used to  
CC generate antibodies for the detection of tumour cells. Detection of the  
CC overexpression of the polynucleotides and their gene products can be used  
CC in the diagnosis of lung cancer or the susceptibility to the disease. The  
CC sequences can also be used to screen for agents potentially useful for  
CC treating lung cancer and to generate transgenic animals (for studying  
CC gene function and for drug screening)

XX  
SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 6 GGGAG 2

Db 5 GGGAG 9

RESULT 50  
AAX86246  
ID AAX86246 standard; DNA; 10 BP.  
XX  
AC AAX86246;  
XX  
DT 22-SEP-1999 (first entry)  
XX  
DE SAGE tag used to identify transcripts which are decreased by p53.  
XX  
KW p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;  
KW neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9914356-A2.  
XX  
PD 25-MAR-1999.  
XX  
PF 17-SEP-1998; 98WO-US019300.  
XX  
PR 17-SEP-1997; 97US-0059153P.  
PR 30-MAR-1998; 98US-0079817P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW, Polyak K;  
XX  
DR WPI; 1999-443793/37.  
XX  
PT Use of p53 transcription tags to determine p53 status in, e.g. cancer  
PT diagnosis.  
XX  
PS Claim 2; Page 29; 73pp; English.  
XX  
CC The specification describes the use of p53 transcription tags for  
CC developing products to determine p53 status, to diagnose cancer and to  
CC evaluate cytotoxicity or carcinogenicity of a test agent. A method for  
CC diagnosing cancer or determining p53 status in a sample suspected for  
CC being neoplastic comprises comparing the level of transcription of an RNA  
CC transcript in a first sample (s1) of a first tissue (t1) to the level of  
CC transcription of the transcript in a second sample (s2) of a second  
CC tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal  
CC human tissue (of the same type) and the transcript is identified by a tag  
CC ; and categorizing s1 as neoplastic or as having a mutant p53 when  
CC transcription is found to be the same or lower in the first, than in s2.  
CC The methods and products can be used to determine p53 status, to diagnose  
CC cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.  
CC AAX86233-64 represent SAGE tags used to identify transcripts which are  
CC decreased by p53  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. NO. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 3 GGGAG 7

Search completed: January 7, 2005, 07:12:01  
Job time : 259.4 secs

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OM nucleic - nucleic search, using sw model  
Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GGGAG  
Perfect score: 5  
Sequence: 1 gggag 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	10	9	CL436411
C 2	5	100.0	10	9	CL436421
C 3	5	100.0	10	9	CL437642
C 4	5	100.0	10	9	CL439219
C 5	5	100.0	11	1	AJ648107
C 6	5	100.0	11	1	AJ655479
C 7	5	100.0	11	1	AJ657108
C 8	5	100.0	11	5	BQ591023
C 9	5	100.0	11	9	CL437735
C 10	5	100.0	11	9	CL657848
C 11	5	100.0	12	1	AJ679735
C 12	5	100.0	12	9	AJ587934
C 13	5	100.0	12	9	AJ592591
C 14	5	100.0	12	9	AJ594389
C 15	5	100.0	13	4	BG926067
C 16	5	100.0	13	4	BM399550
C 17	5	100.0	13	9	AJ593426
C 18	5	100.0	13	9	CL437499
C 19	5	100.0	13	9	CL690995
C 20	5	100.0	14	1	AJ686563
C 21	5	100.0	14	5	BQ593808
C 22	5	100.0	15	1	AJ682954
C 23	5	100.0	15	1	AJ686764
C 24	5	100.0	15	6	CF304766

25	5	100.0	16	1	AA968729	AA968729	or69hl1.8
C 26	5	100.0	16	1	AI075064	AI075064	ou61gl1.x
C 27	5	100.0	16	1	AI094839	AI094839	qa22c08.x
C 28	5	100.0	16	1	AI274782	AI274782	qv67h03.x
C 29	5	100.0	16	1	AI560058	AI560058	tc38hl1.x
C 30	5	100.0	16	1	AI569544	AI569544	tc28dl0.x
C 31	5	100.0	16	5	BQ588093	BQ588093	E012336-0
C 32	5	100.0	16	8	BZ424445	BZ424445	100012843
C 33	5	100.0	16	9	AJ589788	AJ589788	Arabidops
C 34	5	100.0	16	9	AJ595245	AJ595245	Arabidops
C 35	5	100.0	16	9	AJ598372	AJ598372	Arabidops
C 36	5	100.0	17	1	AJ666397	AJ666397	AJ666397
C 37	5	100.0	17	2	AW246940	AW246940	2822481.5
C 38	5	100.0	17	4	BG926068	BG926068	HNC23-1-E
C 39	5	100.0	17	9	AJ589066	AJ589066	Arabidops
C 40	5	100.0	17	9	AJ599163	AJ599163	Arabidops
C 41	5	100.0	18	1	AJ648240	AJ648240	Arabidops
C 42	5	100.0	18	2	AW250267	AW250267	2821151.5
C 43	5	100.0	18	4	BG896958	BG896958	HOA59-1-D
C 44	5	100.0	18	4	BG925410	BG925410	HNC5-1-B6
C 45	5	100.0	18	4	BG925569	BG925569	HNC5-1-E2
C 46	5	100.0	18	4	BM397051	BM397051	5009-0-28
C 47	5	100.0	18	4	BM397051	BM397051	5009-0-28
C 48	5	100.0	18	4	BM397954	BM397954	5009-0-39
C 49	5	100.0	18	4	BM398017	BM398017	5009-0-4-
C 50	5	100.0	18	4	BM399858	BM399858	5009-0-62
C 51	5	100.0	18	6	CF306437	CF306437	HDA1--03-
C 52	5	100.0	18	7	CR555236	CR555236	DKFZp468N
C 53	5	100.0	18	9	AJ587621	AJ587621	Arabidops
C 54	5	100.0	18	9	AJ600946	AJ600946	Arabidops
C 55	5	100.0	18	9	CL438119	CL438119	PST6842-N
C 56	5	100.0	18	9	CL438990	CL438990	PST8480-N
C 57	5	100.0	19	1	AA885444	AA885444	aml4h07.8
C 58	5	100.0	19	1	AA912825	AA912825	ol43dl1.8
C 59	5	100.0	19	1	AA918795	AA918795	ol69c05.8
C 60	5	100.0	19	1	AA934650	AA934650	oo7ldl0.8
C 61	5	100.0	19	1	AI033338	AI033338	ox02d04.8
C 62	5	100.0	19	1	AI049374	AI049374	ub33a03.r
C 63	5	100.0	19	1	AI251781	AI251781	qu76g01.x
C 64	5	100.0	19	1	AI360784	AI360784	qx98g07.x
C 65	5	100.0	19	1	AI648553	AI648553	tz55e07.x
C 66	5	100.0	19	1	AI696833	AI696833	wc74e09.x
C 67	5	100.0	19	1	AI719958	AI719958	aa4ld06.x
C 68	5	100.0	19	1	AI747751	AI747751	ul2lh05.x
C 69	5	100.0	19	1	AI758301	AI758301	ty06a07.x
C 70	5	100.0	19	1	AI811474	AI811474	tw43c04.x
C 71	5	100.0	19	1	AJ660242	AJ660242	AJ660242
C 72	5	100.0	19	1	AJ662060	AJ662060	AJ662060
C 73	5	100.0	19	1	AJ666284	AJ666284	AJ666284
C 74	5	100.0	19	1	AJ686305	AJ686305	AJ686305
C 75	5	100.0	19	1	AJ696991	AJ696991	AJ696991
C 76	5	100.0	19	5	BQ593604	BQ593604	E012766-0
C 77	5	100.0	19	5	BX557717	BX557717	BX557717
C 78	5	100.0	19	6	C00981	C00981	HUMGS000337
C 79	5	100.0	19	6	CF306225	CF306225	HDA1--03-
C 80	5	100.0	19	6	CF307006	CF307006	HDA1--05-
C 81	5	100.0	19	6	CF307304	CF307304	HDA1--06-
C 82	5	100.0	19	6	CF307439	CF307439	HDA1--06-
C 83	5	100.0	19	8	AZ307462	AZ307462	1M0009I08
C 84	5	100.0	19	8	AZ307686	AZ307686	1M0009B05
C 85	5	100.0	19	8	AZ309643	AZ309643	1M0016E23
C 86	5	100.0	19	8	AZ309874	AZ309874	1M0017C14
C 87	5	100.0	19	8	AZ313113	AZ313113	1M0029N17
C 88	5	100.0	19	8	AZ324165	AZ324165	1M0046C06
C 89	5	100.0	19	8	AZ343228	AZ343228	1M0076M05
C 90	5	100.0	19	8	AZ345792	AZ345792	1M0080G12
C 91	5	100.0	19	8	AZ379786	AZ379786	1M0135K09
C 92	5	100.0	19	8	AZ400662	AZ400662	1M0167K06
C 93	5	100.0	19	8	AZ412553	AZ412553	1M0186M03
C 94	5	100.0	19	8	AZ418201	AZ418201	1M0194M12
C 95	5	100.0	19	8	AZ420252	AZ420252	1M0198G01
C 96	5	100.0	19	8	AZ422762	AZ422762	1M0201P12
C 97	5	100.0	19	8	AZ430028	AZ430028	1M0214L16

98	5	100.0	19	8	AZ432757	1M0218L14
C 99	5	100.0	19	8	AZ440106	1M0231G04
C 100	5	100.0	19	8	AZ442378	1M0236KP8
C 101	5	100.0	19	8	AZ443948	1M0238P04
C 102	5	100.0	19	8	AZ445563	1M0241P18
C 103	5	100.0	19	8	AZ447248	1M0244H23
C 104	5	100.0	19	8	AZ447414	1M0244L06
C 105	5	100.0	19	8	AZ463791	1M0272C22
106	5	100.0	19	8	AZ477353	1M0296K16
C 107	5	100.0	19	8	AZ505490	1M0346N08
C 108	5	100.0	19	8	AZ510143	1M0354P21
C 109	5	100.0	19	8	AZ512762	1M0358M04
C 110	5	100.0	19	8	AZ514405	1M0361L03
C 111	5	100.0	19	8	AZ579189	1M0363I12
C 112	5	100.0	19	8	AZ595016	1M0407C19
C 113	5	100.0	19	8	AZ597219	1M0411K23
114	5	100.0	19	8	AZ600709	1M0418H10
C 115	5	100.0	19	8	AZ647364	1M0513O16
116	5	100.0	19	8	AZ654214	1M0528H13
117	5	100.0	19	8	AZ656937	1M0532K13
118	5	100.0	19	8	AZ759944	1M0553O10
C 119	5	100.0	19	8	AZ760597	1M0554N21
120	5	100.0	19	8	AZ762504	1M0557M14
C 121	5	100.0	19	8	AZ783420	2M0025D07
122	5	100.0	19	8	AZ786308	2M0031B17
123	5	100.0	19	8	AZ804081	2M0064I18
124	5	100.0	19	8	AZ807034	2M0069B05
125	5	100.0	19	8	AZ808178	2M0071A15
126	5	100.0	19	8	AZ819494	2M0091I10
127	5	100.0	19	8	AZ822954	2M0096I10
C 128	5	100.0	19	8	AZ835034	2M0129K04
C 129	5	100.0	19	8	AZ842379	2M0140N17
130	5	100.0	19	8	AZ949895	2M0213N08
131	5	100.0	19	8	AZ967656	2M0238M09
C 132	5	100.0	19	8	AZ990851	2M0274E15
C 133	5	100.0	19	8	BH000474	2M0288B20
C 134	5	100.0	19	9	AJ600497	Arabidops
135	5	100.0	19	9	CL657666	PR1012a_H
C 136	5	100.0	20	1	AJ652453	AJ652453
C 137	5	100.0	20	1	AJ696560	AJ696560
138	5	100.0	20	1	AJ798166	AJ798166
139	5	100.0	20	1	AJ808084	AJ808084
C 140	5	100.0	20	4	BM397553	5009-0-34
C 141	5	100.0	20	4	BM398892	5009-0-50
C 142	5	100.0	20	4	BM399755	5009-0-60
143	5	100.0	20	5	BX558127	BX558127
C 144	5	100.0	20	6	C21208	HUMGS000223
C 145	5	100.0	20	6	CF293092	30DGS--02
C 146	5	100.0	20	6	CF302285	7LEAF--07
C 147	5	100.0	20	6	CF306206	HDA1--03-
C 148	5	100.0	20	6	CF306357	HDA1--03-
149	5	100.0	20	6	CF306620	HDA1--04-
C 150	5	100.0	20	6	CF307027	HDA1--05-
C 151	5	100.0	20	6	CF307105	HDA1--05-
C 152	5	100.0	20	6	CF307109	HDA1--05-
C 153	5	100.0	20	6	CF307258	HDA1--06-
C 154	5	100.0	20	6	CF307503	HDA1--06-
155	5	100.0	20	6	CF327699	NACL--02-
C 156	5	100.0	20	6	CF339843	RCL1--06-
C 157	5	100.0	20	7	CF932153	SP1-A4 (P6
158	5	100.0	20	7	CN752083	ApHL3SD-X
159	5	100.0	20	7	CO779101	BL005C_F0
C 160	5	100.0	20	7	CO785157	BL282C_H0
161	5	100.0	20	8	AQ074235	21_pUC8_P
162	5	100.0	20	8	AZ308179	1M0010K19
C 163	5	100.0	20	8	AZ308311	1M0011J12
C 164	5	100.0	20	8	AZ309592	1M0016N09
165	5	100.0	20	8	AZ313204	1M0029P19
C 166	5	100.0	20	8	AZ345513	1M0080J04
C 167	5	100.0	20	8	AZ345583	1M0080L18
168	5	100.0	20	8	AZ357114	1M0098B06
C 169	5	100.0	20	8	AZ368205	1M0118L07
170	5	100.0	20	8	AZ388212	1M0148A10

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C 265	5	100.0	21	8	AZ808542	2M0072E10
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287	5	100.0	21	9	CL695388	PR1016b
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C 291	5	100.0	21	9	AG203673	Pan trogl
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295	5	100.0	22	1	AA912871	cl27a02.s
296	5	100.0	22	1	AA927363	om69g11.s
C 297	5	100.0	22	1	AA953209	oo87b11.s
C 298	5	100.0	22	1	AA953755	on89b03.s
299	5	100.0	22	1	AA996014	os26d08.s
C 300	5	100.0	22	1	AI040053	ox28b01.x
C 301	5	100.0	22	1	AI088271	qa86g08.s
C 302	5	100.0	22	1	AI118718	uc11h07.r
C 303	5	100.0	22	1	AI183338	qd41a12.x
C 304	5	100.0	22	1	AI339084	qq29h01.x
C 305	5	100.0	22	1	AI416500	sal10g04.x
306	5	100.0	22	1	AI434548	ti49d05.x
C 307	5	100.0	22	1	AI440140	ti62d04.x
C 308	5	100.0	22	1	AI473941	tm04c11.x
309	5	100.0	22	1	AI560825	tg40d09.x
C 310	5	100.0	22	1	AI567845	tg87e02.x
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C 312	5	100.0	22	1	AI582080	ar96b07.x
C 313	5	100.0	22	1	AI630912	tz31g03.x
314	5	100.0	22	1	AI664440	ue62c03.r
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C 323	5	100.0	22	1	AJ684402	AJ684402
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C 326	5	100.0	22	4	BM398330	5009-0-44
C 327	5	100.0	22	4	BM399475	5009-0-58
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385	5	100.0	22	9	TA223E07P	AL480269 T. brucei
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C 391	5	100.0	23	1	AU007064	AU007064	AU007064
C 392	5	100.0	23	1	AU258717	AU258717	AU258717
C 393	5	100.0	23	2	AW245303	2822872.3	AW245303
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C 397	5	100.0	23	4	BG926063	HNC23-1-E	BG926063
C 398	5	100.0	23	4	BG926069	HNC23-1-E	BG926069
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401	5	100.0	23	4	BM394302	50072-2-3	BM394302
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C 403	5	100.0	23	4	BM399821	5009-0-62	BM399821
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C 417	5	100.0	23	8	AZ445460	1M0241J16	AZ445460
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C 419	5	100.0	23	8	AZ451117	1M0250A16	AZ451117
C 420	5	100.0	23	8	AZ456925	1M0260J06	AZ456925
C 421	5	100.0	23	8	AZ462625	1M0269C11	AZ462625
C 422	5	100.0	23	8	AZ467018	1M0278E09	AZ467018
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C 429	5	100.0	23	8	AZ512174	1M0357K05	AZ512174
C 430	5	100.0	23	8	AZ512953	1M0358B20	AZ512953
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C 452	5	100.0	23	8	AZ800632	2M0058E17	AZ800632
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C 455	5	100.0	23	8	AZ814933	2M0082G21	AZ814933
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C 474	5	100.0	23	9	AG202994	Pan trogl	AG202994
475	5	100.0	24	1	AJ647132	AJ647132	AJ647132
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478	5	100.0	24	1	AJ685689	AJ685689	AJ685689
C 479	5	100.0	24	4	BG925568	HNC5-1-E1	BG925568
C 480	5	100.0	24	4	BG925905	HNC6-1-B1	BG925905
C 481	5	100.0	24	4	BM398765	5009-0-49	BM398765
C 482	5	100.0	24	5	BQ593128	E012795-0	BQ593128
C 483	5	100.0	24	6	CF306279	HDA1--03-	CF306279
C 484	5	100.0	24	8	AZ304036	1M0003L04	AZ304036
485	5	100.0	24	8	AZ309564	1M0016E09	AZ309564
C 486	5	100.0	24	8	AZ309633	1M0016B22	AZ309633
C 487	5	100.0	24	8	AZ331594	1M0059D12	AZ331594
488	5	100.0	24	8	AZ331928	1M0060G03	AZ331928
489	5	100.0	24	8	AZ335328	1M0065C13	AZ335328
C 490	5	100.0	24	8	AZ346795	1M0082N09	AZ346795
C 491	5	100.0	24	8	AZ347010	1M0082J04	AZ347010
C 492	5	100.0	24	8	AZ374417	1M0127G07	AZ374417
493	5	100.0	24	8	AZ379773	1M0135H09	AZ379773
494	5	100.0	24	8	AZ404465	1M0172P09	AZ404465
495	5	100.0	24	8	AZ416344	1M0191J06	AZ416344
496	5	100.0	24	8	AZ436588	1M0224H20	AZ436588
C 497	5	100.0	24	8	AZ448189	1M0245A16	AZ448189
C 498	5	100.0	24	8	AZ451705	1M0251O10	AZ451705
C 499	5	100.0	24	8	AZ490379	1M0323L18	AZ490379
C 500	5	100.0	24	8	AZ586050	1M0391N08	AZ586050

ALIGNMENTS

RESULT 1	CL436411/c	10 bp	DNA	linear	GSS 18-MAR-2004
LOCUS	CL436411				
DEFINITION	PST292-1.seq MICB1 Mus musculus genomic clone				PST292-1.seq similar to D17ERTD808E, genomic survey sequence.
ACCESSION	CL436411				
VERSION	CL436411.1				GI:45571178
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 10)				
TITLE	Hicks,G.G.				
JOURNAL	www.EScells.ca				
COMMENT	Unpublished (2002)				
	Contact: Hicks GG				
	Mammalian Functional Genomics Centre				
	Manitoba Institute of Cell Biology, University of Manitoba				
	ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada				
	Tel: 204 787 2133				
	Fax: 204 787 2190				
	Email: hicksgg@cc.umanitoba.ca				
	U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from				
	http://140.193.242.7/esdb/public_search_frame.php?PST=PST292-1.seq				
	Class: Gene Trap.				
	Location/Qualifiers				

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source
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST292-1.seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      6 GGGAG 2

RESULT 2
CL436421/c
LOCUS
DEFINITION
PST295-1.seq MICB1 Mus musculus genomic clone PST295-1.seq, genomic
survey sequence.
CL436421
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hicks,G.G.
TITLE
www.EScells.ca
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ONS029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST295-1.seq
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST295-1.seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      6 GGGAG 2

RESULT 3
CL437642
LOCUS
DEFINITION
PST6016-NR.Seq MICB1 Mus musculus genomic clone PST6016-NR.Seq
similar to 5730410I19Rik, genomic survey sequence.
CL437642
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hicks,G.G.
TITLE
www.EScells.ca
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ONS029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST6016-NR.Se
q
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST6016-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 4
CL439219/c
LOCUS
DEFINITION
PST8879-NL.Seq MICB1 Mus musculus genomic clone PST8879-NL.Seq,
genomic survey sequence.
CL439219
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Hicks,G.G.
TITLE
www.EScells.ca
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba

```

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada  
Tel: 204 787 2133  
Fax: 204 787 2190  
Email: hicksgg@cc.umanitoba.ca  
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional  
sequence information and target gene cloning can be generated. ES  
cell line harboring insertion mutation of target gene is available.  
Sequence analysis available from  
http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST8879-NL.Se

q  
Class: Gene Trap.  
Location/Qualifiers  
1. .10  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129 sv"  
/db\_xref="taxon:10090"  
/clone="PST8879-NL.Seq"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="D3H (J1 subclone)"  
/clone\_lib="MICB1"  
/note="Vector: U3NeoSV1"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 8 GGGAG 4

RESULT 5  
AJ648107/c  
LOCUS AJ648107 CSEQRAN19 Sus scrofa cDNA clone C0003263\_K08, mRNA  
DEFINITION sequence.  
ACCESSION AJ648107  
VERSION AJ648107.1 GI:49324952  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBlueScriptII(KS) R. Sitel: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled ovaries. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.ark-genomics.org.

FEATURES  
source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0003263\_K08"  
/tissue\_type="ovary"  
/clone\_lib="CSEQRAN19"  
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing; Normalised library  
constructed from pooled ovaries"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 5 GGGAG 1

RESULT 6  
AJ655479/c  
LOCUS AJ655479 KN277 Sus scrofa cDNA clone C0005190\_H03, mRNA sequence.  
DEFINITION  
ACCESSION AJ655479  
VERSION AJ655479.1 GI:49339511  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -mismatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled early embryos, from 8- cell stage to blastocysts.  
Clones available from UK Centre for Functional Genomics in Farm  
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
www.arkgenomics.org.

FEATURES  
source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005190\_H03"  
/tissue\_type="embryo"  
/clone\_lib="KN277"  
/note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pooled early embryos, from 8-cell stage  
to blastocysts."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 11 GGGAG 7

RESULT 7  
AJ657108  
LOCUS AJ657108 KN277 Sus scrofa cDNA clone C0005196\_K06, mRNA sequence.  
DEFINITION  
ACCESSION AJ657108  
VERSION AJ657108.1 GI:49341140  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.



REFERENCE 1 (bases 1 to 11)  
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

JOURNAL Unpublished (2004)  
 COMMENT Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES Location/Qualifiers  
 source 1..11  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0005196 K06"  
 /tissue\_type="embryo"  
 /clone\_lib="KN277"

/note="Vector: pBlueScriptII(SK+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 3 GGGAG 7

RESULT 8  
 BQ591023/c  
 LOCUS BQ591023 11 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012596-024-018-C03-SP6 MP12-ADIS-024-storage root Beta vulgaris cDNA clone 024-018-C03 5-PRIME, mRNA sequence.

ACCESSION BQ591023  
 VERSION BQ591023.1 GI:26120606  
 KEYWORDS EST.

SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 11)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de  
 Insert Length: 11 Std Error: 0.00  
 Plate: 18 row: C column: 03

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES Location/Qualifiers

source 1..11

/organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:189098"  
 /db\_xref="taxon:161934"  
 /clone="024-018-C03"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP12-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 9 GGGAG 5

## RESULT 9

CL437735/c

LOCUS CL437735 11 bp DNA linear GSS 18-MAR-2004

DEFINITION PST6197-NR.Seg MICB1 Mus musculus genomic clone PST6197-NR.Seg similar to Dnclcl, genomic survey sequence.

ACCESSION CL437735

VERSION CL437735.1 GI:45573647

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 11)

AUTHORS Hicks,G.G.

TITLE www.Escells.ca

JOURNAL Unpublished (2002)

COMMENT Contact: Hicks GG

Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicks@gcc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PS6197-NR.Se

q

Class: Gene Trap.

Location/Qualifiers

1..11

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="129 sv"

/db\_xref="taxon:10090"

/clone="PST6197-NR.Seg"

/sex="Male"

/cell\_type="Embryonic stem cell"

/cell\_line="D3H (J1 subclone)"

/clone\_lib="MICB1"

/note="Vector: U3NeosV1"



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ORIGIN
  Query Match      100.0%; Score 5; DB 9; Length 11;
  Best Local Similarity 100.0%; Pred. No. 1.2e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      1 GGGAG 5
         |||||
  Db      9 GGGAG 5

RESULT 10
CL657848/c
LOCUS
DEFINITION
  CL657848      11 bp      DNA      linear      GSS 09-JUL-2004
  PRI012c_H02 - PRI012c.B21 (11) Mixed stage fosmid library of P.
  pacificus var. California Pristionchus pacificus genomic, genomic
  survey sequence.

ACCESSION
  CL657848
VERSION
  CL657848.1 GI:50139878
KEYWORDS
  GSS.
SOURCE
  Pristionchus pacificus
  Pristionchus pacificus
  Pristionchus pacificus
  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
  Neodiplogasteridae; Pristionchus.
REFERENCE
  1 (bases 1 to 11)
AUTHORS
  Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
  AppaDB: an AcedB database for the nematode satellite organism
  Pristionchus pacificus
JOURNAL
  Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
  Contact: Sommer RJ
  Evolutionary Biology
  Max-Planck-Institute for Developmental Biology
  Spemannstr. 37-39, Tuebingen D-72076, Germany
  Tel: 00497071601371
  Fax: 00497071601498
  Email: ralf.sommer@tuebingen.mpg.de
  This library was generated at Caltech, Pasadena, USA and end
  sequenced at Vancouver, Canada.
  Seq primer: T7
  Class: fosmid ends.
  Location/Qualifiers
    1..11
      /organism="Pristionchus pacificus"
      /mol_type="genomic DNA"
      /strain="California"
      /db_xref="taxon:54126"
      /clone_lib="Mixed stage fosmid library of P. pacificus
      var. California"
      /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
  Query Match      100.0%; Score 5; DB 9; Length 11;
  Best Local Similarity 100.0%; Pred. No. 1.2e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      1 GGGAG 5
         |||||
  Db      9 GGGAG 5

RESULT 11
AJ679735/c
LOCUS
DEFINITION
  AJ679735      12 bp      mRNA      linear      EST 29-JUN-2004
  CSEQRAN04 Sus scrofa cDNA clone C0001780_A09, mRNA
  sequence.
ACCESSION
  AJ679735
VERSION
  AJ679735.1 GI:49412322
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
ORGANISM
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  1 (bases 1 to 12)

```

---

```

AUTHORS
  Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE
  Development of cDNA and EST resources for studying reproduction and
  embryo development in pigs and cattle
JOURNAL
  Unpublished (2004)
COMMENT
  Contact: Anderson SI
  Genomics and Bioinformatics
  Roslin Institute
  Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
  Single pass sequencing. Bases called and trimmed with phred
  v0.020425.c. Vector identified by cross_match with the -minscore 20
  and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
  R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
  from pig uterus. Clones available from UK Centre for Functional
  Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
  EH25 9PS, www.arkgenomics.org.
FEATURES
  Location/Qualifiers
    1..12
      /organism="Sus scrofa"
      /mol_type="mRNA"
      /db_xref="taxon:9823"
      /clone="C0001780_A09"
      /tissue_type="uterus"
      /clone_lib="CSEQRAN04"
      /note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site_2:
      NotI; Single pass sequencing. Normalised library
      constructed from pig uterus."
ORIGIN
  Query Match      100.0%; Score 5; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.2e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      1 GGGAG 5
         |||||
  Db      6 GGGAG 2

RESULT 12
AJ587934
LOCUS
DEFINITION
  AJ587934      12 bp      DNA      linear      GSS 15-JAN-2004
  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
  342D03, genomic survey sequence.
ACCESSION
  AJ587934
VERSION
  AJ587934.1 GI:37937558
KEYWORDS
  GSS; left border; T-DNA flanking sequence.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1
  Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
  Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
  Lepiniec,L., Caboche,M. and Lecharny,A.
  T-DNA integration into the Arabidopsis genome depends on sequences
  of pre-insertion sites
JOURNAL
  EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
  22363535
PUBMED
  12446565
REFERENCE
  2 (bases 1 to 12)
  Balzerque,S.
  Direct Submission
  Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
  Gaston Cremieux, 91057 Evry cedex, FRANCE
  PCR was performed on DNA from transformants of Arabidopsis thaliana
  plants from INRA (Versailles). The DNA fragment(s) resulting from
  the PCR were directly sequenced from the left or the right border
  to determine the genomic sequence flanking the insertion. T-DNA
  derived sequences were removed. Information to order the
  corresponding mutant line and a link to a database providing a
  graphical display of the insertion site are available at
  http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
  been generated in the framework of the French plant genomics

```

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program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1. .12
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            /cultivar="Wassillewskija"
            /db_xref="taxon:3702"
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            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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            /note="T-DNA flanking sequence
            left border"
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                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
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                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                right border"
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        Best Local Similarity 100.0%; Pred. No. 1.2e+07;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1 GGGAG 5
            |||||
        Db 6 GGGAG 10
    RESULT 13
    AJ592591
    LOCUS
    DEFINITION
        Arabidopsis thaliana T-DNA flanking sequence, right border, clone
        624D10, genomic survey sequence.
    ACCESSION
        AJ592591
    VERSION
        AJ592591.1 GI:37942215
    KEYWORDS
        GSS; right border; T-DNA flanking sequence.
    SOURCE
        Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    REFERENCE
        1
    AUTHORS
        Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
        Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
        Lepiniec,L., Caboche,M. and Lecharny,A.
    TITLE
        T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
    JOURNAL
        EMBO Rep. 3 (12), 1152-1157 (2002)
    MEDLINE
        22363535
    PUBMED
        12446565
    REFERENCE
        2 (bases 1 to 12)
    AUTHORS
        Balzergue,S.
    TITLE
        Direct Submission
    JOURNAL
        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
    COMMENT
        PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
    FEATURES
        source
            1. .12
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                /mol_type="genomic DNA"
                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
                /clone="624D10"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            1. .12
                /note="T-DNA flanking sequence
                right border"
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                /mol_type="genomic DNA"
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                right border"
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        Query Match      100.0%; Score 5; DB 9; Length 12;
        Best Local Similarity 100.0%; Pred. No. 1.2e+07;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1 GGGAG 5
            |||||
        Db 6 GGGAG 10
    RESULT 14
    AJ594389
    LOCUS
    DEFINITION
        Arabidopsis thaliana T-DNA flanking sequence, left border, clone
        397G07, genomic survey sequence.
    ACCESSION
        AJ594389
    VERSION
        AJ594389.1 GI:37944013
    KEYWORDS
        GSS; left border; T-DNA flanking sequence.
    SOURCE
        Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    REFERENCE
        1
    AUTHORS
        Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
        Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
        Lepiniec,L., Caboche,M. and Lecharny,A.
    TITLE
        T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
    JOURNAL
        EMBO Rep. 3 (12), 1152-1157 (2002)
    MEDLINE
        22363535
    PUBMED
        12446565
    REFERENCE
        2 (bases 1 to 12)
    AUTHORS
        Balzergue,S.
    TITLE
        Direct Submission
    JOURNAL
        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
    COMMENT
        PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
    FEATURES
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                /note="T-DNA flanking sequence
                left border"
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                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            1. .12
                /note="T-DNA flanking sequence
                left border"
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        Query Match      100.0%; Score 5; DB 9; Length 12;
        Best Local Similarity 100.0%; Pred. No. 1.2e+07;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1 GGGAG 5
            |||||
        Db 4 GGGAG 8
    RESULT 15
    BG926067/c
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ORIGIN
    Query Match      100.0%; Score 5; DB 9; Length 12;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 GGGAG 5
        |||||
    Db 6 GGGAG 10
    RESULT 14
    AJ594389
    LOCUS
    DEFINITION
        Arabidopsis thaliana T-DNA flanking sequence, left border, clone
        397G07, genomic survey sequence.
    ACCESSION
        AJ594389
    VERSION
        AJ594389.1 GI:37944013
    KEYWORDS
        GSS; left border; T-DNA flanking sequence.
    SOURCE
        Arabidopsis thaliana (thale cress)
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    REFERENCE
        1
    AUTHORS
        Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
        Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
        Lepiniec,L., Caboche,M. and Lecharny,A.
    TITLE
        T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
    JOURNAL
        EMBO Rep. 3 (12), 1152-1157 (2002)
    MEDLINE
        22363535
    PUBMED
        12446565
    REFERENCE
        2 (bases 1 to 12)
    AUTHORS
        Balzergue,S.
    TITLE
        Direct Submission
    JOURNAL
        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
    COMMENT
        PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
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        source
            1. .12
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                /db_xref="taxon:3702"
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            1. .12
                /note="T-DNA flanking sequence
                left border"
        misc_feature
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                /mol_type="genomic DNA"
                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
                /clone="397G07"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            1. .12
                /note="T-DNA flanking sequence
                left border"
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        Query Match      100.0%; Score 5; DB 9; Length 12;
        Best Local Similarity 100.0%; Pred. No. 1.2e+07;
        Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        QY 1 GGGAG 5
            |||||
        Db 4 GGGAG 8
    RESULT 15
    BG926067/c
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LOCUS BG926067 13 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BG926067  
VERSION BG926067.1 GI:14320590  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
TITLE Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PUBMED 11597177  
COMMENT Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay\_kumar-l@gsk.com  
Seq primer: T7.  
FEATURES Location/Qualifiers  
source 1..13  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI;  
Directional"  
ORIGIN  
Query Match 100.0%; Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
|||||  
Db 5 GGGAG 1  
RESULT 16  
BM399550/c  
LOCUS BM399550 13 bp mRNA linear EST 17-JAN-2002  
DEFINITION Tetrahymena thermophila cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM399550  
VERSION BM399550.1 GI:18199603  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu

Seq primer: T3.  
FEATURES Location/Qualifiers  
source 1..13  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 2  
RESULT 17  
AJ593426 13 bp DNA linear GSS 15-JAN-2004  
LOCUS AJ593426  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
380B04, genomic survey sequence.  
ACCESSION AJ593426  
VERSION AJ593426.1 GI:37943050  
KEYWORDS GSS; left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1  
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 13)  
AUTHORS Balzerque,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).  
FEATURES Location/Qualifiers  
source 1..13  
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/cultiivar="WasillewskiJa"  
/db\_xref="taxon:3702"  
/clone="380B04"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1..13  
/note="T-DNA flanking sequence  
left border"  
ORIGIN



/clone lib="CSEQRAN04"  
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site\_2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 14 GGGAG 10

RESULT 21

BQ593808/c 14 bp mRNA linear EST 06-DEC-2002  
LOCUS  
DEFINITION  
E012763-024-026-007-SP6 MP12-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-026-007 5-PRIME, mRNA sequence.

ACCESSION BQ593808  
VERSION BQ593808.1 GI:26123391  
KEYWORDS  
SOURCE EST.

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 26 row: 0 column: 07  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

source

1..14  
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line)"  
/db\_xref="GABI:193044"  
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/clone="024-026-007"  
/tissue\_type="developing root"  
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/clone\_lib="MP12-ADIS-024-developing root"  
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CDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 12 GGGAG 8

RESULT 22

AJ682954/c 15 bp mRNA linear EST 29-JUN-2004  
LOCUS  
DEFINITION  
AJ682954 CSEQRAN04 Sus scrofa cDNA clone C0001800\_K20, mRNA  
sequence.

ACCESSION AJ682954  
VERSION AJ682954.1 GI:49415544  
KEYWORDS  
SOURCE EST.

ORGANISM

Sus scrofa (pig)  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

AUTHORS  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle

JOURNAL

COMMENT

Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.

FEATURES

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constructed from pig uterus."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 11 GGGAG 7

RESULT 23

AJ686764/c 15 bp mRNA linear EST 29-JUN-2004  
LOCUS  
DEFINITION  
AJ686764 CSEQRAN04 Sus scrofa cDNA clone C0001812\_M09, mRNA  
sequence.

ACCESSION AJ686764  
VERSION AJ686764.1 GI:49419354  
KEYWORDS  
SOURCE EST.

ORGANISM

Sus scrofa (pig)  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

AUTHORS  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle

JOURNAL

Unpublished (2004)

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COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES     Location/Qualifiers
source       1..15
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_M09"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
       |||||
Db      10 GGGAG 6

RESULT 24
LOCUS   CF304766
DEFINITION
CF304766
CF304766.1 GI:33676527
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
source       1..15
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--05-006"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBlueScript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into"

COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES     Location/Qualifiers
source       1..15
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_M09"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
       |||||
Db      10 GGGAG 6

RESULT 24
LOCUS   CF304766
DEFINITION
CF304766
CF304766.1 GI:33676527
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
source       1..15
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--05-006"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBlueScript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into"

COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES     Location/Qualifiers
source       1..15
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_M09"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
       |||||
Db      10 GGGAG 6

RESULT 25
LOCUS   AA968729
DEFINITION
AA968729
AA968729.1 GI:3143909
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 514 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES     Location/Qualifiers
source       1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI-CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

```
lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
       |||||
Db      6 GGGAG 10

RESULT 25
LOCUS   AA968729
DEFINITION
AA968729
AA968729.1 GI:3143909
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 514 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES     Location/Qualifiers
source       1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI-CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
```



Db 5 GGGAG 9

RESULT 26  
AI075064/c  
LOCUS  
DEFINITION  
ou61g11.x1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:1632356 3'  
similar to TR:Q24348 Q24348 FIBRILLARIN ;, mRNA sequence.

ACCESSION  
AI075064  
VERSION  
AI075064.1 GI:3399844  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI/NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 712 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1632356"  
/sex="female, pooled"  
/tissue\_type="breast"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Br2"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from pooled bulk  
breast tumor tissue, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. This library is the normalized version of  
NCI\_CGAP Br1.1. Library was constructed by Bento Soares  
and M. Fatima Bonaldo."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
|||||  
Db 16 GGGAG 12

RESULT 27  
AI094839/c  
LOCUS  
DEFINITION  
qa22c08.x1 NCI\_CGAP Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'  
similar to TR:O00599 O00599 CON1. ;contains element MSRI repetitive  
element ;, mRNA sequence.

ACCESSION  
AI094839  
VERSION  
AI094839.1 GI:3433815  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI/NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1687502"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Brn23"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGGCATATCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
|||||  
Db 10 GGGAG 6

RESULT 28  
AI274782/c  
LOCUS  
DEFINITION  
AI274782 16 bp mRNA linear EST 21-DEC-1998  
qv67h03.x1 NCI\_CGAP Ut1 Homo sapiens cDNA clone IMAGE:1986677 3'  
similar to WP:F59E12.9 CE11534 ;contains element MSRI repetitive  
element ;, mRNA sequence.

ACCESSION  
AI274782  
VERSION  
AI274782.1 GI:3897056  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov



Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1556 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1986677"  
/tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 10 GGGAG 6

RESULT 29

AI560058

LOCUS

DEFINITION  
AI560058 16 bp mRNA linear EST 13-MAY-1999  
similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15  
PRECURSOR. ;contains MSRI.t2 MSRI repetitive element ;, mRNA  
sequence.

ACCESSION  
AI560058  
VERSION  
AI560058.1 GI:4510263  
KEYWORDS  
EST.

SOURCE

ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

JOURNAL

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 2104 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2211141"  
/tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 8 GGGAG 12

RESULT 30

AI569544/c

LOCUS

DEFINITION  
AI569544 16 bp mRNA linear EST 12-MAY-1999  
similar to TR:Q18444 Q18444 COSMID C34D4. ;contains MSRI.b2 MSRI  
repetitive element ;, mRNA sequence.

ACCESSION  
AI569544  
VERSION  
AI569544.1 GI:4532918  
KEYWORDS  
EST.

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1683 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2180371"  
/tissue\_type="serous papillary carcinoma, high grade, 2 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 8 GGGAG 4

RESULT 31

BQ588093  
LOCUS  
DEFINITION BQ588093 16 bp mRNA linear EST 06-DEC-2002  
E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-009-A19 5-PRIME, mRNA sequence.

ACCESSION BQ588093  
VERSION BQ588093.1 GI:26117675  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 9 row: A column: 19

Seq primer: SP6; CATACGATTTAGGTGACACTATAG.

FEATURES

source

1. .16  
Location/Qualifiers

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"

/db\_xref="GABI:184766"

/db\_xref="taxon:161934"

/clone="024-009-A19"

/tissue\_type="leaf"

/lab\_host="EMDH108"

/clone\_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 7 GGGAG 11

RESULT 32

BZ424445/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .16

/organism="Aspergillus terreus"

/mol\_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db\_xref="taxon:33178"

/lab\_host="Escherichia coli"

/clone\_lib="Aspergillus terreus random genomic DNA clone  
library"

/note="Vector: pZerOTM-2; Site 1: Sau3A; Site 2: BamHI;  
Sau3A genomic fragments ligated into BamHI digested  
pZerOTM-2 "

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|  
|  
|  
|

Db 16 GGGAG 12

RESULT 33

AJ589788/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1

Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

Query Match 100.0%; Score 5; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|  
|  
|  
|

Db 16 GGGAG 12

RESULT 33

AJ589788/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1

Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

Query Match 100.0%; Score 5; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

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|  
|  
|

Db 7 GGGAG 11

BZ424445 16 bp DNA linear GSS 13-DEC-2002  
10012843-4357 Aspergillus terreus random genomic DNA clone library  
Aspergillus terreus genomic, genomic survey sequence.

BZ424445 BZ424445.1 GI:26665900

GSS.

Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 16)

Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,

Zimmer,D.P., Boers,M-E., Blomquist,P.R., Martinez,E.J.,

Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,

Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and

Madden,K.T.

Integrating transcriptional and metabolite profiles to direct the

engineering of lovastatin-producing strains

Unpublished (2002)

Contact: Zimmer DP

Microbia, Inc.

One Kendall Square Building 1400 W, Cambridge, MA 02139, USA

Tel: 617-621-8322

Fax: 617-

Email: dzimmer@microbia.com

Class: plasmid ends.

Location/Qualifiers

1. .16

/organism="Aspergillus terreus"

/mol\_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db\_xref="taxon:33178"

/lab\_host="Escherichia coli"

/clone\_lib="Aspergillus terreus random genomic DNA clone  
library"

/note="Vector: pZerOTM-2; Site 1: Sau3A; Site 2: BamHI;  
Sau3A genomic fragments ligated into BamHI digested  
pZerOTM-2 "

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|  
|  
|  
|

Db 16 GGGAG 12

RESULT 33

AJ589788/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1

Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

Query Match 100.0%; Score 5; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|  
|  
|  
|

Db 7 GGGAG 11

MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

22363535  
12446565  
2 (bases 1 to 16)  
Balzergue,S.  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. .16  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="558A09"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

misc\_feature  
1. .16  
/note="T-DNA flanking sequence  
right border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 2

RESULT 34  
AJ595245/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
413H04, genomic survey sequence.

ACCESSION  
AJ595245  
VERSION  
AJ595245.1 GI:37944869  
KEYWORDS  
GSS; right border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
AUTHORS  
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 16)  
AUTHORS  
Balzergue,S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. .16  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="467B08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 2

RESULT 35  
AJ598372/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
467B08, genomic survey sequence.

ACCESSION  
AJ598372  
VERSION  
AJ598372.1 GI:37948000  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
AUTHORS  
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 16)  
AUTHORS  
Balzergue,S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. .16  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="467B08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. .16  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="413H04"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

misc\_feature  
1. .16  
/note="T-DNA flanking sequence  
right border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 6 GGGAG 2

RESULT 35  
AJ598372/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
467B08, genomic survey sequence.

ACCESSION  
AJ598372  
VERSION  
AJ598372.1 GI:37948000  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
AUTHORS  
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
Lepiniec,L., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
2 (bases 1 to 16)  
AUTHORS  
Balzergue,S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (<http://www.genoplante.com> and  
<http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
1. .16  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="467B08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

misc\_feature 1..16  
/note="T-DNA flanking sequence  
left border"

ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 6 GGGAG 2

RESULT 36  
AJ666397/c

LOCUS  
DEFINITION AJ666397 CSEQRAN09 Sus scrofa cDNA clone C0000033\_K10, mRNA  
sequence.

ACCESSION AJ666397

VERSION AJ666397.1 GI:49350848

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS 1 (bases 1 to 17)

TITLE Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:  
EcoRI R. Site 2: NotI Description: Normalised library constructed  
from pooled tissue from day 30 placentas. Clones available from UK  
Centre for Functional Genomics in Farm Animals, Roslin Institute,  
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES  
source 1..17  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0000033\_K10"  
/tissue\_type="placenta"  
/clone\_lib="CSEQRAN09"  
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 12 GGGAG 8

RESULT 37  
AW246940

LOCUS  
DEFINITION AW246940 17 bp mRNA linear EST 07-JAN-2000  
2822481.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822481 5',  
mRNA sequence.

ACCESSION AW246940

VERSION AW246940.1 GI:6589933

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 17)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT Other\_ESTs: 2822481.3prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence.  
Plate: LLCM9 row: I column: 10.

FEATURES  
Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822481"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 5; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 9 GGGAG 13

RESULT 38  
BG926068/c

LOCUS  
DEFINITION BG926068 17 bp mRNA linear EST 06-NOV-2001  
HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG926068

VERSION BG926068.1 GI:14320591

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 17)

TITLE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries



QY 1 GGGAG 5  
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|  
|  
|  
Db 11 GGGAG 15

RESULT 41  
AJ648240/c

LOCUS  
DEFINITION AJ648240 CSEQRAN19 Sus scrofa cDNA clone C0003264\_A22, mRNA

ACCESSION  
VERSION AJ648240  
KEYWORDS AJ648240.1 GI:49325085  
SOURCE EST.  
ORGANISM Sus scrofa (pig)

REFERENCE  
AUTHORS Sus scrofa  
TITLE Sus scrofa  
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
COMMENT Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 18)  
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
Unpublished (2004)  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.

FEATURES  
source  
1. .18  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0003264\_A22"  
/tissue\_type="ovary"  
/clone\_lib="CSEQRAN19"  
/note="Vector: pBlueScriptII(KS+); Site\_1: EcoRI; Site\_2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
|  
Db 16 GGGAG 12

RESULT 42  
AW250267

LOCUS  
DEFINITION AW250267 18 bp mRNA linear EST 07-JAN-2000  
2821151.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821151 5', mRNA sequence.

ACCESSION  
VERSION AW250267  
KEYWORDS AW250267.1 GI:6593260  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL 1 (bases 1 to 18)  
COMMENT NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821151.3prime

Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 16 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence.  
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High quality sequence stop: 16.  
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ORIGIN

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Db 9 GGGAG 13

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HOA59-1-D4.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION  
VERSION BG896958  
KEYWORDS BG896958.1 GI:14307199  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177  
Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA



```
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-l@gsk.com
Seq primer: T7.

FEATURES
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ACCESSION
  BG925410
VERSION
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KEYWORDS
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SOURCE
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  ORGANISM
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 18)
    Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
    Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
    Lark,M.W.
  Identification and initial characterization of 5000 expressed
  sequenced tags (ESTs) each from adult human normal and
  osteoarthritic cartilage cDNA libraries
  Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  21482651
  11597177
  Contact: Sanjay Kumar
  UW2109
  GlaxoSmithKline
  709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
  Tel: 610-270-7245
  Fax: 610-270-5598
  Email: sanjay_kumar-l@gsk.com
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RESULT 45
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VERSION
  BG925569.1 GI:14320092
KEYWORDS
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 18)
    Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
    Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
    Lark,M.W.
  Identification and initial characterization of 5000 expressed
  sequenced tags (ESTs) each from adult human normal and
  osteoarthritic cartilage cDNA libraries
  Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  21482651
  11597177
  Contact: Sanjay Kumar
  UW2109
  GlaxoSmithKline
  709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
  Tel: 610-270-7245
  Fax: 610-270-5598
  Email: sanjay_kumar-l@gsk.com
  Seq primer: T7.
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RESULT 46
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DEFINITION
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  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
  BM397051
VERSION
  BM397051.1 GI:18197104
KEYWORDS
  EST.
SOURCE
  Tetrahymena thermophila
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    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
    Hymenostomatida; Tetrahymenina; Tetrahymena.
  1 (bases 1 to 18)
    Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
    Frankel,J. and Klobutcher,L.
  EST from Tetrahymena thermophila, strain CU428.1, growing cells
  Unpublished (2002)
  Contact: Turkewitz AP
  Molecular Genetics and Cell Biology
```



```

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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ACCESSION
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VERSION
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 18)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
TITLE
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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```

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920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
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Db      13 GGGAG 9

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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ACCESSION BM399858  
VERSION BM399858.1 GI:18199911  
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SOURCE Tetrahymena thermophila  
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GGGAG  
Perfect score: 5  
Sequence: 1 gggag 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	5	100.0	10	1 US-08-074-879-3	Sequence 3, Appli
4	5	100.0	10	1 US-08-468-057A-3	Sequence 3, Appli
5	5	100.0	10	1 US-08-171-718-30	Sequence 30, Appl
6	5	100.0	10	2 US-08-480-994-20	Sequence 20, Appl
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361 5 100.0 13 4 US-09-474-432B-120 Sequence 120, App  
362 5 100.0 13 4 US-09-474-432B-173 Sequence 173, App  
363 5 100.0 13 4 US-09-474-432B-175 Sequence 175, App  
364 5 100.0 13 4 US-09-474-432B-183 Sequence 183, App  
365 5 100.0 13 4 US-09-535-370-30 Sequence 30, Appl  
366 5 100.0 13 4 US-09-282-734-11 Sequence 11, Appl  
C 367 5 100.0 13 4 US-09-647-344A-23 Sequence 23, Appl  
C 368 5 100.0 13 4 US-09-770-158-31 Sequence 31, Appl  
C 369 5 100.0 13 4 US-09-770-158-32 Sequence 32, Appl  
370 5 100.0 13 4 US-09-136-159A-30 Sequence 30, Appl  
371 5 100.0 13 4 US-09-965-346-1 Sequence 1, Appl  
372 5 100.0 13 4 US-09-476-387-120 Sequence 120, App  
373 5 100.0 13 4 US-09-476-387-173 Sequence 173, App  
374 5 100.0 13 4 US-09-476-387-175 Sequence 175, App  
375 5 100.0 13 4 US-09-476-387-183 Sequence 183, App  
376 5 100.0 13 4 US-09-663-667-30 Sequence 30, Appl  
377 5 100.0 13 4 US-09-500-700-27 Sequence 27, Appl  
C 378 5 100.0 13 6 5256775-2 Patent No. 5256775  
C 379 5 100.0 14 1 US-08-151-574-50 Sequence 50, Appl  
C 380 5 100.0 14 1 US-07-832-855-7 Sequence 7, Appl  
381 5 100.0 14 1 US-08-050-073-232 Sequence 232, App  
C 382 5 100.0 14 1 US-08-050-073-233 Sequence 233, App  
383 5 100.0 14 1 US-08-050-073-281 Sequence 281, App  
C 384 5 100.0 14 1 US-08-485-112-2 Sequence 2, Appl  
385 5 100.0 14 1 US-07-724-500B-12 Sequence 12, Appl  
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400 5 100.0 14 2 US-08-461-418B-8 Sequence 8, Appli  
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402 5 100.0 14 2 US-08-485-133-79 Sequence 79, Appl  
C 403 5 100.0 14 2 US-08-810-599-15 Sequence 15, Appl  
C 404 5 100.0 14 2 US-08-514-542C-5 Sequence 5, Appli  
C 405 5 100.0 14 2 US-08-904-901-9 Sequence 9, Appli  
406 5 100.0 14 3 US-08-544-381B-6 Sequence 6, Appli  
C 407 5 100.0 14 3 US-08-985-162-1825 Sequence 1825, Ap  
C 408 5 100.0 14 3 US-08-985-162-1830 Sequence 1830, Ap  
C 409 5 100.0 14 3 US-08-777-266A-89 Sequence 89, Appl  
C 410 5 100.0 14 3 US-08-998-099-333 Sequence 333, App  
C 411 5 100.0 14 3 US-08-998-099-359 Sequence 359, App  
412 5 100.0 14 3 US-08-534-220-1 Sequence 1, Appli  
C 413 5 100.0 14 3 US-09-249-730-9 Sequence 9, Appli  
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C 415 5 100.0 14 3 US-08-871-678C-75 Sequence 75, Appl  
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C 418 5 100.0 14 3 US-09-326-186B-89 Sequence 89, Appl  
C 419 5 100.0 14 3 US-09-233-510-50 Sequence 50, Appl  
C 420 5 100.0 14 3 US-08-666-341A-37 Sequence 37, Appl  
421 5 100.0 14 3 US-09-255-899-8 Sequence 8, Appli  
C 422 5 100.0 14 3 US-09-593-012-50 Sequence 50, Appl  
C 423 5 100.0 14 4 US-08-937-067-15 Sequence 15, Appl  
C 424 5 100.0 14 4 US-09-328-174A-21 Sequence 21, Appl  
C 425 5 100.0 14 4 US-09-475-947A-76 Sequence 76, Appl  
C 426 5 100.0 14 4 US-09-698-505A-38 Sequence 38, Appl  
C 427 5 100.0 14 4 US-07-936-532-2 Sequence 2, Appli  
C 428 5 100.0 14 4 US-09-922-445-4 Sequence 4, Appli  
C 429 5 100.0 14 4 US-09-922-445-39 Sequence 39, Appl  
C 430 5 100.0 14 4 US-09-230-652-26 Sequence 26, Appl  
C 431 5 100.0 14 4 US-09-491-894A-1 Sequence 1, Appli  
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433 5 100.0 14 4 US-09-829-855-196 Sequence 196, App  
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C 435 5 100.0 14 4 US-09-401-063-1830 Sequence 1830, Ap  
436 5 100.0 14 4 US-09-723-909-104 Sequence 104, App  
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C 438 5 100.0 14 4 US-09-904-420A-5 Sequence 5, Appli  
439 5 100.0 14 4 US-09-688-990-1 Sequence 1, Appli  
440 5 100.0 14 4 US-10-032-307-57 Sequence 57, Appl  
C 441 5 100.0 14 4 US-09-777-430C-55 Sequence 55, Appl  
C 442 5 100.0 14 4 US-09-777-430C-83 Sequence 83, Appl  
443 5 100.0 14 5 PCT-US93-08743-104 Sequence 104, App  
C 444 5 100.0 14 6 5276019-5 Patent No. 5276019  
C 445 5 100.0 14 6 5486603-1 Patent No. 5486603  
446 5 100.0 14 6 5486603-2 Patent No. 5486603  
C 447 5 100.0 15 1 US-07-664-989B-121 Sequence 121, App  
448 5 100.0 15 1 US-08-050-073-261 Sequence 261, App  
449 5 100.0 15 1 US-08-137-701-18 Sequence 18, Appl  
C 450 5 100.0 15 1 US-08-311-760A-58 Sequence 58, Appl  
C 451 5 100.0 15 1 US-08-311-760A-71 Sequence 71, Appl  
C 452 5 100.0 15 1 US-08-311-760A-231 Sequence 231, App  
C 453 5 100.0 15 1 US-08-182-968A-3 Sequence 3, Appli  
C 454 5 100.0 15 1 US-08-182-968A-3 Sequence 3, Appli  
C 455 5 100.0 15 1 US-08-182-968A-16 Sequence 16, Appl  
C 456 5 100.0 15 1 US-08-182-968A-39 Sequence 39, Appl  
457 5 100.0 15 1 US-08-182-968A-64 Sequence 64, Appl  
458 5 100.0 15 1 US-08-182-968A-65 Sequence 65, Appl  
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C 466 5 100.0 15 1 US-08-182-968A-296 Sequence 296, App  
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C 468 5 100.0 15 1 US-08-182-968A-324 Sequence 324, App  
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C 471 5 100.0 15 1 US-08-182-968A-360 Sequence 360, App  
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C 473 5 100.0 15 1 US-08-182-968A-363 Sequence 363, App  
C 474 5 100.0 15 1 US-08-182-968A-493 Sequence 493, App  
475 5 100.0 15 1 US-08-182-968A-494 Sequence 494, App  
C 476 5 100.0 15 1 US-08-266-414-5 Sequence 5, Appli  
C 477 5 100.0 15 1 US-08-319-492B-434 Sequence 434, App  
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C 479 5 100.0 15 1 US-08-319-492B-436 Sequence 436, App  
C 480 5 100.0 15 1 US-08-319-492B-437 Sequence 437, App  
481 5 100.0 15 1 US-08-231-227-1 Sequence 1, Appli  
C 482 5 100.0 15 1 US-08-231-227-2 Sequence 2, Appli  
483 5 100.0 15 1 US-08-241-372-10 Sequence 10, Appl  
C 484 5 100.0 15 1 US-08-291-932A-29 Sequence 29, Appl  
C 485 5 100.0 15 1 US-08-291-932A-30 Sequence 30, Appl  
C 486 5 100.0 15 1 US-08-291-932A-107 Sequence 107, App  
487 5 100.0 15 1 US-08-291-932A-135 Sequence 135, App  
C 488 5 100.0 15 1 US-08-291-932A-155 Sequence 155, App  
C 489 5 100.0 15 1 US-08-291-932A-168 Sequence 168, App  
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C 492 5 100.0 15 1 US-08-291-932A-242 Sequence 242, App  
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C 495 5 100.0 15 1 US-08-291-932A-296 Sequence 296, App  
C 496 5 100.0 15 1 US-08-291-932A-347 Sequence 347, App  
C 497 5 100.0 15 1 US-08-291-932A-380 Sequence 380, App  
498 5 100.0 15 1 US-08-580-242-2 Sequence 2, Appli  
499 5 100.0 15 1 US-08-580-242-9 Sequence 9, Appli  
C 500 5 100.0 15 1 US-08-334-847-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-07-963-723A-3/c  
; Sequence 3, Application US/07963723A  
; Patent No. 5494794  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Douglas C.  
; TITLE OF INVENTION: Detection of Mitochondrial DNA Mutations  
; TITLE OF INVENTION: Associated with Alzheimer's Disease and Parkinson's  
; TITLE OF INVENTION: Disease  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Needle & Rosenberg, P.C.  
; STREET: 133 Carnegie Way, N.W., Suite 400  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/963,723A  
; FILING DATE: 19921020  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 0510.027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880



; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-963-723A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 9 GGGAG 5

RESULT 2

US-08-202-927-14  
; Sequence 14, Application US/08202927  
; Patent No. 5646126

; GENERAL INFORMATION:  
; APPLICANT: Cheng, Yung-chi  
; APPLICANT: Lukhtanov, Eugene A.  
; APPLICANT: Meyer Jr., Rich B.  
; APPLICANT: Pai, Balakrishna S.  
; APPLICANT: Reed, Michael W.  
; APPLICANT: Zhou, James H.  
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
; TITLE OF INVENTION: Anticancer Activity  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klein & Szekeres  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92715

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/202,927  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Szekeres, Gabor L.  
; REGISTRATION NUMBER: 28,675  
; REFERENCE/DOCKET NUMBER: 491-07-PA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 854-5502  
; TELEFAX: (714) 854-4897  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 10  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
; OTHER INFORMATION: formula 3)."  
US-08-202-927-14

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 6 GGGAG 10

RESULT 3

US-08-074-879-3  
; Sequence 3, Application US/08074879  
; Patent No. 5656423

; GENERAL INFORMATION:  
; APPLICANT: Orth, Gerard  
; APPLICANT: Volpers, Christoph  
; APPLICANT: Streek, Rolf  
; TITLE OF INVENTION: DNA Sequences Derived from the Genome of  
; TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis  
; TITLE OF INVENTION: and for the Production of an Immunogenic Composition  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/074,879  
; FILING DATE: 16-JUN-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 92/1136  
; FILING DATE: 09-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 02356.0066-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-074-879-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 4 GGGAG 8

RESULT 4

US-08-468-057A-3  
; Sequence 3, Application US/08468057A  
; Patent No. 5665535

; GENERAL INFORMATION:  
; APPLICANT: Orth, Gerard  
; APPLICANT: Volpers, Christoph

;; APPLICANT: Streek, Rolf  
;; TITLE OF INVENTION: DNA Sequences Derived from the Genome of  
;; the Papillomavirus HPV39, Their Use in In Vitro Diagnosis  
;; TITLE OF INVENTION: and for the Production of an Immunogenic Composition  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
;; ADDRESSES: Dunner  
;; STREET: 1300 I Street, N.W.  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3315  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/468,057A  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/074,879  
;; FILING DATE: 16-JUN-1993  
;; APPLICATION NUMBER: WO 92/1136  
;; FILING DATE: 09-JUL-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Potter, Jane E.R.  
;; REGISTRATION NUMBER: 33,332  
;; REFERENCE/DOCKET NUMBER: 02356.0066-00000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-468-057A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 4 GGGAG 8

RESULT 5  
US-08-171-718-30/c  
; Sequence 30, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/171,718  
;; FILING DATE: 22-DEC-1993  
;; CLASSIFICATION: 436  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/108,808  
;; FILING DATE: 19-AUG-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/022,034  
;; FILING DATE: 25-FEB-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/026,063  
;; FILING DATE: 04-MAR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Brown, Anne  
;; REGISTRATION NUMBER: 36,463  
;; REFERENCE/DOCKET NUMBER: 0609.3850003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-171-718-30

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 5 GGGAG 1

RESULT 6  
US-08-480-994-20/c  
; Sequence 20, Application US/08480994  
; Patent No. 5834248  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,994  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-480-994-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|  
|  
|  
|  
|  
Db 6 GGGAG 2

RESULT 7  
US-08-480-994-30  
Sequence 30, Application US/08480994  
Patent No. 5834248  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,994  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-480-994-30

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
|  
|  
|  
|  
|  
Db 6 GGGAG 10

RESULT 8  
US-08-441-887A-40  
Sequence 40, Application US/08441887A  
Patent No. 5837832  
GENERAL INFORMATION:  
APPLICANT: Chee, Mark  
APPLICANT: Cronin, Maureen T.  
APPLICANT: Fodor, Stephen P.A.  
APPLICANT: Huang, Xiaohua X.  
APPLICANT: Hubbell, Earl A.  
APPLICANT: Lipshutz, Robert J.  
APPLICANT: Lobban, Peter E.  
APPLICANT: Morris, Macdonald S.  
APPLICANT: Sheldon, Edward L.  
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
TITLE OF INVENTION: Biological Chips  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,887A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,312  
FILING DATE: 26-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,937  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joseph O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-004160US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-326-2400  
TELEFAX: 650-326-2422  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
US-08-441-887A-40

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
|  
|  
|  
|  
|  
Db 6 GGGAG 10

```
RESULT 9
US-08-441-887A-96
; Sequence 96, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-96

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 5 GGGAG 9

RESULT 10
US-08-441-887A-348/c
; Sequence 348, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
```

```
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 348:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-348

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 7 GGGAG 3

RESULT 11
US-08-441-887A-349/c
; Sequence 349, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
```

;/ TITLE OF INVENTION: Biological Chips  
;/ NUMBER OF SEQUENCES: 360  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, 8th Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/441,887A  
;/ FILING DATE: 16-MAY-1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/143,312  
;/ FILING DATE: 26-OCT-1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/082,937  
;/ FILING DATE: 25-JUN-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Liebeschuetz, Joseph O.  
;/ REGISTRATION NUMBER: 37,505  
;/ REFERENCE/DOCKET NUMBER: 018547-004160US  
;/ TELEPHONE: 650-326-2400  
;/ TELEFAX: 650-326-2422  
;/ INFORMATION FOR SEQ ID NO: 349:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (probe)  
;/  
;/ US-08-441-887A-349

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 8 GGGAG 4

RESULT 12  
US-08-441-887A-350/c  
;/ Sequence 350, Application US/08441887A  
;/ Patent No. 5837832  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Chee, Mark  
;/ APPLICANT: Cronin, Maureen T.  
;/ APPLICANT: Fodor, Stephen P.A.  
;/ APPLICANT: Huang, Xiaohua X.  
;/ APPLICANT: Hubbell, Earl A.  
;/ APPLICANT: Lipshutz, Robert J.  
;/ APPLICANT: Lobban, Peter E.  
;/ APPLICANT: Morris, Macdonald S.  
;/ APPLICANT: Sheldon, Edward L.  
;/ TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
;/ TITLE OF INVENTION: Biological Chips  
;/ NUMBER OF SEQUENCES: 360  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, 8th Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA

;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/441,887A  
;/ FILING DATE: 16-MAY-1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/143,312  
;/ FILING DATE: 26-OCT-1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 08/082,937  
;/ FILING DATE: 25-JUN-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Liebeschuetz, Joseph O.  
;/ REGISTRATION NUMBER: 37,505  
;/ REFERENCE/DOCKET NUMBER: 018547-004160US  
;/ TELEPHONE: 650-326-2400  
;/ TELEFAX: 650-326-2422  
;/ INFORMATION FOR SEQ ID NO: 350:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (probe)  
;/  
;/ US-08-441-887A-350

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 9 GGGAG 5

RESULT 13  
US-08-441-887A-351/c  
;/ Sequence 351, Application US/08441887A  
;/ Patent No. 5837832  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Chee, Mark  
;/ APPLICANT: Cronin, Maureen T.  
;/ APPLICANT: Fodor, Stephen P.A.  
;/ APPLICANT: Huang, Xiaohua X.  
;/ APPLICANT: Hubbell, Earl A.  
;/ APPLICANT: Lipshutz, Robert J.  
;/ APPLICANT: Lobban, Peter E.  
;/ APPLICANT: Morris, Macdonald S.  
;/ APPLICANT: Sheldon, Edward L.  
;/ TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
;/ TITLE OF INVENTION: Biological Chips  
;/ NUMBER OF SEQUENCES: 360  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend and Crew LLP  
;/ STREET: Two Embarcadero Center, 8th Floor  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/441,887A

;  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 351:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
; US-08-441-887A-351

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 10 GGGAG 6

RESULT 14

US-08-616-844-20/c  
; Sequence 20, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/616,844  
; FILING DATE: 15-MAR-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-053  
; TELECOMMUNICATION INFORMATION:

;  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"  
; HYPOTHETICAL: NO  
; US-08-616-844-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 6 GGGAG 2

RESULT 15

US-08-616-844-30  
; Sequence 30, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/616,844  
; FILING DATE: 15-MAR-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"

```

; HYPOTHETICAL: NO
US-08-616-844-30

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      6 GGGAG 10

RESULT 16
US-08-173-489C-169
; Sequence 169, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus ayw isolate,
; DESCRIPTION: nucleotides 3071 to 3080
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: ayw
; PUBLICATION INFORMATION:
; AUTHORS: Galibert, F, Mandart, E, Fitoussi, F,
; AUTHORS: Tiollais, P, Charnay, P.
; TITLE: Nucleotide sequence of the
; TITLE: Hepatitis B virus genome (subtype ayw) cloned
; JOURNAL: Nature
; VOLUME: 281
; PAGES: 646-650
; DATE: 1979
; RELEVANT RESIDUES IN SEQ ID NO: 169 :FROM 1 TO 10

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US-08-173-489C-169

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      3 GGGAG 7

RESULT 17
US-08-173-489C-200/c
; Sequence 200, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from Hepatitis B
; DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244199
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 200 :FROM 1 TO 10
US-08-173-489C-200

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      7 GGGAG 3

RESULT 18
US-08-173-489C-287

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; Sequence 287, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEFAX: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 287:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; DESCRIPTION: 16S rRNA gene from Clostridium  
; DESCRIPTION: pasteurianum (Accession # M23930) nucleotides  
; DESCRIPTION: 149 to 158  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; ORIGINAL SOURCE:  
; ORGANISM: Clostridium pasteurianum  
; PUBLICATION INFORMATION:  
; AUTHORS: Weisburg, W G, Tully, J G, Rose, D L,  
; AUTHORS: Petzel, J P, Oyaizu, H, Yang, D, Mandelco,  
; AUTHORS: L, Sechrest, J, Lawrence, T G, Van Etten, J,  
; AUTHORS: Maniloff, J, Woese, C R.  
; TITLE: A phylogenetic analysis of  
; TITLE: the mycoplasmas: Basis for their classification  
; JOURNAL: Journal of Bacteriology  
; VOLUME: 171  
; PAGES: 6455-6467  
; DATE: 1989  
; RELEVANT RESIDUES IN SEQ ID NO: 287 :FROM 1 TO 10  
; US-08-173-489C-287

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 19  
US-08-590-571-19/c

; Sequence 19, Application US/08590571  
; Patent No. 5861246  
; GENERAL INFORMATION:  
; APPLICANT: Sherman Weissman and Girish N. Nallur  
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yahwak & Associates  
; STREET: 25 Skytop Drive  
; CITY: Trumbull  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06611  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,571  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George M. Yahwak  
; REGISTRATION NUMBER: 26,824  
; REFERENCE/DOCKET NUMBER: Yale  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203)268-1951  
; TELEFAX: (203)268-1951  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-590-571-19

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
Db 9 GGGAG 5

RESULT 20  
US-08-590-571-29  
; Sequence 29, Application US/08590571  
; Patent No. 5861246  
; GENERAL INFORMATION:  
; APPLICANT: Sherman Weissman and Girish N. Nallur  
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yahwak & Associates  
; STREET: 25 Skytop Drive  
; CITY: Trumbull  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06611  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,571  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George M. Yahwak

; REGISTRATION NUMBER: 26,824  
; REFERENCE/DOCKET NUMBER: Yale  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203)268-1951  
; TELEFAX: (203)268-1951  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-590-571-29

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 3 GGGAG 7

## RESULT 21

US-08-590-571-31/c  
; Sequence 31, Application US/08590571  
; Patent No. 5861246

; GENERAL INFORMATION:  
; APPLICANT: Sherman Weissman and Girish N. Nallur  
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yahwak & Associates  
; STREET: 25 Skytop Drive  
; CITY: Trumbull  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06611

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,571  
; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: George M. Yahwak  
; REGISTRATION NUMBER: 26,824  
; REFERENCE/DOCKET NUMBER: Yale

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203)268-1951

; TELEFAX: (203)268-1951

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-590-571-31

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 9 GGGAG 5

## RESULT 22

US-08-590-571-32  
; Sequence 32, Application US/08590571  
; Patent No. 5861246

; GENERAL INFORMATION:

; APPLICANT: Sherman Weissman and Girish N. Nallur

; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yahwak & Associates

; STREET: 25 Skytop Drive

; CITY: Trumbull

; STATE: Connecticut

; COUNTRY: USA

; ZIP: 06611

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/590,571

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: George M. Yahwak

; REGISTRATION NUMBER: 26,824

; REFERENCE/DOCKET NUMBER: Yale

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203)268-1951

; TELEFAX: (203)268-1951

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-590-571-32

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

## RESULT 23

US-08-599-654-20/c

; Sequence 20, Application US/08599654

; Patent No. 5882925

; GENERAL INFORMATION:

; APPLICANT: FALB, DEAN A

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/599,654

; FILING DATE: 09-FEB-1996

; CLASSIFICATION: 800

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-599-654-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 6 GGGAG 2

RESULT 24
US-08-599-654-30
; Sequence 30, Application US/08599654
; Patent No. 5882925
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,654
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
```

```
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-599-654-30

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 6 GGGAG 10

RESULT 25
US-08-545-253A-15/c
; Sequence 15, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-545-253A-15

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
```

```
Db      |||||
        10 GGGAG 6

RESULT 26
US-08-053-451B-135
; Sequence 135, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Dittlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-053-451B-135

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      5 GGGAG 9

RESULT 27
US-08-485-573-20/c
; Sequence 20, Application US/08485573
; Patent No. 5968770
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      5 GGGAG 9

RESULT 28
US-08-485-573-30
; Sequence 30, Application US/08485573
; Patent No. 5968770
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,573
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
US-08-485-573-20

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      6 GGGAG 2
```

TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-485-573-30

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 29

US-08-265-484B-1/C  
Sequence 1, Application US/08265484B  
Patent No. 5998193

GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid

US-08-265-484B-1

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 10 GGGAG 6

RESULT 30

US-08-265-484B-2  
Sequence 2, Application US/08265484B  
Patent No. 5998193

GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid

US-08-265-484B-2

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 1 GGGAG 5

RESULT 31

US-08-265-484B-4  
Sequence 4, Application US/08265484B  
Patent No. 5998193

GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid

US-08-265-484B-4

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-4

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      1 GGGAG 5

RESULT 32
US-08-265-484B-9
; Sequence 9, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-9

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      1 GGGAG 5

RESULT 33
US-08-265-484B-10
; Sequence 10, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-10

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      1 GGGAG 5

RESULT 34
US-08-265-484B-27/c
; Sequence 27, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
```

; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
; TITLE OF INVENTION: Ribozymes and Compositions Thereof  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,484B  
; FILING DATE: 24-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 45284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other Nucleic Acid  
; US-08-265-484B-27

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 10 GGGAG 6

RESULT 35  
US-08-388-353-86  
; Sequence 86, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353

; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-388-353-86

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 6 GGGAG 10

RESULT 36  
US-08-388-353-87  
; Sequence 87, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-388-353-87



Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 37  
US-08-388-353-88  
; Sequence 88, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-88

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 4 GGGAG 8

RESULT 38  
US-08-388-353-89  
; Sequence 89, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 89:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-89

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 3 GGGAG 7

RESULT 39  
US-08-388-353-90  
; Sequence 90, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:

; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 90:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-90

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 2 GGGAG 6

RESULT 40  
US-08-388-353-91  
; Sequence 91, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-91

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 1 GGGAG 5  
RESULT 41  
US-08-388-353-302/c  
; Sequence 302, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 302:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-302

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 10 GGGAG 6

RESULT 42  
US-08-388-353-303/c  
; Sequence 303, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 303:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-303

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
Db 9 GGGAG 5

RESULT 43  
US-08-388-353-304/c  
Sequence 304, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 304:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-304

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db 8 GGGAG 4

RESULT 44  
US-08-388-353-305/c  
Sequence 305, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 305:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-305

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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Db          7 GGGAG 3

RESULT 45
US-08-388-353-306/c
; Sequence 306, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-306

Query Match      100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGAG 5
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Db          6 GGGAG 2

RESULT 46
US-08-388-353-307/c
; Sequence 307, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City

Query Match      100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGAG 5
           |||||
Db          6 GGGAG 2

RESULT 47
US-08-388-353-694
; Sequence 694, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-306
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TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 694:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-694

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 48  
US-08-388-353-695  
Sequence 695, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 695:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-695

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 49  
US-08-388-353-696  
Sequence 696, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 696:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-696

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 4 GGGAG 8

RESULT 50  
US-08-388-353-697  
Sequence 697, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 697:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-697

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
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Db 3 GGGAG 7

Search completed: January 7, 2005, 11:05:38  
Job time : 61 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
(without alignments)  
106.177 Million cell updates/sec

Title: GGGAG  
Perfect score: 5  
Sequence: 1 gggag 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	5	100.0	10	9	US-09-989-789-569
5	5	100.0	10	9	US-09-989-789-570
6	5	100.0	10	9	US-09-989-789-601
7	5	100.0	10	9	US-09-989-789-604
8	5	100.0	10	9	US-09-989-789-605
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10	5	100.0	10	9	US-09-989-789-610
11	5	100.0	10	9	US-09-989-789-645
12	5	100.0	10	9	US-09-989-789-1271

13	5	100.0	10	9	US-09-989-789-1272	Sequence 1272, Ap
14	5	100.0	10	9	US-09-989-789-1283	Sequence 1283, Ap
15	5	100.0	10	9	US-09-989-789-1288	Sequence 1288, Ap
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19	5	100.0	10	9	US-09-989-789-1345	Sequence 1345, Ap
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44	5	100.0	10	9	US-09-986-718-20	Sequence 20, Appl
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53	5	100.0	10	10	US-09-990-186-609	Sequence 609, App
54	5	100.0	10	10	US-09-990-186-610	Sequence 610, App
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83	5	100.0	10	10	US-09-979-593-38	Sequence 38, Appl
84	5	100.0	10	10	US-09-979-593-49	Sequence 49, Appl
85	5	100.0	10	10	US-09-989-994-569	Sequence 569, App



86	5	100.0	10	10	US-09-989-994-570	Sequence 570, App	Sequence 570, App
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93	5	100.0	10	10	US-09-989-994-1271	Sequence 1271, App	Sequence 1271, App
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297	5	100.0	10	18	US-10-487-934-116	Sequence 116, App	C 370	5	100.0	11	17	US-10-450-797-407	Sequence 407, App
298	5	100.0	10	18	US-10-487-934-134	Sequence 134, App	C 371	5	100.0	11	17	US-10-450-797-441	Sequence 441, App
299	5	100.0	10	18	US-10-487-934-152	Sequence 152, App	372	5	100.0	11	17	US-10-450-797-444	Sequence 444, App
C 300	5	100.0	10	18	US-10-487-934-159	Sequence 159, App	373	5	100.0	11	17	US-10-450-797-551	Sequence 551, App
301	5	100.0	10	18	US-10-487-934-176	Sequence 176, App	374	5	100.0	11	17	US-10-450-797-556	Sequence 556, App
C 302	5	100.0	10	18	US-10-487-934-204	Sequence 204, App	375	5	100.0	11	17	US-10-450-797-572	Sequence 572, App
303	5	100.0	10	18	US-10-487-934-318	Sequence 318, App	C 376	5	100.0	11	17	US-10-450-797-607	Sequence 607, App
C 304	5	100.0	10	18	US-10-602-494-372	Sequence 372, App	377	5	100.0	11	17	US-10-450-797-620	Sequence 620, App

C 378 US-10-450-797-691 Sequence 691, App  
C 379 US-10-450-797-705 Sequence 705, App  
C 380 US-10-450-797-730 Sequence 730, App  
C 381 US-10-450-797-736 Sequence 736, App  
C 382 US-10-450-797-760 Sequence 760, App  
C 383 US-10-450-797-831 Sequence 831, App  
C 384 US-10-450-797-900 Sequence 900, App  
C 385 US-10-450-797-910 Sequence 910, App  
C 386 US-10-450-797-920 Sequence 920, App  
C 387 US-10-450-797-926 Sequence 926, App  
C 388 US-10-450-797-940 Sequence 940, App  
C 389 US-10-450-797-977 Sequence 977, App  
C 390 US-10-450-797-1159 Sequence 1159, Ap  
C 391 US-10-450-797-1160 Sequence 1160, Ap  
C 392 US-10-450-797-1205 Sequence 1205, Ap  
C 393 US-10-450-797-1242 Sequence 1242, Ap  
C 394 US-10-450-797-1267 Sequence 1267, Ap  
C 395 US-10-450-797-1278 Sequence 1278, Ap  
C 396 US-10-450-797-1299 Sequence 1299, Ap  
C 397 US-10-450-797-1340 Sequence 1340, Ap  
C 398 US-10-450-797-1368 Sequence 1368, Ap  
C 399 US-10-450-797-1373 Sequence 1373, Ap  
C 400 US-10-450-797-1394 Sequence 1394, Ap  
C 401 US-10-474-794-14 Sequence 114, App  
C 402 US-10-474-794-114 Sequence 86, Appl  
C 403 US-10-641-962-86 Sequence 1, Appl  
C 404 US-09-559-402-1 Sequence 14, Appl  
C 405 US-09-773-876-14 Sequence 11, Appl  
C 406 US-09-946-893-11 Sequence 5, Appl  
C 407 US-09-256-650-5 Sequence 1, Appl  
C 408 US-09-761-116-1 Sequence 430, App  
C 409 US-09-263-959-430 Sequence 456, App  
C 410 US-09-263-959-456 Sequence 497, App  
C 411 US-09-263-959-497 Sequence 516, App  
C 412 US-09-263-959-516 Sequence 554, App  
C 413 US-09-263-959-554 Sequence 582, App  
C 414 US-09-263-959-582 Sequence 656, App  
C 415 US-09-263-959-656 Sequence 671, App  
C 416 US-09-263-959-671 Sequence 688, App  
C 417 US-09-263-959-688 Sequence 697, App  
C 418 US-09-263-959-697 Sequence 953, App  
C 419 US-09-263-959-953 Sequence 35, Appl  
C 420 US-09-879-813-35 Sequence 46, Appl  
C 421 US-09-879-813-46 Sequence 64, Appl  
C 422 US-09-928-457-64 Sequence 43, Appl  
C 423 US-09-841-157A-43 Sequence 23, Appl  
C 424 US-09-996-263-23 Sequence 30, Appl  
C 425 US-09-765-061B-30 Sequence 40, Appl  
C 426 US-09-765-061B-40 Sequence 7, Appl  
C 427 US-09-923-005-7 Sequence 8, Appl  
C 428 US-09-923-005-8 Sequence 9, Appl  
C 429 US-09-923-005-9 Sequence 10, Appl  
C 430 US-09-923-005-10 Sequence 11, Appl  
C 431 US-09-923-005-11 Sequence 87, Appl  
C 432 US-09-851-871-87 Sequence 6, Appl  
C 433 US-10-073-718-6 Sequence 2, Appl  
C 434 US-10-215-854-2 Sequence 6, Appl  
C 435 US-10-154-993-6 Sequence 48, Appl  
C 436 US-10-078-958-48 Sequence 28, Appl  
C 437 US-10-155-233-28 Sequence 18, Appl  
C 438 US-10-193-451A-18 Sequence 24, Appl  
C 439 US-10-193-451A-24 Sequence 116, App  
C 440 US-10-211-088-116 Sequence 35, Appl  
C 441 US-10-146-505-35 Sequence 46, Appl  
C 442 US-10-146-505-46 Sequence 4, Appl  
C 443 US-10-212-962-4 Sequence 12, Appl  
C 444 US-10-265-031-12 Sequence 11, Appl  
C 445 US-10-325-403-11 Sequence 4, Appl  
C 446 US-10-165-410A-4 Sequence 43, Appl  
C 447 US-10-165-410A-43 Sequence 6, Appl  
C 448 US-10-284-742-6 Sequence 3, Appl  
C 449 US-10-240-580-3 Sequence 299, App  
C 450 US-10-223-666-299

C 451 US-10-352-586-23 Sequence 23, Appl  
C 452 US-10-091-281-177 Sequence 177, App  
C 453 US-10-080-979-11 Sequence 11, Appl  
C 454 US-10-182-329-73 Sequence 73, Appl  
C 455 US-10-444-206-87 Sequence 87, Appl  
C 456 US-10-325-403-11 Sequence 11, Appl  
C 457 US-10-602-837-11 Sequence 11, Appl  
C 458 US-10-461-194-82 Sequence 82, Appl  
C 459 US-10-297-058-16 Sequence 16, Appl  
C 460 US-10-661-165-375 Sequence 375, App  
C 461 US-10-661-165-527 Sequence 527, App  
C 462 US-10-780-439-11 Sequence 11, Appl  
C 463 US-10-793-094-5 Sequence 5, Appl  
C 464 US-10-717-897-74 Sequence 74, Appl  
C 465 US-10-745-462-1 Sequence 1, Appl  
C 466 US-10-830-283-1 Sequence 1, Appl  
C 467 US-10-670-011-385 Sequence 385, App  
C 468 US-10-311-645A-40 Sequence 40, Appl  
C 469 US-10-849-072-8 Sequence 8, Appl  
C 470 US-10-641-962-87 Sequence 87, Appl  
C 471 US-10-836-670-22 Sequence 22, Appl  
C 472 US-10-836-670-26 Sequence 26, Appl  
C 473 US-10-257-017B-267100 Sequence 267100,  
C 474 US-10-257-017B-267239 Sequence 267239,  
C 475 US-10-257-017B-267247 Sequence 267247,  
C 476 US-10-257-017B-267401 Sequence 267401,  
C 477 US-10-257-017B-267405 Sequence 267405,  
C 478 US-10-257-017B-267411 Sequence 267411,  
C 479 US-10-257-017B-267455 Sequence 267455,  
C 480 US-10-257-017B-267456 Sequence 267456,  
C 481 US-10-257-017B-267611 Sequence 267611,  
C 482 US-10-257-017B-267663 Sequence 267663,  
C 483 US-10-257-017B-267729 Sequence 267729,  
C 484 US-10-257-017B-267761 Sequence 267761,  
C 485 US-10-257-017B-267762 Sequence 267762,  
C 486 US-10-257-017B-267822 Sequence 267822,  
C 487 US-10-257-017B-267933 Sequence 267933,  
C 488 US-10-257-017B-268012 Sequence 268012,  
C 489 US-10-257-017B-268137 Sequence 268137,  
C 490 US-10-257-017B-268174 Sequence 268174,  
C 491 US-10-257-017B-268195 Sequence 268195,  
C 492 US-10-257-017B-268240 Sequence 268240,  
C 493 US-10-257-017B-268609 Sequence 268609,  
C 494 US-10-257-017B-268794 Sequence 268794,  
C 495 US-10-257-017B-268862 Sequence 268862,  
C 496 US-10-257-017B-269046 Sequence 269046,  
C 497 US-10-257-017B-269047 Sequence 269047,  
C 498 US-10-257-017B-269145 Sequence 269145,  
C 499 US-10-257-017B-269218 Sequence 269218,  
C 500 US-10-257-017B-306175 Sequence 306175,

ALIGNMENTS

RESULT 1  
US-09-907-074A-14  
; Sequence 14, Application US/09907074A  
; Publication No. US20010055773A1  
; GENERAL INFORMATION:  
; APPLICANT: Jayasena, Sumedha  
; APPLICANT: Gold, Larry  
; TITLE OF INVENTION: Homogeneous Detection of a Target Through Nucleic Acid  
; FILE OF INVENTION: Ligand-Ligand Beacon Interaction  
; FILE REFERENCE: NEX64/PCT-USC  
; CURRENT APPLICATION NUMBER: US/09/907,074A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/581,326  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: PCT/US98/26599  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/068,135  
; PRIOR FILING DATE: 1997-12-15

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; PRIOR APPLICATION NUMBER: 09/157,206
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-907-074A-14

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 2
US-09-907-074A-15/c
; Sequence 15, Application US/09907074A
; Publication No. US20010055773A1
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Homogeneous Detection of a Target Through Nucleic Acid
; TITLE OF INVENTION: Ligand-Ligand Beacon Interaction
; FILE REFERENCE: NEX64/PCT-USC
; CURRENT APPLICATION NUMBER: US/09/907,074A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/581,326
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US98/26599
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/068,135
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: 09/157,206
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-907-074A-15

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      8 GGGAG 4

RESULT 3
US-09-154-750A-49
; Sequence 49, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
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; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Sequence
US-09-154-750A-49

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 4
US-09-989-789-569
; Sequence 569, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 569
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-569

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 5
US-09-989-789-570
; Sequence 570, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 570
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
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; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 610  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-610

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 2 GGGAG 6

RESULT 11  
US-09-989-789-645  
; Sequence 645, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 645  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-645

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 2 GGGAG 6

RESULT 12  
US-09-989-789-1271  
; Sequence 1271, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1271  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1271

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 3 GGGAG 7

RESULT 13  
US-09-989-789-1272  
; Sequence 1272, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1272  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1272

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 3 GGGAG 7

RESULT 14  
US-09-989-789-1283  
; Sequence 1283, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1283  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1283

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
Db 2 GGGAG 6

RESULT 15  
US-09-989-789-1288



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; Sequence 1288, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1288
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-989-789-1288

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      2 GGGAG 6

RESULT 16
US-09-989-789-1303
; Sequence 1303, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1303
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-989-789-1303

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      2 GGGAG 6

RESULT 17
US-09-989-789-1304
; Sequence 1304, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 1304
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-989-789-1304

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      3 GGGAG 7

RESULT 18
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      3 GGGAG 7

RESULT 19
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
;
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      3 GGGAG 7
```



```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
   |||||
Db 3 GGGAG 7

RESULT 20
US-09-989-789-1620
; Sequence 1620, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1620
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1620

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
   |||||
Db 3 GGGAG 7

RESULT 21
US-09-989-789-1630
; Sequence 1630, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1630

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
   |||||
Db 3 GGGAG 7

RESULT 22
US-09-989-789-1631
; Sequence 1631, Application US/09989789
; Patent No. US20020063379A1
```

```
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1631

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
   |||||
Db 3 GGGAG 7

RESULT 23
US-09-989-789-1655
; Sequence 1655, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1655
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1655

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
   |||||
Db 3 GGGAG 7

RESULT 24
US-09-989-789-1656
; Sequence 1656, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1656
; LENGTH: 10
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1656

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7

RESULT 25
US-09-989-789-1657
; Sequence 1657, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1657
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1657

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7

RESULT 26
US-09-989-789-1666
; Sequence 1666, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1666

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7

RESULT 27
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       5 GGGAG 9

RESULT 28
US-09-989-789-1674
; Sequence 1674, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1674

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       5 GGGAG 9

RESULT 29
US-09-989-789-1685
; Sequence 1685, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
```

```
QY      1 GGGAG 5
        |||||
Db       5 GGGAG 9

RESULT 27
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       5 GGGAG 9

RESULT 28
US-09-989-789-1674
; Sequence 1674, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1674

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db       5 GGGAG 9

RESULT 29
US-09-989-789-1685
; Sequence 1685, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
```

```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1685
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1685
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7
```

## RESULT 30

```
US-09-989-789-1696
; Sequence 1696, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1696
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1696
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7
```

## RESULT 31

```
US-09-989-789-1697
; Sequence 1697, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1697
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1697
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGAG 5
        |||||
Db       3 GGGAG 7
```

## RESULT 32

```
US-09-989-789-1698
; Sequence 1698, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1698
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1698
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGAG 5
        |||||
Db       2 GGGAG 6
```

## RESULT 33

```
US-09-989-789-1699
; Sequence 1699, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1699
```

```
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGAG 5
        |||||
```

Db 3 GGGAG 7

RESULT 34

US-09-989-789-1700

; Sequence 1700, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1700

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-1700

Query Match 100.0%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|||||

Db 3 GGGAG 7

RESULT 35

US-09-989-789-1701

; Sequence 1701, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1701

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-1701

Query Match 100.0%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|||||

Db 3 GGGAG 7

RESULT 36

US-09-989-789-1702

; Sequence 1702, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1702

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-1702

Query Match 100.0%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|||||

Db 2 GGGAG 6

RESULT 37

US-09-989-789-1703

; Sequence 1703, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1703

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-789-1703

Query Match 100.0%; Score 5; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|||||

Db 3 GGGAG 7

RESULT 38

US-09-989-789-1704

; Sequence 1704, Application US/09989789

; Patent No. US20020063379A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1704

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target



```
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-371-900-30

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      6 GGGAG 10

RESULT 42
US-09-970-820-20/c
; Sequence 20, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-970-820-20

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
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Db      6 GGGAG 10

RESULT 44
US-09-986-718-20/c
; Sequence 20, Application US/09986718
; Patent No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```
Db      |||||
      6 GGGAG 2

RESULT 43
US-09-970-820-30
; Sequence 30, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-970-820-30

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      6 GGGAG 10

RESULT 44
US-09-986-718-20/c
; Sequence 20, Application US/09986718
; Patent No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,718  
FILING DATE: 09-No. US20020178458A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/485,573  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-986-718-20  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||  
6 GGGAG 2  
RESULT 45  
US-09-986-718-30  
Sequence 30, Application US/09986718  
Patent No. US20020178458A1  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,718  
FILING DATE: 09-No. US20020178458A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/485,573  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-986-718-30  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||  
6 GGGAG 10  
RESULT 46  
US-09-846-033B-142  
Sequence 142, Application US/09846033B  
Publication No. US2003004404A1  
GENERAL INFORMATION:  
APPLICANT: Rebar, Edward  
APPLICANT: Jamieson, Andrew  
APPLICANT: Liu, Qiang  
APPLICANT: Liu, Pei-Qi  
APPLICANT: Wolffe, Alan  
APPLICANT: Eisenberg, Stephen P.  
APPLICANT: Jarvis, Eric  
APPLICANT: Sangamo BioSciences, Inc.  
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
FILE REFERENCE: 019496-005820US  
CURRENT APPLICATION NUMBER: US/09/846,033B  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 09/733,604  
PRIOR FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: US 09/736,083  
PRIOR FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 252  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 142  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: target  
US-09-846-033B-142  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGAG 5  
Db |||||  
2 GGGAG 6  
RESULT 47  
US-09-846-033B-146  
Sequence 146, Application US/09846033B  
Publication No. US2003004404A1  
GENERAL INFORMATION:  
APPLICANT: Rebar, Edward



```

; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolfe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; TITLE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-146

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      5 GGGAG 9

RESULT 48
US-09-990-186-569
; Sequence 569, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 569
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-569

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 49
US-09-990-186-570
; Sequence 570, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 570
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-570

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      3 GGGAG 7

RESULT 50
US-09-990-186-601
; Sequence 601, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-601

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
      |||||
Db      2 GGGAG 6

Search completed: January 7, 2005, 11:31:24
Job time : 273.2 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGGGG

Perfect score: 5

Sequence: 1 ggggg 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	100.0	10	6	A19426
2	5	100.0	10	6	A19427
3	5	100.0	10	6	A72419
4	5	100.0	10	6	A72420
5	5	100.0	10	6	A76186
6	5	100.0	10	6	A76256
7	5	100.0	10	6	A76259
8	5	100.0	10	6	A80129
9	5	100.0	10	6	A80130
10	5	100.0	10	6	A82122
11	5	100.0	10	6	A82123
12	5	100.0	10	6	AR016487
13	5	100.0	10	6	AR030034
14	5	100.0	10	6	AR030035
15	5	100.0	10	6	AR030217
16	5	100.0	10	6	AR030222
17	5	100.0	10	6	AR030233
18	5	100.0	10	6	AR030236
19	5	100.0	10	6	AR030238

C 93	5	100.0	10	6	BD239299	BD239299	Preparati
C 94	5	100.0	10	6	BD239303	BD239303	Preparati
C 95	5	100.0	10	6	BD239308	BD239308	Preparati
C 96	5	100.0	10	6	BD239382	BD239382	Preparati
C 97	5	100.0	10	6	BD239427	BD239427	Preparati
C 98	5	100.0	10	6	BD239542	BD239542	Preparati
C 99	5	100.0	10	6	BD239623	BD239623	Preparati
100	5	100.0	10	6	BD239625	BD239625	Preparati
101	5	100.0	10	6	BD239641	BD239641	Preparati
102	5	100.0	10	6	BD239883	BD239883	Preparati
C 103	5	100.0	10	6	BD239927	BD239927	Preparati
C 104	5	100.0	10	6	BD239953	BD239953	Preparati
C 105	5	100.0	10	6	BD239967	BD239967	Preparati
C 106	5	100.0	10	6	BD240009	BD240009	Preparati
C 107	5	100.0	10	6	BD240196	BD240196	Preparati
C 108	5	100.0	10	6	BD240240	BD240240	Preparati
C 109	5	100.0	10	6	BD240315	BD240315	Preparati
110	5	100.0	10	6	BD240330	BD240330	Preparati
C 111	5	100.0	10	6	BD240380	BD240380	Preparati
C 112	5	100.0	10	6	BD240447	BD240447	Preparati
C 113	5	100.0	10	6	BD240565	BD240565	Preparati
C 114	5	100.0	10	6	BD240602	BD240602	Preparati
C 115	5	100.0	10	6	BD240680	BD240680	Preparati
C 116	5	100.0	10	6	BD240686	BD240686	Preparati
C 117	5	100.0	10	6	BD243162	BD243162	Preparati
C 118	5	100.0	10	6	CQ766713	CQ766713	Sequence
C 119	5	100.0	10	6	CQ786560	CQ786560	Sequence
C 120	5	100.0	10	6	E11167	E11167	Oligonucleo
C 121	5	100.0	10	6	E17309	E17309	PCR primer
C 122	5	100.0	10	6	E39492	E39492	Genes with
C 123	5	100.0	10	6	E39516	E39516	Genes with
C 124	5	100.0	10	6	E39544	E39544	Genes with
C 125	5	100.0	10	6	E39586	E39586	Genes with
C 126	5	100.0	10	6	E39601	E39601	Genes with
C 127	5	100.0	10	6	E39656	E39656	Genes with
C 128	5	100.0	10	6	E39685	E39685	Genes with
C 129	5	100.0	10	6	E39692	E39692	Genes with
C 130	5	100.0	10	6	E39706	E39706	Genes with
C 131	5	100.0	10	6	E39746	E39746	Genes with
C 132	5	100.0	10	6	E39750	E39750	Genes with
C 133	5	100.0	10	6	E54811	E54811	Human norma
C 134	5	100.0	10	6	I13448	I13448	Sequence 51
C 135	5	100.0	10	6	I13449	I13449	Sequence 52
C 136	5	100.0	10	6	I17723	I17723	Sequence 3
C 137	5	100.0	10	6	I21132	I21132	Sequence 17
C 138	5	100.0	10	6	I21133	I21133	Sequence 18
C 139	5	100.0	10	6	I21707	I21707	Sequence 3
C 140	5	100.0	10	6	I22192	I22192	Sequence 6
C 141	5	100.0	10	6	I36118	I36118	Sequence 18
C 142	5	100.0	10	6	I48951	I48951	Sequence 4
C 143	5	100.0	10	6	I54926	I54926	Sequence 16
C 144	5	100.0	10	6	I58808	I58808	Sequence 3
C 145	5	100.0	10	6	I58809	I58809	Sequence 4
C 146	5	100.0	10	6	I59753	I59753	Sequence 17
C 147	5	100.0	10	6	I59754	I59754	Sequence 18
C 148	5	100.0	10	6	I79745	I79745	Sequence 41
C 149	5	100.0	10	6	I90237	I90237	Sequence 18
C 150	5	100.0	10	6	AR195167	AR195167	Sequence
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C 156	5	100.0	10	6	AR266729	AR266729	Sequence
C 157	5	100.0	10	6	AR266732	AR266732	Sequence
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C 159	5	100.0	10	6	AR266734	AR266734	Sequence
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C 162	5	100.0	10	6	AR306131	AR306131	Sequence
C 163	5	100.0	10	6	AR306856	AR306856	Sequence
C 164	5	100.0	10	6	AR306862	AR306862	Sequence
C 165	5	100.0	10	6	AR306866	AR306866	Sequence

C 166	5	100.0	10	6	AR306872	AR306872	Sequence
C 167	5	100.0	10	6	AR336862	AR336862	Sequence
C 168	5	100.0	10	6	AR351638	AR351638	Sequence
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C 182	5	100.0	10	6	AX039269	AX039269	Sequence
C 183	5	100.0	10	6	AX063647	AX063647	Sequence
C 184	5	100.0	10	6	AX074495	AX074495	Sequence
C 185	5	100.0	10	6	AX074498	AX074498	Sequence
C 186	5	100.0	10	6	AX074498	AX074498	Sequence
C 187	5	100.0	10	6	AX099009	AX099009	Sequence
C 188	5	100.0	10	6	AX099010	AX099010	Sequence
C 189	5	100.0	10	6	AX138244	AX138244	Sequence
C 190	5	100.0	10	6	AX138247	AX138247	Sequence
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C 192	5	100.0	10	6	AX147749	AX147749	Sequence
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C 194	5	100.0	10	6	AX152116	AX152116	Sequence
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C 208	5	100.0	10	6	AX152784	AX152784	Sequence
C 209	5	100.0	10	6	AX152785	AX152785	Sequence
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C 211	5	100.0	10	6	AX152905	AX152905	Sequence
C 212	5	100.0	10	6	AX152910	AX152910	Sequence
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ORGANISM	synthetic construct						
REFERENCE	1 (bases 1 to 10)						
AUTHORS	van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A., Veenstra,A.E., Luiten,R.G.M. and Seltlen,G.C.M.						
TITLE	Cloning and expression of microbial phytase						
JOURNAL	Patent: EP 0420358-A 15 03-APR-1991;						
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REFERENCE 1 (bases 1 to 10)
AUTHORS van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A.,
TITLE Veenstra,A.E., Luiten,R.G.M. and Selten,G.C.M.
JOURNAL Cloning and expression of microbial phytase
Patent: EP 0420358-A 16 03-APR-1991;
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ACCESSION A72419
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KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530747-A 6 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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VERSION A72420.1 GI:6063743
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ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530747-A 7 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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VERSION A76186.1 GI:6088296
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Taylor,P.N.
TITLE IMPROVEMENTS IN OR RELATING TO DNA CLONING TECHNIQUES AND PRODUCTS
FOR USE THEREWITH
JOURNAL Patent: WO 9319186-A 14 30-SEP-1993;
UNIV HULL (GB)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db 6 GGGGG 10

RESULT 6
A76256
LOCUS A76256
DEFINITION Sequence 27 from Patent WO9319181.
ACCESSION A76256
VERSION A76256.1 GI:6088355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Sandal,N. and Marcker,K.
TITLE BIOLOGICAL MATERIAL
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JOURNAL Patent: WO 9319181-A 27 30-SEP-1993;
SANDOZ AG (AT); SANDOZ AG (DE)
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QY      1 GGGGG 5
      |||||
Db      2 GGGGG 6
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RESULT 7
LOCUS A76259 A76259 10 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 30 from Patent WO9319181.
ACCESSION A76259
VERSION A76259.1 GI:6088358
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Sandal,N. and Marcker,K.
TITLE BIOLOGICAL MATERIAL
JOURNAL Patent: WO 9319181-A 30 30-SEP-1993;
SANDOZ AG (AT); SANDOZ AG (DE)
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QY      1 GGGGG 5
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Db      2 GGGGG 6
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RESULT 8
LOCUS A80129 A80129 10 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 6 from Patent WO9530748.
ACCESSION A80129
VERSION A80129.1 GI:6092861
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530748-A 6 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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  Best Local Similarity 100.0%; Pred. No. 3.1e+07;
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QY      1 GGGGG 5
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Db      2 GGGGG 6
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JOURNAL Patent: WO 9319181-A 27 30-SEP-1993;
SANDOZ AG (AT); SANDOZ AG (DE)
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  Best Local Similarity 100.0%; Pred. No. 3.1e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGG 5
      |||||
Db      2 GGGGG 6
      |||||
RESULT 9
LOCUS A80130 A80130 10 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 7 from Patent WO9530748.
ACCESSION A80130
VERSION A80130.1 GI:6092862
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530748-A 7 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGG 5
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Db      3 GGGGG 7
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RESULT 10
LOCUS A82122 A82122 10 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent EP0887405.
ACCESSION A82122
VERSION A82122.1 GI:6731987
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Brown,J.W.
TITLE Process for producing stabilised RNA molecules within cells, RNA
          molecules thus produced and nucleic acid precursors of such
          molecules
JOURNAL Patent: EP 0887405-A 1 30-DEC-1998;
GENE SHEARS PTY LTD (AU)
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  Best Local Similarity 100.0%; Pred. No. 3.1e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGG 5
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Db      3 GGGGG 7
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RESULT 11
LOCUS A82123 A82123 10 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent EP0887405.
ACCESSION A82123
VERSION A82123.1 GI:6731987
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Brown,J.W.
TITLE Process for producing stabilised RNA molecules within cells, RNA
          molecules thus produced and nucleic acid precursors of such
          molecules
JOURNAL Patent: EP 0887405-A 1 30-DEC-1998;
GENE SHEARS PTY LTD (AU)
FEATURES
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  Best Local Similarity 100.0%; Pred. No. 3.1e+07;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGG 5
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Db      3 GGGGG 7
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LOCUS A82123 10 bp DNA linear PAT 21-JAN-2000  
DEFINITION Sequence 2 from Patent EP0887405.  
ACCESSION A82123  
VERSION A82123.1 GI:6731988  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Leader,D.J. and Brown,J.W.  
TITLE Process for producing stabilised RNA molecules within cells, RNA molecules thus produced and nucleic acid precursors of such molecules  
JOURNAL Patent: EP 0887405-A 2 30-DEC-1998;  
FEATURES GENE SHEARS PTY LTD (AU)  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 8 GGGGG 4  
RESULT 12  
LOCUS AR016487 10 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 2 from patent US 5776744.  
ACCESSION AR016487  
VERSION AR016487.1 GI:3972764  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Glazer,P.M., Lin,L.Michael. and George,J.  
TITLE Methods and compositions for effecting homologous recombination  
JOURNAL Patent: US 5776744-A 2 07-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..10  
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/mol\_type="unassigned DNA"  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 6 GGGGG 10  
RESULT 13  
LOCUS AR030034 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 223 from patent US 5861244.  
ACCESSION AR030034  
VERSION AR030034.1 GI:5943248  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation

JOURNAL Patent: US 5861244-A 223 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 4 GGGGG 8  
RESULT 14  
LOCUS AR030035/c 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 224 from patent US 5861244.  
ACCESSION AR030035  
VERSION AR030035.1 GI:5943249  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 224 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 9 GGGGG 5  
RESULT 15  
LOCUS AR030217 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 28 from patent US 5861246.  
ACCESSION AR030217  
VERSION AR030217.1 GI:5943431  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 28 19-JAN-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 3 GGGGG 7

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RESULT 16
AR030222 LOCUS AR030222 Sequence 33 from patent US 5861246. 10 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR030222
VERSION AR030222.1 GI:5943436
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding proteins
JOURNAL Patent: US 5861246-A 33 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..10
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db |||||
1 GGGGG 5
RESULT 17
AR030233 LOCUS AR030233 Sequence 44 from patent US 5861246. 10 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR030233
VERSION AR030233.1 GI:5943447
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding proteins
JOURNAL Patent: US 5861246-A 44 19-JAN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db |||||
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RESULT 18
AR030236 LOCUS AR030236 Sequence 47 from patent US 5861246. 10 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR030236
VERSION AR030236.1 GI:5943450
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
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AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding proteins
JOURNAL Patent: US 5861246-A 47 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..10
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db |||||
5 GGGGG 9
RESULT 19
AR030238 LOCUS AR030238 Sequence 49 from patent US 5861246. 10 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR030238
VERSION AR030238.1 GI:5943452
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding proteins
JOURNAL Patent: US 5861246-A 49 19-JAN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db |||||
3 GGGGG 7
RESULT 20
AR032142/c LOCUS AR032142 Sequence 3 from patent US 5866700. 10 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR032142
VERSION AR032142.1 GI:5946431
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Pfeleiderer,W., Schnell,R. and Matysiak,S.
TITLE Solid-phase synthesis of oligoribonucleotides
JOURNAL Patent: US 5866700-A 3 02-FEB-1999;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGG 5
Db |||||
3 GGGGG 7
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QY      1 GGGGG 5
        |||||
Db      10 GGGGG 6

RESULT 21
AR032143 LOCUS      AR032143      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 4 from patent US 5866700.
ACCESSION      AR032143
VERSION      AR032143.1 GI:5946432
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Pfeleiderer,W., Schnell,R. and Matysiak,S.
TITLE      Solid-phase synthesis of oligoribonucleotides
JOURNAL      Patent: US 5866700-A 4 02-FEB-1999;
FEATURES      Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      1 GGGGG 5

RESULT 22
AR043161/c LOCUS      AR043161      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 45 from patent US 5814453.
ACCESSION      AR043161
VERSION      AR043161.1 GI:5964169
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Beck,J.Joseph.
TITLE      Detection of fungal pathogens using the polymerase chain reaction
JOURNAL      Patent: US 5814453-A 45 29-SEP-1998;
FEATURES      Location/Qualifiers
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                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      6 GGGGG 2

RESULT 23
AR043654/c LOCUS      AR043654      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 24 from patent US 5814517.
ACCESSION      AR043654
VERSION      AR043654.1 GI:5964662
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Beck,J.Joseph.
TITLE      Detection of fungal pathogens using the polymerase chain reaction
JOURNAL      Patent: US 5814453-A 45 29-SEP-1998;
FEATURES      Location/Qualifiers
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                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      6 GGGGG 2
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REFERENCE      1 (bases 1 to 10)
AUTHORS      Seidel,H.Martin. and Lamb,I.Peter.
TITLE      DNA spacer regulatory elements responsive to cytokines and methods
                for their use
JOURNAL      Patent: US 5814517-A 24 29-SEP-1998;
FEATURES      Location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      7 GGGGG 3

RESULT 24
AR049732 LOCUS      AR049732      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 35 from patent US 5824770.
ACCESSION      AR049732
VERSION      AR049732.1 GI:5971724
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Georgopoulos,K.
TITLE      Ikaros polypeptides
JOURNAL      Patent: US 5824770-A 35 20-OCT-1998;
FEATURES      Location/Qualifiers
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                /organism="unknown"
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ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      3 GGGGG 7

RESULT 25
AR058463 LOCUS      AR058463      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 40 from patent US 5837832.
ACCESSION      AR058463
VERSION      AR058463.1 GI:5984040
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
                Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE      Arrays of nucleic acid probes on biological chips
JOURNAL      Patent: US 5837832-A 40 17-NOV-1998;
FEATURES      Location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGGG 5  
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Db 4 GGGGG 8

RESULT 26  
AR058487  
LOCUS AR058487 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 64 from patent US 5837832.  
ACCESSION AR058487  
VERSION AR058487.1 GI:5984064  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,  
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldom,E.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 5837832-A 64 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 3 GGGGG 7

RESULT 27  
AR058519  
LOCUS AR058519 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 96 from patent US 5837832.  
ACCESSION AR058519  
VERSION AR058519.1 GI:5984096  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,  
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldom,E.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 5837832-A 96 17-NOV-1998;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 3 GGGGG 7

RESULT 28  
AR074337  
LOCUS AR074337 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 145 from patent US 5952490.  
ACCESSION AR074337  
VERSION AR074337.1 GI:10001092  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,  
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and  
Imbach,J.Louis.  
TITLE Oligonucleotides having a conserved G4 core sequence  
JOURNAL Patent: US 5952490-A 145 14-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
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Db 1 GGGGG 5

RESULT 29  
AR074448/c  
LOCUS AR074448 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 19 from patent US 5955075.  
ACCESSION AR074448  
VERSION AR074448.1 GI:10001203  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 19 21-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..10  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
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Db 6 GGGGG 2

RESULT 30  
AR074449/c  
LOCUS AR074449 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 20 from patent US 5955075.  
ACCESSION AR074449  
VERSION AR074449.1 GI:10001204  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 20 21-SEP-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
      |||||
Db      8 GGGGG 4

RESULT 31
AR074661/c
LOCUS      AR074661      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION      Sequence 45 from patent US 595274.
ACCESSION      AR074661
VERSION      AR074661.1 GI:10001414
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Ligon,J.M. and Beck,J.J.
TITLE      Detection of fungal pathogens using the polymerase chain reaction
JOURNAL      Patent: US 595274-A 45 21-SEP-1999;
FEATURES
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      /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
      |||||
Db      6 GGGGG 2

RESULT 32
AR078332
LOCUS      AR078332      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION      Sequence 1 from patent US 5962426.
ACCESSION      AR078332
VERSION      AR078332.1 GI:10005078
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Glazer,P.M.
TITLE      Triple-helix forming oligonucleotides for targeted mutagenesis
JOURNAL      Patent: US 5962426-A 1 05-OCT-1999;
FEATURES
      source
      1..10
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      /mol_type="unassigned DNA"

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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 33
AR081128/c
LOCUS      AR081128      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION      Sequence 19 from patent US 5972353.
ACCESSION      AR081128
VERSION      AR081128.1 GI:10007856
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KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL      Patent: US 5972353-A 19 26-OCT-1999;
FEATURES
      Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
      |||||
Db      6 GGGGG 2

RESULT 34
AR081129/c
LOCUS      AR081129      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION      Sequence 20 from patent US 5972353.
ACCESSION      AR081129
VERSION      AR081129.1 GI:10007857
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL      Patent: US 5972353-A 20 26-OCT-1999;
FEATURES
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
      |||||
Db      8 GGGGG 4

RESULT 35
AR085325/c
LOCUS      AR085325      10 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION      Sequence 19 from patent US 5981711.
ACCESSION      AR085325
VERSION      AR085325.1 GI:10012094
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN-specific antibodies and hybridomas
JOURNAL      Patent: US 5981711-A 19 09-NOV-1999;
FEATURES
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Query Match      100.0%; Score 5; DB 6; Length 10;
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGG 5  
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|  
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|  
6 GGGG 2

Db

RESULT 36  
AR085326/c  
LOCUS AR085326 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 20 from patent US 5981711.  
ACCESSION AR085326  
VERSION AR085326.1 GI:10012095  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 20 09-NOV-1999;  
FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGG 5  
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|  
|  
8 GGGG 4

Db

RESULT 37  
AR088073/c  
LOCUS AR088073 10 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 19 from patent US 5989838.  
ACCESSION AR088073  
VERSION AR088073.1 GI:10014836  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 19 23-NOV-1999;  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGG 5  
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|  
|  
|  
|  
6 GGGG 2

Db

RESULT 38  
AR088074/c  
LOCUS AR088074 10 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 20 from patent US 5989838.  
ACCESSION AR088074  
VERSION AR088074.1 GI:10014837  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 20 23-NOV-1999;  
FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGG 5  
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|  
|  
8 GGGG 4

Db

RESULT 39  
AR092699/c  
LOCUS AR092699 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 11 from patent US 5998193.  
ACCESSION AR092699  
VERSION AR092699.1 GI:10019451  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 11 07-DEC-1999;  
FEATURES  
source  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGG 5  
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|  
|  
|  
|  
7 GGGG 3

Db

RESULT 40  
AR092700  
LOCUS AR092700 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 12 from patent US 5998193.  
ACCESSION AR092700  
VERSION AR092700.1 GI:10019452  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 12 07-DEC-1999;  
FEATURES  
source  
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 4 GGGGG 8

## RESULT 41

AR092702 LOCUS AR092702 Sequence 14 from patent US 5998193. 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION  
ACCESSION AR092702  
VERSION AR092702.1 GI:10019454  
KEYWORDS  
SOURCE  
ORGANISM  
Unassigned.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stapper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 14 07-DEC-1999;  
source Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 3 GGGGG 7

## RESULT 42

AR092706 LOCUS AR092706 Sequence 18 from patent US 5998193. 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION  
ACCESSION AR092706  
VERSION AR092706.1 GI:10019458  
KEYWORDS  
SOURCE  
ORGANISM  
Unassigned.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stapper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 18 07-DEC-1999;  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 4 GGGGG 8

## RESULT 43

AR092708 LOCUS AR092708 Sequence 20 from patent US 5998193. 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION

ACCESSION AR092708  
VERSION AR092708.1 GI:10019460  
KEYWORDS  
SOURCE  
ORGANISM  
Unassigned.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stapper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 20 07-DEC-1999;  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 4 GGGGG 8

## RESULT 44

AR092709 LOCUS AR092709 Sequence 21 from patent US 5998193. 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION  
ACCESSION AR092709  
VERSION AR092709.1 GI:10019461  
KEYWORDS  
SOURCE  
ORGANISM  
Unassigned.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stapper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 21 07-DEC-1999;  
source Location/Qualifiers  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 3 GGGGG 7

## RESULT 45

AR092710 LOCUS AR092710 Sequence 22 from patent US 5998193. 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION  
ACCESSION AR092710  
VERSION AR092710.1 GI:10019462  
KEYWORDS  
SOURCE  
ORGANISM  
Unassigned.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stapper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 22 07-DEC-1999;  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
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Db      6 GGGGG 10

RESULT 46
LOCUS      AR092711      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 23 from patent US 5998193.
ACCESSION  AR092711
VERSION     AR092711.1 GI:10019463
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Keese,P., Stapper,M. and Perriman,R.
TITLE      Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
           embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 23 07-DEC-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      4 GGGGG 8

RESULT 47
AR092712/c
LOCUS      AR092712      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 24 from patent US 5998193.
ACCESSION  AR092712
VERSION     AR092712.1 GI:10019464
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Keese,P., Stapper,M. and Perriman,R.
TITLE      Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
           embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 24 07-DEC-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 3
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/organism="unknown"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      4 GGGGG 8

RESULT 48
LOCUS      AR094553      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6001657.
ACCESSION  AR094553
VERSION     AR094553.1 GI:10021585
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Hardin,C.C., Brown,B.A. II, Roberts,J.F. and Pelsue,S.C.
TITLE      Antibodies that selectively bind quadruplex nucleic acids
JOURNAL    Patent: US 6001657-A 1 14-DEC-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      4 GGGGG 8

RESULT 49
AR096853/c
LOCUS      AR096853      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 4 from patent US 6008400.
ACCESSION  AR096853
VERSION     AR096853.1 GI:10026024
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Scaringe,S. and Caruthers,M.H.
TITLE      Orthoester reagents for use as protecting groups in oligonucleotide
           synthesis
JOURNAL    Patent: US 6008400-A 4 28-DEC-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      9 GGGGG 5

RESULT 50
AR098905
LOCUS      AR098905      10 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 41 from patent US 6077685.
ACCESSION  AR098905
VERSION     AR098905.1 GI:12808671
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE      Tumor suppressor merlin and antibodies thereof
JOURNAL    Patent: US 6077685-A 41 20-JUN-2000;
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Matches       5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;  
  
QY                      1 GGGGG 5  
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Db                      5 GGGGG 9

Search completed: January 7, 2005, 07:55:24  
Job time : 520 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:35:05 ; Search time 254.4 Seconds  
(without alignments)  
103.173 Million cell updates/sec

Title: GGGGG  
Perfect score: 5  
Sequence: 1 ggggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3979404

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : N\_Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
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3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	100.0	10	2	AAQ49546 Primer to
3	5	100.0	10	2	AAQ79368 Regulator
4	5	100.0	10	2	AAQ79367 Regulator
5	5	100.0	10	2	AAQ79359 Sequence
6	5	100.0	10	2	AAQ79358 Sequence
7	5	100.0	10	2	AAQ71100 Merlin ex
8	5	100.0	10	2	AAQ64610 Alzheimer
9	5	100.0	10	2	AAT08734 U4snRNA
10	5	100.0	10	2	AAX32616 Anticance
11	5	100.0	10	2	AAT08758 U4snRNA
12	5	100.0	10	2	AAQ96682 HIV-1 NL4
13	5	100.0	10	2	AAQ96685 HIV-1 NL4
14	5	100.0	10	2	AAQ96686 HIV-1 NL4
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20	5	100.0	10	2	AAQ88461 Human mit
21	5	100.0	10	2	AAQ88437 Human mit

22	5	100.0	10	2	AAQ88493 Human mit
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26	5	100.0	10	2	Aeq81070 supF gene
27	5	100.0	10	2	AAT27213 HIV-1 det
28	5	100.0	10	2	AAT35000 HIV inhib
29	5	100.0	10	2	AAT35713 Primer UB
30	5	100.0	10	2	AAT10084 Hammerhea
31	5	100.0	10	2	AAT98862 Core-bind
32	5	100.0	10	2	AAT98847 Binding s
33	5	100.0	10	2	AAT98859 Core-bind
34	5	100.0	10	2	AAT98864 Core-bind
35	5	100.0	10	2	AAT98851 Binding s
36	5	100.0	10	2	AAT70006 Triplex-f
37	5	100.0	10	2	AAT70007 Oligonuc
38	5	100.0	10	2	AAT80370 Oligo HCV
39	5	100.0	10	2	AAT47062 Oligonuc
40	5	100.0	10	2	AAV62570 Septoria
41	5	100.0	10	2	AAV45390 Mouse CD3
42	5	100.0	10	2	AAV67001 CD3-epsil
43	5	100.0	10	2	Aaz86960 PCR prime
44	5	100.0	10	2	AAV32461 Oligonuc
45	5	100.0	10	2	AAV56865 Regulator
46	5	100.0	10	2	AAV50112 Yeast tag
47	5	100.0	10	2	AAV50068 Yeast tag
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49	5	100.0	10	2	AAV4582 Inverted
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51	5	100.0	10	2	AAX54730 Tumour ne
52	5	100.0	10	2	AAX54777 Inducible
53	5	100.0	10	2	AAX14836 Triple he
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58	5	100.0	10	3	AAA07996 DNA seque
59	5	100.0	10	3	AAA07995 DNA seque
60	5	100.0	10	3	AAA34177 Human ade
61	5	100.0	10	3	AAA34224 Human ade
62	5	100.0	10	3	Aaz78372 Human den
63	5	100.0	10	3	Aaz77991 Human den
64	5	100.0	10	3	Aaz78289 Human den
65	5	100.0	10	3	Aaz78293 Human den
66	5	100.0	10	3	Aaz78417 Human den
67	5	100.0	10	3	Aaz78615 Human den
68	5	100.0	10	3	Aaz79320 Human den
69	5	100.0	10	3	Aaz79555 Human den
70	5	100.0	10	3	Aaz79676 Human den
71	5	100.0	10	3	Aaz78097 Human den
72	5	100.0	10	3	Aaz79592 Human den
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79	5	100.0	10	3	Aaz78532 Human den
80	5	100.0	10	3	Aaz78631 Human den
81	5	100.0	10	3	Aaz79186 Human den
82	5	100.0	10	3	Aaz79437 Human den
83	5	100.0	10	3	Aaz79670 Human den
84	5	100.0	10	3	Aaz78250 Human den
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86	5	100.0	10	3	Aaz78150 Human den
87	5	100.0	10	3	Aaz77893 Human den
88	5	100.0	10	3	Aaz79230 Human den
89	5	100.0	10	3	Aaz78298 Human den
90	5	100.0	10	3	Aaz78873 Human den
91	5	100.0	10	3	Aaz78957 Human den
92	5	100.0	10	3	Aaz77789 Human den
93	5	100.0	10	3	Aaz78185 Human den
94	5	100.0	10	3	Aaz78613 Human den

C 95	5	100.0	10	3	AAZ78917	Aaz78917	Human den
C 96	5	100.0	10	3	AAZ78999	Aaz78999	Human den
C 97	5	100.0	10	3	AAZ79305	Aaz79305	Human den
C 98	5	100.0	10	3	AAZ77828	Aaz77828	Human den
C 99	5	100.0	10	3	AAZ78943	Aaz78943	Human den
C 100	5	100.0	10	3	AAZ77707	Aaz77707	Human den
C 101	5	100.0	10	3	AAZ81922	Aaz81922	Metastati
C 102	5	100.0	10	3	AAZ81974	Aaz81974	Metastati
C 103	5	100.0	10	3	AAZ82416	Aaz82416	Metastati
C 104	5	100.0	10	3	AAZ83861	Aaz83861	Metastati
C 105	5	100.0	10	3	AAZ83994	Aaz83994	Metastati
C 106	5	100.0	10	3	AAZ84216	Aaz84216	Metastati
C 107	5	100.0	10	3	AAZ84412	Aaz84412	Metastati
C 108	5	100.0	10	3	AAZ85416	Aaz85416	Metastati
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C 112	5	100.0	10	3	AAZ81900	Aaz81900	Metastati
C 113	5	100.0	10	3	AAZ82527	Aaz82527	Metastati
C 114	5	100.0	10	3	AAZ83394	Aaz83394	Metastati
C 115	5	100.0	10	3	AAZ83803	Aaz83803	Metastati
C 116	5	100.0	10	3	AAZ84716	Aaz84716	Metastati
C 117	5	100.0	10	3	AAZ84926	Aaz84926	Metastati
C 118	5	100.0	10	3	AAZ85143	Aaz85143	Metastati
C 119	5	100.0	10	3	AAZ85703	Aaz85703	Metastati
C 120	5	100.0	10	3	AAZ85747	Aaz85747	Metastati
C 121	5	100.0	10	3	AAZ81975	Aaz81975	Metastati
C 122	5	100.0	10	3	AAZ82651	Aaz82651	Metastati
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C 125	5	100.0	10	3	AAZ84949	Aaz84949	Metastati
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C 127	5	100.0	10	3	AAZ85429	Aaz85429	Metastati
C 128	5	100.0	10	3	AAZ85597	Aaz85597	Metastati
C 129	5	100.0	10	3	AAZ85929	Aaz85929	Metastati
C 130	5	100.0	10	3	AAZ85979	Aaz85979	Metastati
C 131	5	100.0	10	3	AAZ86039	Aaz86039	Metastati
C 132	5	100.0	10	3	AAZ86048	Aaz86048	Metastati
C 133	5	100.0	10	3	AAZ86049	Aaz86049	Metastati
C 134	5	100.0	10	3	AAZ81472	Aaz81472	Metastati
C 135	5	100.0	10	3	AAZ83866	Aaz83866	Metastati
C 136	5	100.0	10	3	AAZ83888	Aaz83888	Metastati
C 137	5	100.0	10	3	AAZ85191	Aaz85191	Metastati
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C 141	5	100.0	10	3	AAZ81725	Aaz81725	Metastati
C 142	5	100.0	10	3	AAZ81943	Aaz81943	Metastati
C 143	5	100.0	10	3	AAZ82313	Aaz82313	Metastati
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C 145	5	100.0	10	3	AAZ83196	Aaz83196	Metastati
C 146	5	100.0	10	3	AAZ83756	Aaz83756	Metastati
C 147	5	100.0	10	3	AAZ81370	Aaz81370	Metastati
C 148	5	100.0	10	3	AAZ81382	Aaz81382	Metastati
C 149	5	100.0	10	3	AAZ81489	Aaz81489	Metastati
C 150	5	100.0	10	3	AAZ83981	Aaz83981	Metastati
C 151	5	100.0	10	3	AAZ84360	Aaz84360	Metastati
C 152	5	100.0	10	3	AAZ85495	Aaz85495	Metastati
C 153	5	100.0	10	3	AAZ86185	Aaz86185	Metastati
C 154	5	100.0	10	3	AAZ86185	Aaz86185	Metastati
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C 156	5	100.0	10	3	AAZ81677	Aaz81677	Metastati
C 157	5	100.0	10	3	AAZ82706	Aaz82706	Metastati
C 158	5	100.0	10	3	AAZ82817	Aaz82817	Metastati
C 159	5	100.0	10	3	AAZ83011	Aaz83011	Metastati
C 160	5	100.0	10	3	AAZ84580	Aaz84580	Metastati
C 161	5	100.0	10	3	AAZ84976	Aaz84976	Metastati
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C 167	5	100.0	10	3	AAZ85018	Aaz85018	Metastati
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C 171	5	100.0	10	3	AAZ86473	Aaz86473	Metastati
C 172	5	100.0	10	3	AAZ80901	Aaz80901	Metastati
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C 174	5	100.0	10	3	AAZ82441	Aaz82441	Metastati
C 175	5	100.0	10	3	AAZ83274	Aaz83274	Metastati
C 176	5	100.0	10	3	AAZ84139	Aaz84139	Metastati
C 177	5	100.0	10	3	AAZ84180	Aaz84180	Metastati
C 178	5	100.0	10	3	AAZ85190	Aaz85190	Metastati
C 179	5	100.0	10	3	AAZ85902	Aaz85902	Metastati
C 180	5	100.0	10	3	AAZ81824	Aaz81824	Metastati
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C 182	5	100.0	10	3	AAZ83060	Aaz83060	Metastati
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C 184	5	100.0	10	3	AAZ85783	Aaz85783	Metastati
C 185	5	100.0	10	3	AAZ85956	Aaz85956	Metastati
C 186	5	100.0	10	3	AAZ81613	Aaz81613	Metastati
C 187	5	100.0	10	3	AAZ81983	Aaz81983	Metastati
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C 189	5	100.0	10	3	AAZ83576	Aaz83576	Metastati
C 190	5	100.0	10	3	AAZ84112	Aaz84112	Metastati
C 191	5	100.0	10	3	AAZ85138	Aaz85138	Metastati
C 192	5	100.0	10	3	AAZ80769	Aaz80769	Metastati
C 193	5	100.0	10	3	AAZ81372	Aaz81372	Metastati
C 194	5	100.0	10	3	AAZ82034	Aaz82034	Metastati
C 195	5	100.0	10	3	AAZ82512	Aaz82512	Metastati
C 196	5	100.0	10	3	AAZ83865	Aaz83865	Metastati
C 197	5	100.0	10	3	AAZ83944	Aaz83944	Metastati
C 198	5	100.0	10	3	AAZ85074	Aaz85074	Metastati
C 199	5	100.0	10	3	AAZ85245	Aaz85245	Metastati
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C 201	5	100.0	10	3	AAZ81218	Aaz81218	Metastati
C 202	5	100.0	10	3	AAZ81282	Aaz81282	Metastati
C 203	5	100.0	10	3	AAZ84137	Aaz84137	Metastati
C 204	5	100.0	10	3	AAZ80794	Aaz80794	Metastati
C 205	5	100.0	10	3	AAZ82240	Aaz82240	Metastati
C 206	5	100.0	10	3	AAZ82326	Aaz82326	Metastati
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C 208	5	100.0	10	3	AAZ80869	Aaz80869	Metastati
C 209	5	100.0	10	3	AAZ83267	Aaz83267	Metastati
C 210	5	100.0	10	3	AAZ83469	Aaz83469	Metastati
C 211	5	100.0	10	3	AAZ83851	Aaz83851	Metastati
C 212	5	100.0	10	3	AAZ84742	Aaz84742	Metastati
C 213	5	100.0	10	3	AAZ86313	Aaz86313	Metastati
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C 215	5	100.0	10	3	AAZ81284	Aaz81284	Metastati
C 216	5	100.0	10	3	AAZ82195	Aaz82195	Metastati
C 217	5	100.0	10	3	AAZ82922	Aaz82922	Metastati
C 218	5	100.0	10	3	AAZ83070	Aaz83070	Metastati
C 219	5	100.0	10	3	AAZ84776	Aaz84776	Metastati
C 220	5	100.0	10	3	AAZ84975	Aaz84975	Metastati
C 221	5	100.0	10	3	AAA39090	Aaa39090	Control s
C 222	5	100.0	10	3	AAA93859	Aaa93859	Oligonuc
C 223	5	100.0	10	3	AAA93854	Aaa93854	Oligonuc
C 224	5	100.0	10	3	AAA93857	Aaa93857	Oligonuc
C 225	5	100.0	10	3	AAZ74192	Aac74192	Human mon
C 226	5	100.0	10	3	AAZ73962	Aac73962	Human den
C 227	5	100.0	10	3	AAZ73990	Aac73990	Human den
C 228	5	100.0	10	3	AAZ74131	Aac74131	Human mon
C 229	5	100.0	10	3	AAZ73938	Aac73938	Human den
C 230	5	100.0	10	3	AAZ74032	Aac74032	Human mon
C 231	5	100.0	10	3	AAZ74152	Aac74152	Human mon
C 232	5	100.0	10	3	AAZ74138	Aac74138	Human den
C 233	5	100.0	10	3	AAZ74102	Aac74102	Human den
C 234	5	100.0	10	3	AAZ74196	Aac74196	Human mon
C 235	5	100.0	10	3	AAZ74047	Aac74047	Human den
C 236	5	100.0	10	3	AAA13751	Aaa13751	Stem cell
C 237	5	100.0	10	3	AAA56447	Aaa56447	Human mac
C 238	5	100.0	10	3	AAA56480	Aaa56480	Human mac
C 239	5	100.0	10	3	AAA56510	Aaa56510	Human mac
C 240	5	100.0	10	3	AAA56568	Aaa56568	Human mac

C 241	5	100.0	10	3	AAA56193	Aaa56193 Human mon
242	5	100.0	10	3	AAA56269	Aaa56269 Human mac
243	5	100.0	10	3	AAA56482	Aaa56482 Human mac
244	5	100.0	10	3	AAA56335	Aaa56335 Human mac
C 245	5	100.0	10	3	AAA56301	Aaa56301 Human mac
C 246	5	100.0	10	3	AAA56192	Aaa56192 Human mon
247	5	100.0	10	3	AAA56572	Aaa56572 Human mac
C 248	5	100.0	10	3	AAA56323	Aaa56323 Human mac
C 249	5	100.0	10	3	AAA56397	Aaa56397 Human mac
C 250	5	100.0	10	3	AAA56423	Aaa56423 Human mac
C 251	5	100.0	10	3	AAA56150	Aaa56150 Human mon
C 252	5	100.0	10	3	AAA56235	Aaa56235 Human mac
C 253	5	100.0	10	3	AAA56519	Aaa56519 Human mac
C 254	5	100.0	10	3	AAA06058	Aaa06058 CTR gene
C 255	5	100.0	10	3	AAZ79800	Aaz79800 Human cys
256	5	100.0	10	3	AAZ79727	Aaz79727 Human col
C 257	5	100.0	10	3	AAZ79780	Aaz79780 Human bre
C 258	5	100.0	10	3	AAZ79801	Aaz79801 Human cys
C 259	5	100.0	10	3	AAA16550	Aaa16550 Initiator
C 260	5	100.0	10	3	AAF20299	Aaf20299 Human tum
261	5	100.0	10	3	AAF20346	Aaf20346 Human ind
C 262	5	100.0	10	3	AAc60401	Aac60401 Example t
C 263	5	100.0	10	3	AAA52469	Aaa52469 Human MN
264	5	100.0	10	3	AAA61030	Aaa61030 Protein b
265	5	100.0	10	3	AAA61012	Aaa61012 Protein b
266	5	100.0	10	3	AAA61028	Aaa61028 Protein b
267	5	100.0	10	3	AAA61025	Aaa61025 Protein b
268	5	100.0	10	3	AAA61016	Aaa61016 Protein b
C 269	5	100.0	10	3	AAA70754	Aaa70754 PCR prime
C 270	5	100.0	10	3	AAc64304	Aac64304 Stem nucl
271	5	100.0	10	4	AAf92220	Aaf92220 Human IGE
C 272	5	100.0	10	4	AAI67381	Aai67381 Human FKB
273	5	100.0	10	4	AAD06119	Aad06119 Human e2
274	5	100.0	10	4	AAF25058	Aaf25058 Consensus
C 275	5	100.0	10	4	AAF25058	Aaf25058 Consensus
C 276	5	100.0	10	4	AAF25055	Aaf25055 5' termin
C 277	5	100.0	10	4	AAH19564	Aah19564 Translati
C 278	5	100.0	10	4	AAF56225	Aaf56225 DNA bindi
279	5	100.0	10	4	AAF90455	Aaf90455 Egr-1 bin
C 280	5	100.0	10	4	AAc04428	Aac04428 Human DAX
281	5	100.0	10	4	AAc04427	Aac04427 Human DAX
C 282	5	100.0	10	4	AAc04439	Aac04439 Human DAX
C 283	5	100.0	10	4	AAH63741	Aah63741 Human ubi
C 284	5	100.0	10	4	AAH63985	Aah63985 Human ubi
C 285	5	100.0	10	4	AAH64002	Aah64002 Human ubi
C 286	5	100.0	10	4	AAH63400	Aah63400 Human can
287	5	100.0	10	4	AAH63782	Aah63782 Human ubi
288	5	100.0	10	4	AAH64351	Aah64351 Human ubi
C 289	5	100.0	10	4	AAH64235	Aah64235 Human ubi
C 290	5	100.0	10	4	AAH63904	Aah63904 Human ubi
C 291	5	100.0	10	4	AAH64507	Aah64507 Human ubi
C 292	5	100.0	10	4	AAH64515	Aah64515 Human ubi
C 293	5	100.0	10	4	AAH64066	Aah64066 Human ubi
294	5	100.0	10	4	AAH64110	Aah64110 Human ubi
295	5	100.0	10	4	AAH64153	Aah64153 Human ubi
296	5	100.0	10	4	AAH64346	Aah64346 Human ubi
C 297	5	100.0	10	4	AAH63980	Aah63980 Human ubi
298	5	100.0	10	4	AAH63519	Aah63519 Human ubi
C 299	5	100.0	10	4	AAH63742	Aah63742 Human ubi
C 300	5	100.0	10	4	AAH63412	Aah63412 Human can
301	5	100.0	10	4	AAH63518	Aah63518 Human ubi
C 302	5	100.0	10	4	AAH63860	Aah63860 Human ubi
C 303	5	100.0	10	4	AAH63859	Aah63859 Human ubi
C 304	5	100.0	10	4	AAH64514	Aah64514 Human ubi
C 305	5	100.0	10	4	AAH63390	Aah63390 Human can
306	5	100.0	10	4	AAH63665	Aah63665 Human ubi
307	5	100.0	10	4	AAH63689	Aah63689 Human ubi
C 308	5	100.0	10	4	AAH64345	Aah64345 Human ubi
C 309	5	100.0	10	4	AAH63191	Aah63191 Human col
310	5	100.0	10	4	AAH64189	Aah64189 Human ubi
311	5	100.0	10	4	AAH64232	Aah64232 Human ubi
C 312	5	100.0	10	4	AAH64510	Aah64510 Human ubi
313	5	100.0	10	4	AAH63171	Aah63171 Human col

314	5	100.0	10	4	AAH63722	Aah63722 Human ubi
315	5	100.0	10	4	AAH64668	Aah64668 Human col
C 316	5	100.0	10	4	AAH63307	Aah63307 Human col
C 317	5	100.0	10	4	AAH63528	Aah63528 Human ubi
C 318	5	100.0	10	4	AAH64180	Aah64180 Human ubi
C 319	5	100.0	10	4	AAH64286	Aah64286 Human CHR
320	5	100.0	10	4	AAH57291	Aah57291 Human CHR
C 321	5	100.0	10	4	AAc93021	Aac93021 C. cibari
C 322	5	100.0	10	4	AAH20553	Aah20553 Human MTR
C 323	5	100.0	10	4	AAH06402	Aad06402 Translati
C 324	5	100.0	10	4	AAH41330	Aah41330 Universal
C 325	5	100.0	10	4	AAH04110	Aas04110 Human SCF
C 326	5	100.0	10	4	AAH010957	Aad10957 E. coli a
C 327	5	100.0	10	4	AAf89090	Aaf89090 Mammalian
C 328	5	100.0	10	4	AAc91834	Aac91834 C. cibari
329	5	100.0	10	4	AAH32831	Aah32831 LPS activ
330	5	100.0	10	4	AAH32884	Aah32884 LPS activ
C 331	5	100.0	10	4	AAH32822	Aah32822 LPS activ
332	5	100.0	10	4	AAH32722	Aah32722 LPS activ
C 333	5	100.0	10	4	AAH32911	Aah32911 LPS activ
C 334	5	100.0	10	4	AAH32850	Aah32850 LPS activ
C 335	5	100.0	10	4	AAH32908	Aah32908 LPS activ
336	5	100.0	10	4	AAH32790	Aah32790 LPS activ
C 337	5	100.0	10	4	AAH32710	Aah32710 LPS activ
C 338	5	100.0	10	4	AAH32764	Aah32764 LPS activ
C 339	5	100.0	10	4	AAH32644	Aah32644 LPS activ
C 340	5	100.0	10	4	AAH32853	Aah32853 LPS activ
C 341	5	100.0	10	4	ABA81670	Aba81670 Human pho
342	5	100.0	10	4	ABA81659	Aba81659 Human pho
343	5	100.0	10	4	ABA81679	Aba81679 Human pho
C 344	5	100.0	10	5	AAH23888	Aah23888 Human SCF
C 345	5	100.0	10	5	AAH41714	Aah41714 Anti-PEP
C 346	5	100.0	10	5	AAH41708	Aah41708 Anti-PEP
347	5	100.0	10	5	AAH41704	Aah41704 Anti-PEP
C 348	5	100.0	10	5	AAH41694	Aah41694 Anti-PEP
349	5	100.0	10	5	ABA06186	Aba06186 Human nor
C 350	5	100.0	10	5	AAc04211	Aac04211 Human SCF
C 351	5	100.0	10	5	AAf70437	Aaf70437 Human DRD
C 352	5	100.0	10	5	AAf69621	Aaf69621 Human IL4
353	5	100.0	10	5	AAf69646	Aaf69646 Human IL4
354	5	100.0	10	5	AAf74015	Aaf74015 Human SLC
355	5	100.0	10	5	AAc02803	Aac02803 Human pre
C 356	5	100.0	10	5	AAc02802	Aac02802 Human pre
C 357	5	100.0	10	5	AAc10446	Aac10446 Human ste
C 358	5	100.0	10	5	ABA83125	Aba83125 Lutheran
C 359	5	100.0	10	5	ABA83162	Aba83162 Lutheran
C 360	5	100.0	10	5	ABA83177	Aba83177 Galectin-
C 361	5	100.0	10	5	ABA83167	Aba83167 Mesotheli
362	5	100.0	10	5	AAf40195	Aaf40195 Yeast NOR
C 363	5	100.0	10	5	AAf35160	Aaf35160 Yeast NOR
C 364	5	100.0	10	5	AAf37508	Aaf37508 Yeast NOR
C 365	5	100.0	10	5	AAf42809	Aaf42809 Yeast NOR
C 366	5	100.0	10	5	AAf33285	Aaf33285 Yeast hig
C 367	5	100.0	10	5	AAf33329	Aaf33329 Yeast NOR
C 368	5	100.0	10	5	AAf39136	Aaf39136 Yeast NOR
C 369	5	100.0	10	5	AAf40930	Aaf40930 Yeast NOR
370	5	100.0	10	5	AAf42413	Aaf42413 Yeast NOR
371	5	100.0	10	5	AAf42422	Aaf42422 Yeast NOR
C 372	5	100.0	10	5	AAf33811	Aaf33811 Yeast NOR
C 373	5	100.0	10	5	AAf35900	Aaf35900 Yeast NOR
374	5	100.0	10	5	AAf39189	Aaf39189 Yeast NOR
375	5	100.0	10	5	AAf40640	Aaf40640 Yeast NOR
C 376	5	100.0	10	5	AAf40931	Aaf40931 Yeast NOR
C 377	5	100.0	10	5	AAf42421	Aaf42421 Yeast NOR
C 378	5	100.0	10	5	AAf34090	Aaf34090 Yeast NOR
C 379	5	100.0	10	5	AAf35288	Aaf35288 Yeast NOR
C 380	5	100.0	10	5	AAf41909	Aaf41909 Yeast NOR
C 381	5	100.0	10	5	AAf42398	Aaf42398 Yeast NOR
C 382	5	100.0	10	5	AAf42810	Aaf42810 Yeast NOR
C 383	5	100.0	10	5	AAf44018	Aaf44018 Yeast NOR
384	5	100.0	10	5	AAf39759	Aaf39759 Yeast NOR
C 385	5	100.0	10	6	AAc16881	Aac16881 Translati
C 386	5	100.0	10	6	ABK52524	Abk52524 RNA3' ter

387	Aas98394	Galanin r	5	100.0	10	6	AAS98394
C 388	Aas98395	Galanin r	5	100.0	10	6	AAS98395
C 389	Aad25297	Human HSD	5	100.0	10	6	AAD25297
C 390	Aal45335	Human KCN	5	100.0	10	6	AAL45335
391	Aas18304	Primer-ex	5	100.0	10	6	AAS18304
C 392	Aas18284	Primer-ex	5	100.0	10	6	AAS18284
393	Aas99276	Human F12	5	100.0	10	6	AAS99276
394	Aad26088	Human apo	5	100.0	10	6	AAD26088
395	Aad26079	Human apo	5	100.0	10	6	AAD26079
C 396	ABL88350	Human CHR	5	100.0	10	6	ABL88350
C 397	ABL88325	Human CHR	5	100.0	10	6	ABL88325
C 398	AAD32208	Human NFK	5	100.0	10	6	AAD32208
399	ABL52191	Human PER	5	100.0	10	6	ABL52191
C 400	ABK85686	Human SCY	5	100.0	10	6	ABK85686
401	ABK95839	Solute Ca	5	100.0	10	6	ABK95839
402	ABK95841	Solute Ca	5	100.0	10	6	ABK95841
403	AAS98818	Colony st	5	100.0	10	6	AAS98818
C 404	AAS98843	Colony st	5	100.0	10	6	AAS98843
C 405	AAS98893	Colony st	5	100.0	10	6	AAS98893
406	ABL01316	Human MMP	5	100.0	10	6	ABL01316
C 407	AAD25882	Primer #4	5	100.0	10	6	AAD25882
C 408	ABL42914	Human mat	5	100.0	10	6	ABL42914
C 409	ABL42664	Human mat	5	100.0	10	6	ABL42664
C 410	ABL42918	Human mat	5	100.0	10	6	ABL42918
411	ABL42800	Human mat	5	100.0	10	6	ABL42800
412	ABL42849	Human mat	5	100.0	10	6	ABL42849
C 413	ABL42858	Human mat	5	100.0	10	6	ABL42858
C 414	ABL42915	Human mat	5	100.0	10	6	ABL42915
415	ABL57663	Human SCY	5	100.0	10	6	ABL57663
C 416	ABL57675	Human SCY	5	100.0	10	6	ABL57675
C 417	ABL57672	Human SCY	5	100.0	10	6	ABL57672
418	ABL60194	Human MUC	5	100.0	10	6	ABL60194
C 419	ABA94621	Nucleotid	5	100.0	10	6	ABA94621
C 420	ABA94626	Nucleotid	5	100.0	10	6	ABA94626
421	ABA94625	Nucleotid	5	100.0	10	6	ABA94625
C 422	ABA94619	Nucleotid	5	100.0	10	6	ABA94619
C 423	ABA94622	Nucleotid	5	100.0	10	6	ABA94622
424	ABA94620	Nucleotid	5	100.0	10	6	ABA94620
425	ABK37021	Human ALA	5	100.0	10	6	ABK37021
426	ABK12726	Oligonucl	5	100.0	10	6	ABK12726
427	ABK12724	Oligonucl	5	100.0	10	6	ABK12724
428	ABN81497	Human HTA	5	100.0	10	6	ABN81497
429	ABK81402	SCYA21 ge	5	100.0	10	6	ABK81402
430	ABK96071	Human LIP	5	100.0	10	6	ABK96071
431	ABK96055	Human LIP	5	100.0	10	6	ABK96055
432	ABK96056	Human LIP	5	100.0	10	6	ABK96056
C 433	ABK96073	Human LIP	5	100.0	10	6	ABK96073
C 434	ABK10419	Synthetic	5	100.0	10	6	ABK10419
C 435	AAS96201	Human Ace	5	100.0	10	6	AAS96201
436	ABA97042	ZFP36 ext	5	100.0	10	6	ABA97042
437	ABA97044	ZFP36 ext	5	100.0	10	6	ABA97044
C 438	ABA97030	ZFP36 ext	5	100.0	10	6	ABA97030
C 439	ABA97036	ZFP36 ext	5	100.0	10	6	ABA97036
C 440	Aad26165	Human end	5	100.0	10	6	AAD26165
441	Aal48057	Human CSF	5	100.0	10	6	AAL48057
442	Aas16393	Primer-ex	5	100.0	10	6	AAS16393
443	Aas95402	Human ICA	5	100.0	10	6	AAS95402
444	Aad26425	Human GRM	5	100.0	10	6	AAD26425
445	Aad26862	Human GPR	5	100.0	10	6	AAD26862
C 446	ABL39511	Human ETF	5	100.0	10	6	ABL39511
C 447	ABL52259	Human PHK	5	100.0	10	6	ABL52259
C 448	ABQ71645	Zinc fing	5	100.0	10	6	ABQ71645
449	ABQ71583	Zinc fing	5	100.0	10	6	ABQ71583
450	ABQ71515	Zinc fing	5	100.0	10	6	ABQ71515
451	ABQ71668	Zinc fing	5	100.0	10	6	ABQ71668
452	ABQ71515	Zinc fing	5	100.0	10	6	ABQ71515
453	ABQ71485	Zinc fing	5	100.0	10	6	ABQ71485
454	ABQ71537	Zinc fing	5	100.0	10	6	ABQ71537
455	ABQ71296	Zinc fing	5	100.0	10	6	ABQ71296
456	ABQ71538	Zinc fing	5	100.0	10	6	ABQ71538
457	ABQ71516	Zinc fing	5	100.0	10	6	ABQ71516
458	ABQ71611	Zinc fing	5	100.0	10	6	ABQ71611
459	ABQ71295	Zinc fing	5	100.0	10	6	ABQ71295

460	5	100.0	10	6	ABQ71676
C 461	5	100.0	10	6	ABQ88701
462	5	100.0	10	6	ABT05365
463	5	100.0	10	6	ABT05351
464	5	100.0	10	6	AAD25202
C 465	5	100.0	10	6	ABA99340
C 466	5	100.0	10	6	ABK46452
C 467	5	100.0	10	6	AAD35463
468	5	100.0	10	6	ABN80617
C 469	5	100.0	10	6	ABN80639
C 470	5	100.0	10	6	ABN80641
C 471	5	100.0	10	6	ABN87956
C 472	5	100.0	10	6	ABV78397
473	5	100.0	10	6	ABV78565
C 474	5	100.0	10	6	ABV78362
C 475	5	100.0	10	6	ABV78447
476	5	100.0	10	6	ABV78405
C 477	5	100.0	10	6	ABV78480
C 478	5	100.0	10	6	ABV78310
479	5	100.0	10	6	ABV84781
C 480	5	100.0	10	6	ABV84352
C 481	5	100.0	10	6	ABV84501
C 482	5	100.0	10	6	ABV84639
C 483	5	100.0	10	6	ABV84547
484	5	100.0	10	6	ABV84249
C 485	5	100.0	10	6	ABV84742
C 486	5	100.0	10	6	ABV84765
C 487	5	100.0	10	6	ABS73847
488	5	100.0	10	6	AAS95618
489	5	100.0	10	6	AAS95620
490	5	100.0	10	6	ABK09440
C 491	5	100.0	10	6	ABK09444
492	5	100.0	10	6	ABK23714
C 493	5	100.0	10	6	ABK23472
494	5	100.0	10	6	ABK23541
C 495	5	100.0	10	6	ABK23664
C 496	5	100.0	10	6	ABK23684
497	5	100.0	10	6	ABK23510
C 498	5	100.0	10	6	ABK23559
C 499	5	100.0	10	6	ABK23811
500	5	100.0	10	12	AD113733

ALIGNMENTS

RESULT 1	
AAQ49543	
ID	AAQ49543 standard; DNA; 10 BP.
XX	XX
AC	AAQ49543;
XX	XX
DT	25-MAR-2003 (revised)
DT	20-APR-1994 (first entry)
XX	XX
DE	Primer to amplify BCNR locus marker B9.2.
XX	XX
KW	Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;
KW	sugar beet; ss.
XX	XX
OS	Synthetic.
XX	XX
PN	WO9319181-A1.
XX	XX
PD	30-SEP-1993.
XX	XX
PF	23-MAR-1993; 93WO-EP000702.
XX	XX
PR	25-MAR-1992; 92DK-00000396.
XX	XX
PA	(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
PA	(SANO ) SANDOZ PATENT GMBH.
PA	(SANO ) SANDOZ LTD.



XX Sandal N, Marcker K, Stiekema W, Lange W, Klein-Lankhorst R;  
PI Steen P;  
XX WPI; 1993-320747/40.  
XX Recombinant DNA comprising Beet Cyst Nematode Resistance Locus - confers  
PT nematode resistance to beet species.  
XX Claim 2; Page 61; 82pp; English.  
XX This primer is used to amplify a BCNR locus marker of ca. 700bp from wild  
CC beet species belonging to section Procumbentes. (Updated on 25-MAR-2003  
CC to correct PN field.)  
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 2 GGGGG 6  
RESULT 2  
AAQ49546  
ID AAQ49546 standard; DNA; 10 BP.  
XX AAQ49546;  
XX 25-MAR-2003 (revised)  
DT 20-APR-1994 (first entry)  
XX Primer to amplify BCNR locus marker B9.1.  
DE  
XX Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;  
KW sugar beet; ss.  
XX Synthetic.  
XX WO9319181-A1.  
XX 30-SEP-1993.  
XX 23-MAR-1993; 93WO-EP000702.  
PF 25-MAR-1992; 92DK-00000396.  
PR (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
PA (SANO ) SANDOZ PATENT GMBH.  
PA (SANO ) SANDOZ LTD.  
XX Sandal N, Marcker K, Stiekema W, Lange W, Klein-Lankhorst R;  
PI Steen P;  
XX WPI; 1993-320747/40.  
XX Recombinant DNA comprising Beet Cyst Nematode Resistance Locus - confers  
PT nematode resistance to beet species.  
XX Claim 2; Page 61; 82pp; English.  
XX This primer is used to amplify a BCNR locus marker of ca. 1100bp from  
CC wild beet species belonging to section Procumbentes. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db 2 GGGGG 6  
RESULT 3  
AAQ79368  
ID AAQ79368 standard; DNA; 10 BP.  
XX AAQ79368;  
AC AAQ79368;  
XX 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX Regulatory element AP2/Rev located at posn. 708 of the extended 3'  
DE flanking region of human erythropoietin.  
DE Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
KW  
XX Synthetic.  
OS  
XX WO9423570-A1.  
PN 27-OCT-1994.  
PD 15-APR-1994; 94WO-US004141.  
PF 15-APR-1993; 93US-00046295.  
XX 23-JUN-1993; 93US-00082850.  
PR (UYN ) UNIV NEW YORK STATE.  
XX Lee-Huang S;  
PI WPI; 1994-341353/42.  
XX New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX Disclosure; Table II, page 14; 81pp; English.  
XX AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
CC 1777 bases of AAQ79753. It corresp. to the non- coding 3' flanking region  
CC of AAQ79753 and includes all the regulatory elements contained therein.  
CC It extends from the 5'-most PstI site 3' of the end of the coding  
CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
CC structures. It also contains TATA boxes in forward and reverse  
CC orientation, and at least about 184 potential transcriptional regulatory  
CC elements. AAQ79365-Q79369 list several of these elements and their  
CC positions. The nucleotide posns. are measured from first nucleotide at  
CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 5 GGGGG 9  
RESULT 4  
AAQ79367  
ID AAQ79367 standard; DNA; 10 BP.  
XX AAQ79367;

XX 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Regulatory element AP2/Rev located at posn. 707 of the extended 3'  
DE flanking region of human erythropoietin.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UUNY ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
PI WPI; 1994-341353/42.  
DR  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table II, page 14; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
CC 1777 bases of AAQ79753. It corresp. to the non- coding 3' flanking region  
CC of AAQ79753 and includes all the regulatory elements contained therein.  
CC It extends from the 5'-most PstI site 3' of the end of the coding  
CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
CC structures. It also contains TATA boxes in forward and reverse  
CC orientation, and at least about 184 potential transcriptional regulatory  
CC elements. AAQ79365-Q79369 list several of these elements and their  
CC positions. The nucleotide posns. are measured from first nucleotide at  
CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 9 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db 6 GGGGG 10  
  
RESULT 5  
ID AAQ79359 standard; DNA; 10 BP.  
XX  
AC AAQ79359;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Sequence of AP2 regulatory sequence located at posn. 2621 in hEpsLH.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX

XX 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UUNY ) UNIV NEW YORK STATE.  
XX  
XX Lee-Huang S;  
PI  
XX WPI; 1994-341353/42.  
DR  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table I, p. 12; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
CC 5' flanking region and includes all the 5' regulatory elements. This  
CC region, consisting of the first 3892 of AAQ79353, was not found in the  
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
CC show several of these elements and their positions. The nucleotide  
CC position of these elements is measured from the BamHI site at the 5' end  
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 8 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db 6 GGGGG 2  
  
RESULT 6  
ID AAQ79358 standard; DNA; 10 BP.  
XX  
AC AAQ79358;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Sequence of AP2 regulatory sequence located at posn. 896 in hEpsLH.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UUNY ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
XX WPI; 1994-341353/42.  
DR  
XX

PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodrn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table I, p. 12; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpoSH. This nucleic acid sequence includes EPO coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
CC 5' flanking region and includes all the 5' regulatory elements. This  
CC region, consisting of the first 3892 of AAQ79353, was not found in the  
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
CC show several of these elements and their positions. The nucleotide  
CC position of these elements is measured from the BamHI site at the 5' end  
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
6 GGGGG 2  
  
RESULT 7  
AAQ71100  
ID AAQ71100 standard; cDNA; 10 BP.  
XX  
AC AAQ71100;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 12 splice donor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX  
PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Trofatter JA, Maccollin MM, Gusella JF;  
XX WPI; 1994-272992/34.  
DR  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
PT tumours and neurofibromatosis (NF2).  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance  
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
5 GGGGG 9  
  
RESULT 8  
AAQ64610/c  
ID AAQ64610 standard; cDNA; 10 BP.  
XX  
AC AAQ64610;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-DEC-1994 (first entry)  
XX  
DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.  
XX  
KW Mitochondrial DNA mutation; associated with Alzheimer's;  
KW Parkinson's disease; mismatch primers; PCR; amplification;  
KW polymerase chain reaction; ss.  
XX Homo sapiens.  
XX WO9409162-A1.  
PN  
XX 28-APR-1994.  
XX  
PF 20-OCT-1993; 93WO-US010072.  
XX  
PR 20-OCT-1992; 92US-00963723.  
XX  
PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
XX  
PI Wallace DC;  
XX  
DR WPI; 1994-151346/18.  
XX  
PT Detection of mitochondrial DNA mutation associated with Alzheimer's  
PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-  
PT disposition to Alzheimer's disease and/or Parkinson's disease in a  
PT patient.  
XX  
PS Disclosure; Page 36; 83pp; English.  
XX  
CC A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene  
CC insertion. Direct sequence analysis revealed that the insertion consisted  
CC of approximately five cytosines within AAQ64610. This mitochondrial DNA  
CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The  
CC detection of the mutations is useful for diagnosing or predicting a pre-  
CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX

SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 5 GGGGG 1

RESULT 9

AAT08734  
ID AAT08734 standard; DNA; 10 BP.  
XX  
AC AAT08734;  
XX  
DT 14-JUN-1996 (first entry)  
XX  
DE U14snRNA inverted repeat sequence.  
XX  
KW snRNA; small nucleolar RNA; U14; non-translated sequence; conserved;  
KW Box C; Box D; processing; pre-ribosomal RNA; ribosome formation;  
KW normal growth phenotype; yeast; plant; maize; potato; 18S rRNA; ss.  
XX  
OS Synthetic.  
XX  
PN WO9530747-A1.  
XX  
PD 16-NOV-1995.  
XX  
PF 04-MAY-1994; 94WO-EP001409.  
XX  
PR 04-MAY-1994; 94WO-EP001409.  
XX  
PA (GENE-) GENE SHEARS PTY LTD.  
XX  
PI Brown JWS, Leader DJ, Waugh R;  
XX  
DR WPI; 1995-404114/51.  
XX  
PT Nucleic acid contg. plant U14 sequences and their derivs. - for  
PT regulating prodn. of ribosomal RNA, also as stabilisers for heterologous  
PT RNA.  
XX  
PS Claim 7; Page 29; 57pp; English.  
XX  
CC U14 small nucleolar RNA (snRNA) is present in genomes as a non-  
CC translated sequence. U14 sequences contain at the extremities of the  
CC coding sequence, a pair of inverted repeats, which usually have a length  
CC of between 4 and 20, e.g. 5-12 nucleotides and which are complementary to  
CC each other to allow the formation of a stem by base- pairing. The stem  
CC structure is thought to protect the U14 gene from digestion by RNase. The  
CC present sequence forms a stem structure by annealing to its complementary  
CC strand. SnRNAs are involved in processing of pre-ribosomal RNA  
CC transcripts and ribosome formation. U14snRNA is required for a normal  
CC growth phenotype and for processing of pre-rRNA transcripts in yeast.  
CC Plant U14 sequences have been identified and characterised in the present  
CC invention, and may be intron encoded  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 3 GGGGG 7

RESULT 10

AAX32616

ID AAX32616 standard; DNA; 10 BP.  
XX  
AC AAX32616;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #16.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 50; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 6 GGGGG 10

RESULT 11

AAT08758  
ID AAT08758 standard; DNA; 10 BP.  
XX  
AC AAT08758;  
XX  
DT 14-JUN-1996 (first entry)  
XX  
DE U14snRNA inverted repeat sequence.  
XX  
KW snRNA; small nucleolar RNA; U14; non-translated sequence; conserved;  
KW Box C; Box D; processing; pre-ribosomal RNA; ribosome formation;  
KW normal growth phenotype; yeast; plant; maize; potato; 18S rRNA; ss.  
XX  
OS Synthetic.  
XX  
PN WO9530748-A2.  
XX

PD 16-NOV-1995.  
XX  
PF 04-MAY-1995; 95WO-EP001694.  
XX  
PR 04-MAY-1994; 94WO-EP001409.  
PR 09-DEC-1994; 94EP-00119487.  
XX  
PA (GENE-) GENE SHEARS PTY LTD.  
XX  
PI Brown JWS, Leader DJ, Waugh R;  
XX  
DR WPI; 1995-404115/51.  
XX  
PT Plant U14 nucleic acid sequences and derivatives - regulate ribosomal RNA  
PT production and accumulation in plants.  
XX  
PS Claim 9; Page 43; 57pp; English.  
XX  
CC U14 small nucleolar RNA (snRNA) is present in genomes as a non-  
CC translated sequence. U14 sequences contain at the extremities of the  
CC coding sequence, a pair of inverted repeats, which usually have a length  
CC of between 4 and 20, e.g. 5-12 nucleotides and which are complementary to  
CC each other to allow the formation of a stem by base-pairing. The stem  
CC structure is thought to protect the U14 gene from digestion by RNase. The  
CC present sequence forms a stem structure by annealing to its complementary  
CC strand. SnRNAs are involved in processing of pre-ribosomal RNA  
CC transcripts and ribosome formation. U14snRNA is required for a normal  
CC growth phenotype and for processing of pre-rRNA transcripts in yeast.  
CC Plant U14 sequences have been identified and characterised in the present  
CC invention, and may be intron encoded  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
3 GGGGG 7  
  
RESULT 12  
AAQ96682  
ID AAQ96682 standard; DNA; 10 BP.  
XX  
AC AAQ96682;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 277.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
3 GGGGG 7  
  
RESULT 13  
AAQ96685  
ID AAQ96685 standard; DNA; 10 BP.  
XX  
AC AAQ96685;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 280.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 191; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
6 GGGGG 10  
  
RESULT 13  
AAQ96685  
ID AAQ96685 standard; DNA; 10 BP.  
XX  
AC AAQ96685;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 280.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.  
  
New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
LTR region - can be used in a vaccine to inhibit/reduce productive  
infection in an individual by a pathogenic strain.  
  
Claim 13; Page 191; 301pp; English.  
  
Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
resulting avirulent HIV strains are still capable of inducing an immune  
response in humans, and enable the generation of therapeutic, diagnostic  
and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
standardise OS field)

```
XX SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
3 GGGGG 7

RESULT 14
AAQ96686
ID AAQ96686 standard; DNA; 10 BP.
XX
AC AAQ96686;
XX
DT 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 281.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
PS Claim 13; Page 191; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
2 GGGGG 6

RESULT 15
AAQ96683
ID AAQ96683 standard; DNA; 10 BP.
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```
XX AAQ96683;
XX
DT 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 278.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
PS Claim 13; Page 191; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
5 GGGGG 9

RESULT 16
AAQ96687
ID AAQ96687 standard; DNA; 10 BP.
XX
AC AAQ96687;
XX
DT 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 282.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
```

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XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
PR PR 21-FEB-1994; 94AU-00004002.
PR PR 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 191; 301pp; English.
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
1 GGGGG 5

RESULT 17
AAQ96684
ID AAQ96684 standard; DNA; 10 BP.
XX AAQ96684;
AC AAQ96684;
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 279.
DE HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
OS WO9521912-A1.
XX 17-AUG-1995.
PD 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 191; 301pp; English.
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
1 GGGGG 5

RESULT 18
AAQ96688
ID AAQ96688 standard; DNA; 10 BP.
XX AAQ96688;
AC AAQ96688;
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 283.
DE HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
OS WO9521912-A1.
XX 17-AUG-1995.
PD 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 191; 301pp; English.
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
SQ

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PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 191; 301pp; English.
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
4 GGGGG 8

RESULT 18
AAQ96688
ID AAQ96688 standard; DNA; 10 BP.
XX AAQ96688;
AC AAQ96688;
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 283.
DE HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
OS WO9521912-A1.
XX 17-AUG-1995.
PD 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 191; 301pp; English.
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
SQ

```



```

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      1 GGGGG 5

RESULT 19
AAQ93130/c
ID AAQ93130 standard; DNA; 10 BP.
XX
AC AAQ93130;
XX
DT 06-MAR-1996 (first entry)
XX
DE Telomerase RNA (telRNA) gene fragment mutated coding sequence.
XX
KW Telomerase; telomere; cancer; gene therapy; euplotes; mutation; tumour;
KW treatment; ss.
XX
OS Tetrahymena sp.
XX
PN EP666313-A2.
XX
PD 09-AUG-1995.
XX
PF 27-JAN-1995; 95EP-00300539.
XX
PR 27-JAN-1994; 94US-00189151.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Henderson E;
XX
WPI; 1995-270495/36.
XX
New gene encoding human telomerase RNA, related vectors and transformed
cells - useful esp. for treatment of cancer by gene therapy.
XX
Example 7; Page 9; 20pp; English.
XX
AAQ93130 is a mutated telomerase RNA gene fragment which when introduced
to a cell results in rapid cell death. A new telomerase gene or gene
fragment coding for telomerase RNA has been identified. Mutations of this
gene can be used in the treatment of tumours. The DNA can be introduced
into cancerous cells in vivo or in vitro so that the mutated telomerase
competes with endogenous telomerase for formation of active telomeres.
This results in the addition of aberrant telomere sequences to the ends
of chromosomes which causes genetic instability and rapid cell death.
CC Telomere-specific ribozymes may also be useful to treat or prevent cancer
CC i.e. it may be present to inactivate any telomerase RNA if a normal cell
CC undergoes transformation. The method is specific for tumour cells since
CC telomerase is inactive in normal cells
XX
SQ Sequence 10 BP; 4 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      8 GGGGG 4

RESULT 20
AAQ8461
ID AAQ8461 standard; DNA; 10 BP.
XX
AC AAQ8461;
```

```

XX      19-DEC-1995 (first entry)
DT
XX      Human mitochondrial D-loop region DNA probe 6-2.
DE
XX
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW D-loop region; biological chip; hybridisation fingerprint;
KW interrogation position; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 10
FT /*tag= a
FT /note= "3'-end of probe is covalently attached to chip
FT surface"
XX
PN WO9511995-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012305.
XX
PR 26-OCT-1993; 93US-00143312.
PR 02-AUG-1994; 94US-00284064.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
DR WPI; 1995-178887/23.
XX
New arrays of oligo:nucleotide probes - used for comparing known
sequences with variants for detection of mutation(s) and sequencing.
PT
XX
PS Disclosure; Page 107; 223pp; English.
XX
CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC fragment of human mitochondrial DNA from the D-loop region, the most
CC polymorphic region of human mitochondrial DNA. The chip comprised a set
CC of 268 overlapping oligonucleotide probes (see AAQ8421-Q88684) of
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC x 1cm array. Each position in the sequence was represented by at least
CC one probe (usually 2 or more). DNA was amplified from six human donors
CC and then transcribed to give the 1.3kb RNA transcripts which were
CC fragmented and hybridised to the chip. For each individual, a unique
CC hybridisation fingerprint was produced on the chip; all differences could
CC be correlated with differences in the cloned genomic DNA sequence
XX
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      3 GGGGG 7

RESULT 21
AAQ88437
ID AAQ88437 standard; DNA; 10 BP.
XX
AC AAQ88437;
XX
DT 19-DEC-1995 (first entry)
XX
DE Human mitochondrial D-loop region DNA probe 16-0.
XX
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW D-loop region; biological chip; hybridisation fingerprint;
```

```
KW interrogation position; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 10
FT /*tag= a
FT /note= "3'-end of probe is covalently attached to chip
FT surface"
XX
PN WO95111995-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012305.
XX
PR 26-OCT-1993; 93US-00143312.
PR 02-AUG-1994; 94US-00284064.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
DR WPI; 1995-178887/23.
XX
PT New arrays of oligo:nucleotide probes - used for comparing known
PT sequences with variants for detection of mutation(s) and sequencing.
XX
PS Disclosure; Page 106; 223pp; English.
XX
CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC fragment of human mitochondrial DNA from the D-loop region, the most
CC polymorphic region of human mitochondrial DNA. The chip comprised a set
CC of 268 overlapping oligonucleotide probes (see AAQ88493-Q88684) of
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC x 1cm array. Each position in the sequence was represented by at least
CC one probe (usually 2 or more). DNA was amplified from six human donors
CC and then transcribed to give the 1.3kb RNA transcripts which were
CC fragmented and hybridised to the chip. For each individual, a unique
CC hybridisation fingerprint was produced on the chip; all differences could
CC be correlated with differences in the cloned genomic DNA sequence
XX
SQ Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
4 GGGGG 8

RESULT 22
AAQ88493
ID AAQ88493 standard; DNA; 10 BP.
XX
AC AAQ88493;
XX
DT 20-DEC-1995 (first entry)
XX
DE Human mitochondrial D-loop region DNA probe 4-4.
XX
KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW D-loop region; biological chip; hybridisation fingerprint;
KW interrogation position; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 10
FT /*tag= a
```

```
FT /note= "3'-end of probe is covalently attached to chip
FT surface"
XX
PN WO95111995-A1.
XX
PD 04-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012305.
XX
PR 26-OCT-1993; 93US-00143312.
PR 02-AUG-1994; 94US-00284064.
XX
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX
DR WPI; 1995-178887/23.
XX
PT New arrays of oligo:nucleotide probes - used for comparing known
PT sequences with variants for detection of mutation(s) and sequencing.
XX
PS Disclosure; Page 107; 223pp; English.
XX
CC A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC fragment of human mitochondrial DNA from the D-loop region, the most
CC polymorphic region of human mitochondrial DNA. The chip comprised a set
CC of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC x 1cm array. Each position in the sequence was represented by at least
CC one probe (usually 2 or more). DNA was amplified from six human donors
CC and then transcribed to give the 1.3kb RNA transcripts which were
CC fragmented and hybridised to the chip. For each individual, a unique
CC hybridisation fingerprint was produced on the chip; all differences could
CC be correlated with differences in the cloned genomic DNA sequence
XX
SQ Sequence 10 BP; 1 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
3 GGGGG 7

RESULT 23
AAT14138/C
ID AAT14138 standard; DNA; 10 BP.
XX
AC AAT14138;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US004477.
XX
PR 14-APR-1994; 94US-00228935.
PR 27-MAR-1995; 95US-00410780.
XX
PA (LIGA-) LIGAND PHARM INC.
```

```
XX Seidel HM, Lamb IP;
PI WPI; 1995-373797/48.
DR
XX DNA spacer regulatory elements responsive to cytokine(s) - for detecting
PT the presence of transcriptional regulatory protein in a sample.
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element TT(Nx)AA,
CC where x is 4-7, and the regulatory element binds an activated
CC transcriptional regulatory protein in response to a signalling mol., i.e.
CC a cytokine. This cytokine responsive DNA spacer regulatory element can be
CC used to detect the presence of a transcriptional regulatory protein in a
CC sample, and in assays for (ant)agonists of gene transcription. The
CC identified cpds. may be used to treat cytokine-induced disease states, or
CC to ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
7 GGGGG 3

RESULT 24
AAT05376/c
ID AAT05376 standard; DNA; 10 BP.
XX
AC AAT05376;
XX
DT 04-JUN-1996 (first entry)
XX
DE Setoria nodorum RAPD primer OPB-19.
XX
KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KW Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
KW internal transcribed region; strain; capture; colourimetric assay;
KW isolate; development; population; random amplified polymorphic DNA; ss.
XX
OS Synthetic.
XX
PN WO9529260-A2.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US004712.
XX
PR 25-APR-1994; 94US-00233608.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ligon JM, Beck JJ;
XX
DR WPI; 1995-383005/49.
XX
CC DNA encoding intervening transcribed sequence - used for detection of
PT plant fungal pathogens.
XX
PS Claim 9; Page 16; 65pp; English.
XX
CC A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,
CC Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR
CC amplification of sequences found in the internal transcribed region (ITS)
CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93
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CC and AAT05357-72. These primers are derived from the ITS sequences of
CC these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The
CC amplification products of the reactions using these primers can be used
CC with the capture primers AAT05378-93 in colourimetric assays. The primers
CC and ITS DNAs can be used for the detection of specific fungal pathogen
CC isolates and in monitoring disease development in plant populations. The
CC primers AAT05373-7 were obtained from purchased random amplified
CC polymorphic DNA (RAPD) primer libraries and used to PCR amplify ITS
CC sequences in conjunction with the primers AAQ94390-3. This primer
CC amplified a 1.1 kb region from S.nodorum
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
6 GGGGG 2

RESULT 25
AAT04915/c
ID AAT04915 standard; cDNA; 10 BP.
XX
AC AAT04915;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 201-7.
XX
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX
PF 04-OCT-1990; 95EP-00105391.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 1995-346090/45.
XX
PT New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.
XX
PS Example 3; Fig 12C; 127pp; English.
XX
CC AAT04915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occurring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
CC stimulate growth of primitive progenitors such as haematopoietic
CC progenitor cells, neural stem cells and primordial germ stem cells. The
CC peptides can be used in a composition for treating leucopenia, anaemia or
CC thrombocytopenia, for enhancing engraftment of bone marrow during
CC transplantation or for bone marrow recovery after chemotherapy or
CC radiation-induced bone marrow aplasia or myelosuppression. They can also
```

CC be used for treating neoplasia, nerve damage, infertility, intestinal  
CC damage or myeloproliferative disorders. Antibodies may be raised against  
CC the peptides for use in detection or neutralisation of SCF in serum. SCF  
CC may be useful for the treatment of AIDS and severe combined  
CC immunodeficiency (SCID) states alone or in combination with other factors  
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 10 BP; 0 A; 8 C; 1 G; 0 T; 0 U; 1 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 8 GGGGG 4

RESULT 26  
AAQ81070  
ID AAQ81070 standard; DNA; 10 BP.  
XX  
AC AAQ81070;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-SEP-1995 (first entry)  
XX  
DE supF gene triplex forming mutagenic oligonucleotide pso-AG10.  
XX  
KW supF gene; triplex forming mutagenic oligonucleotide; pso-AG10;  
KW 4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.  
XX  
OS Synthetic.  
XX

Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /note= "4'hydroxymethyl-4,5', 8-trimethylpsoralenated"  
XX  
PN W09501364-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 24-JUN-1994; 94WO-US007234.  
XX  
PR 25-JUN-1993; 93US-00083088.  
XX

(UYVA ) UNIV YALE.  
PA  
XX  
PI Glazer PM, Havre PA;  
XX  
DR WPI; 1995-060943/08.  
XX  
PT New mutagenic oligo:nucleotide(s) - having a mutagen incorporated in an  
PT oligo:nucleotide which forms a triplex, for site-directed mutagenesis.  
XX  
PS Example 5; Page 5; 72pp; English.  
XX

CC AAQ81070 is the supF gene triplex forming mutagenic oligonucleotide pso-  
CC AG10. It forms a triplex (a triple stranded nucleic acid) with a specific  
CC site on the supF genome, enabling the covalently bound 4'hydroxymethyl-  
CC 4,5',8-trimethylpsoralen group to produce a site specific mutation.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 6 GGGGG 10

RESULT 27  
AAT27213  
ID AAT27213 standard; DNA; 10 BP.  
XX  
AC AAT27213;  
XX

DT 10-DEC-1996 (first entry)  
XX  
DE HIV-1 detection probe DNA A(-)1.  
XX

KW Human immunodeficiency virus; HIV; manufacture; immobilised probe;  
KW magnetic microparticle; carboxy group; primary amino group;  
KW hybridisation; ss.  
XX

OS Synthetic.  
XX  
PN JP08089294-A.  
XX  
PD 09-APR-1996.  
XX

PF 28-SEP-1994; 94JP-00233448.  
XX  
PR 28-SEP-1994; 94JP-00233448.  
XX  
PA (JAPS ) NIPPON GOSEI GOMU KK.  
XX

DR WPI; 1996-233380/24.  
XX

PT Powder mfr. for detecting specific nucleic acids, useful for diagnosis -  
PT comprises fixing single stranded oligo:nucleotide having fixed and  
PT hybridisable regions to insol. microparticles having superficial carboxyl  
PT gps.  
XX

PS Example 1; Page 6; 8pp; Japanese.  
XX

CC The probes AAT27211-4 are examples of probes, used to detect HIV-1  
CC sequences, which are generated by a novel method of manufacturing an  
CC immobilised probe. The method involves fixing a nucleic acid probe  
CC sequence to the surface of an insol. magnetic microparticle via carboxy  
CC gps. on the surface of the particle. The nucleic acid is single stranded,  
CC of length 10-150 nucleotides and has a fixed region of 5-30 nucleotides  
CC contg. prim. amino gps. and a hybridising region comprising 5 similar  
CC nucleotides positioned away from the terminus of the oligonucleotide  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

RESULT 28  
AAT35000  
ID AAT35000 standard; DNA; 10 BP.  
XX

AC AAT35000;  
XX

DT 25-MAR-2003 (revised)  
DT 03-DEC-1996 (first entry)  
XX

DE HIV inhibitor #3.  
XX

KW HIV; infection inhibitor; triplex forming; purine rich promoter; V3 loop;  
KW transcription inhibitor; gp120 protein; viral growth; enzyme inhibitor;  
KW PLA2; telomere length; glove coating; condom; ss.  
XX

OS Synthetic.

XX US5523389-A.  
PN  
XX  
PD 04-JUN-1996.  
XX  
PF 28-SEP-1993; 93US-00128011.  
XX  
PR 29-SEP-1992; 92US-00954185.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Imbach JL, Ecker DJ, Wyatt JR;  
XX WPI; 1996-285782/29.  
DR  
XX New octa:nucleotide with guanosine quartet and phosphoro:thioate links -  
PT is inhibitor of HIV infection by binding to the V3 loop.  
PT  
XX Disclosure; Col 2; 14pp; English.  
XX  
CC AAT34998-T35001 represent HIV inhibitors. Sequences containing only G and  
CC T residues (such as these sequences) are triplex forming  
CC oligonucleotides, and form purine rich promoter elements used to inhibit  
CC transcription. These sequences bind to the HIV gp120 protein at the V3  
CC loop via the internal guanosine quartet. This binding prevents cell-to-  
CC cell and virus-to-cell infection. The sequences may also be used for  
CC inhibiting viral growth, and other viral genes, for inhibiting the enzyme  
CC PLA2, and to modulate telomere length. In some cases these sequences need  
CC to be chemically modified. The chemically modified oligonucleotides  
CC preferably include at least one phosphorothioate linkage. Other modified  
CC intersugar links, or 2'-modified sugar residues can also be used. These  
CC oligonucleotides can be used for coating gloves, condoms, etc, or for  
CC topical application. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
1 GGGGG 5  
  
RESULT 29  
AAT35713  
ID AAT35713 standard; DNA; 10 BP.  
XX  
AC AAT35713;  
XX  
DT 08-OCT-1996 (first entry)  
XX  
DE Primer UBC515 for V.dahliae RAPD reaction.  
XX  
KW RAPD; random amplified polymorphic DNA; diagnostic assay; quantitative;  
KW PCR; primer; qualitative; soil sample; agricultural field; potatoe;  
KW V.albo-atrum; soil fumigation; amplify; polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN US5527671-A.  
XX  
PD 18-JUN-1996.  
XX  
PF 07-NOV-1994; 94US-00335565.  
XX  
PR 07-NOV-1994; 94US-00335565.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
XX  
PI German TL, Li K, Rouse DI;  
XX

DR WPI; 1996-299849/30.  
XX Assay for Verticillium dahliae - by amplification of specific DNA  
PT sequence.  
XX  
PS Example; Col 9; 16pp; English.  
XX  
CC AAT35710-T35738 represent amplification primers used in a random  
CC amplified polymorphic DNA (RAPD) reaction on V.dahliae DNA. These  
CC sequences were used to isolate the sequence represented by AAT35706 for  
CC use in the diagnostic assays of the invention. The qualitative assays of  
CC the invention comprise analysing a sample for the presence of the  
CC V.dahliae sequence. Detection of the V.dahliae sequence in the sample  
CC shows that the sample is infected by V.dahliae. A quantitative assay of  
CC the invention, comprises taking a sample and isolating nucleic acids from  
CC it. A sequence that acts as an internal standard (see AAT35707) is added  
CC to the isolated nucleic acids. The internal standard competes with the  
CC V.dahliae sequence for the PCR primers used in the reaction (such as the  
CC sequences represented by AAT35708 and AAT35709). The amplified portion of the  
CC the internal standard is a different size to the amplified portion of the  
CC V.dahliae sequence. The amounts of amplified DNA of each sequence is then  
CC compared to indicate the number of V.dahliae present in the sample. The  
CC sample used in these assays is normally a soil sample from an  
CC agricultural field that is going to be used for growing potatoes. These  
CC assays are faster and more accurate than methods based on culturing soil  
CC samples in selective media. The assays can also distinguish between  
CC V.dahliae and V.albo-atrum. By using these assays, unnecessary soil  
CC fumigation can be avoided  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
1 GGGGG 5  
  
RESULT 30  
AAT10084/c  
ID AAT10084 standard; DNA; 10 BP.  
XX  
AC AAT10084;  
XX  
DT 29-AUG-1996 (first entry)  
XX  
DE Hammerhead ribozyme RNA complementary oligonucleotide.  
XX  
KW Hammerhead; ribozyme; enhanced RNA cleavage; cleavage efficiency;  
KW viral inactivation; viral RNA transcript; hybridisation; target RNA;  
KW complementary oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
PN WO9600232-A1.  
XX  
PD 04-JAN-1996.  
XX  
PF 21-JUN-1995; 95WO-AU0000359.  
XX  
PR 24-JUN-1994; 94US-00265484.  
XX  
PA (GENE-) GENE SHEARS PTY LTD.  
XX  
PI Keese P, Stapper M, Perriman R;  
XX WPI; 1996-068825/07.  
DR  
XX Improved catalytic hammer-head ribozyme(s) and enhanced RNA cleavage -  
PT useful in activating target sequences in e.g. infectious viruses.  
XX

PS Example 3; Page 64; 122pp; English.

XX The present oligonucleotide is a complementary oligonucleotide (CO) for

CC the ribozyme given in AAT10062 or AAT10072, which are specific examples

CC of a claimed, highly generic, hammerhead ribozyme with enhanced RNA

CC cleavage. The CO alters the cleavage efficiency of the ribozymes, i.e.

CC the cleavage efficiency of the CO in combination with a ribozyme as a %

CC of a control without the CO is 152. The ribozymes of the invention (opt.

CC in conjunction with a CO) have extensive therapeutic and biological

CC applications, e.g. disease causing viruses in man, animals and plants may

CC be inactivated by administering to an infected subject a ribozyme adapted

CC to hybridise to, and cleave RNA transcripts of the virus

XX Sequence 10 BP; 0 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db |||||

7 GGGGG 3

RESULT 31

AAT98862

ID AAT98862 standard; DNA; 10 BP.

XX AAT98862;

AC AAT98862;

XX 20-MAR-1998 (first entry)

DT Core-binding site clone 6-9-1.

DE Protein-binding site isolation; transcription factor modification;

XX DNA-binding protein; inhibitor identification; ss.

OS Synthetic.

XX WO9727330-A1.

PN 31-JUL-1997.

XX 24-JAN-1997; 97WO-US001230.

PF 24-JAN-1996; 96US-00590571.

XX (UYVA ) UNIV YALE.

PA Weissman SM, Kulkarni P, Nallur GN;

XX WPI; 1997-393714/36.

DR Identifying protein-binding sites for DNA-binding proteins - using

XX duplexes having 5' and 3' sequences for annealing to amplification

PT primers with an internal potential protein-binding site sequence.

XX Example 3; Page 22; 52pp; English.

PS This sequence represents a core-binding site identified using the method

CC of the invention. This sequence was identified using the 32P-labelled

CC oligonucleotide duplex shown in AAT76581 and the primers shown in

CC AAT76582-T76583 in the method of the invention. The method is for

CC simultaneously isolating protein-binding sites for DNA-binding proteins.

CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes

CC having 5' and 3' sequences capable of annealing to primers for

CC amplification and an internal sequence having a potential protein-binding

CC site, a non-specific inhibitor and a sample containing DNA-binding

CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed

CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form

CC amplified duplexes; thereby isolating protein-binding sites for the DNA-

CC binding proteins. The methods can be used to identify protein-binding

CC sites which can be used to identify corresponding DNA-binding proteins in

CC an expression library. They can also be used to develop products to

CC inhibit the function of a given DNA-binding protein or for the

CC modification of transcription factors

XX Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db |||||

5 GGGGG 9

RESULT 32

AAT98847

ID AAT98847 standard; DNA; 10 BP.

XX AAT98847;

AC AAT98847;

XX 20-MAR-1998 (first entry)

DT Binding site BSN1 identified using the method of the invention.

XX Protein-binding site isolation; transcription factor modification;

KW DNA-binding protein; inhibitor identification; ss.

XX Synthetic.

OS WO9727330-A1.

XX 31-JUL-1997.

PD 24-JAN-1997; 97WO-US001230.

PF 24-JAN-1996; 96US-00590571.

XX (UYVA ) UNIV YALE.

PA Weissman SM, Kulkarni P, Nallur GN;

XX WPI; 1997-393714/36.

DR Identifying protein-binding sites for DNA-binding proteins - using

XX duplexes having 5' and 3' sequences for annealing to amplification

PT primers with an internal potential protein-binding site sequence.

XX Example 3; Page 19; 52pp; English.

PS This sequence represents a binding site identified using the method of

CC the invention. This sequence was identified using the 32P-labelled

CC oligonucleotide duplex shown in AAT76581 and the primers shown in

CC AAT76582-T76583 in the method of the invention. The method is for

CC simultaneously isolating protein-binding sites for DNA-binding proteins.

CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes

CC having 5' and 3' sequences capable of annealing to primers for

CC amplification and an internal sequence having a potential protein-binding

CC site, a non-specific inhibitor and a sample containing DNA-binding

CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed

CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form

CC amplified duplexes; thereby isolating protein-binding sites for the DNA-

CC binding proteins. The methods can be used to identify protein-binding

CC sites which can be used to identify corresponding DNA-binding proteins in

CC an expression library. They can also be used to develop products to

CC inhibit the function of a given DNA-binding protein or for the

CC modification of transcription factors

XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
QY      1 GGGG 5
        |||||
Db      3 GGGG 7

RESULT 33
AAT98859
ID  AAT98859 standard; DNA; 10 BP.
XX
AC  AAT98859;
XX
DT  20-MAR-1998 (first entry)
XX
DE  Core-binding site clone 6-6-2.
XX
KW  Protein-binding site isolation; transcription factor modification;
KW  DNA-binding protein; inhibitor identification; ss.
XX
OS  Synthetic.
XX
PN  WO9727330-A1.
XX
PD  31-JUL-1997.
XX
PF  24-JAN-1997; 97WO-US001230.
XX
PR  24-JAN-1996; 96US-00590571.
XX
PA  (UYVA ) UNIV YALE.
XX
PI  Weissman SM, Kulkarni P, Nallur GN;
XX
DR  WPI; 1997-393714/36.
XX
PT  Identifying protein-binding sites for DNA-binding proteins - using
PT  duplexes having 5' and 3' sequences for annealing to amplification
PT  primers with an internal potential protein-binding site sequence.
XX
PS  Example 3; Page 22; 52pp; English.
XX
CC  This sequence represents a core-binding site identified using the method
CC  of the invention. This sequence was identified using the 32P-labelled
CC  oligonucleotide duplex shown in AAT76581 and the primers shown in
CC  AAT76582-T76583 in the method of the invention. The method is for
CC  simultaneously isolating protein-binding sites for DNA-binding proteins.
CC  The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC  having 5' and 3' sequences capable of annealing to primers for
CC  amplification and an internal sequence having a potential protein-binding
CC  site, a non-specific inhibitor and a sample containing DNA-binding
CC  proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC  with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC  amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC  binding proteins. The methods can be used to identify protein-binding
CC  sites which can be used to identify corresponding DNA-binding proteins in
CC  an expression library. They can also be used to develop products to
CC  inhibit the function of a given DNA-binding protein or for the
CC  modification of transcription factors
XX
SQ  Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGG 5
        |||||
Db      4 GGGG 8

RESULT 34
AAT98864
ID  AAT98864 standard; DNA; 10 BP.
```

```
XX  AAT98864;
AC
XX
DT  20-MAR-1998 (first entry)
XX
DE  Core-binding site clone 6-12-2R.
XX
KW  Protein-binding site isolation; transcription factor modification;
KW  DNA-binding protein; inhibitor identification; ss.
XX
OS  Synthetic.
XX
PN  WO9727330-A1.
XX
PD  31-JUL-1997.
XX
PF  24-JAN-1997; 97WO-US001230.
XX
PR  24-JAN-1996; 96US-00590571.
XX
PA  (UYVA ) UNIV YALE.
XX
PI  Weissman SM, Kulkarni P, Nallur GN;
XX
DR  WPI; 1997-393714/36.
XX
PT  Identifying protein-binding sites for DNA-binding proteins - using
PT  duplexes having 5' and 3' sequences for annealing to amplification
PT  primers with an internal potential protein-binding site sequence.
XX
PS  Example 3; Page 22; 52pp; English.
XX
CC  This sequence represents a core-binding site identified using the method
CC  of the invention. This sequence was identified using the 32P-labelled
CC  oligonucleotide duplex shown in AAT76581 and the primers shown in
CC  AAT76582-T76583 in the method of the invention. The method is for
CC  simultaneously isolating protein-binding sites for DNA-binding proteins.
CC  The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC  having 5' and 3' sequences capable of annealing to primers for
CC  amplification and an internal sequence having a potential protein-binding
CC  site, a non-specific inhibitor and a sample containing DNA-binding
CC  proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC  with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC  amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC  binding proteins. The methods can be used to identify protein-binding
CC  sites which can be used to identify corresponding DNA-binding proteins in
CC  an expression library. They can also be used to develop products to
CC  inhibit the function of a given DNA-binding protein or for the
CC  modification of transcription factors
XX
SQ  Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      3 GGGGG 7

RESULT 35
AAT98851
ID  AAT98851 standard; DNA; 10 BP.
XX
AC  AAT98851;
XX
DT  20-MAR-1998 (first entry)
XX
DE  Binding site BSN14 identified using the method of the invention.
XX
KW  Protein-binding site isolation; transcription factor modification;
KW  DNA-binding protein; inhibitor identification; ss.
```



```
XX OS Synthetic.
XX PN WO9727330-A1.
XX PD 31-JUL-1997.
XX PF 24-JAN-1997; 97WO-US001230.
XX PR 24-JAN-1996; 96US-00590571.
XX PA (UYYA ) UNIV YALE.
XX PI Weissman SM, Kulkarni P, Nallur GN;
XX DR WPI; 1997-393714/36.
XX PT Identifying protein-binding sites for DNA-binding proteins - using
XX PT duplexes having 5' and 3' sequences for annealing to amplification
XX PT primers with an internal potential protein-binding site sequence.
XX PS Example 3; Page 19; 52pp; English.
XX CC This sequence represents a binding site identified using the method of
XX CC the invention. This sequence was identified using the 32P-labelled
XX CC oligonucleotide duplex shown in AAT76581 and the primers shown in
XX CC AAT76582-T76583 in the method of the invention. The method is for
XX CC simultaneously isolating protein-binding sites for DNA-binding proteins.
XX CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
XX CC having 5' and 3' sequences capable of annealing to primers for
XX CC amplification and an internal sequence having a potential protein-binding
XX CC site, a non-specific inhibitor and a sample containing DNA-binding
XX CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
XX CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
XX CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
XX CC binding proteins. The methods can be used to identify protein-binding
XX CC sites which can be used to identify corresponding DNA-binding proteins in
XX CC an expression library. They can also be used to develop products to
XX CC inhibit the function of a given DNA-binding protein or for the
XX CC modification of transcription factors
XX SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
1 GGGGG 5

RESULT 36
AAT70006
ID AAT70006 standard; DNA; 10 BP.
XX AC
XX AC AAT70006;
XX DT 25-AUG-1997 (first entry)
XX DE Triplex-forming oligonucleotide AG10.
XX KW Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;
XX KW oncogene inactivation; supF gene; ss.
XX OS Synthetic.
XX PN WO9639195-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-US008883.
XX PR 25-AUG-1997 (first entry)
XX PA Triplex-forming oligonucleotide AG10.
XX PI Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;
XX KW oncogene inactivation; supF gene; ss.
XX OS Synthetic.
XX PN WO9639195-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-US008883.
XX XX
```

```
PR 06-JUN-1995; 95US-00463519.
XX (UYYA ) UNIV YALE.
XX PI Glazer PM, Havre PA;
XX DR WPI; 1997-042873/04.
XX XX Triple-helix forming oligo:nucleotide linked to a mutagen - useful for
XX PT site-specific mutagenesis of target gene, e.g. for gene therapy or to
XX PT inactivate oncogene(s) or viral genes.
XX PS Example 1; Fig 1; 68pp; English.
XX CC Homopurine oligonucleotide AG10 (AAT70006) can be linked to psoralen at
XX CC its 5' end and used to achieve site-specific, targeted mutagenesis of a
XX CC specific gene. It is based on a homopurine/ homopyrimidine 10-bp motif
XX CC found at bp 167-176 of the supF gene (see also AAT70005), an E. coli
XX CC amber suppressor tyrosine tRNA gene. Targeted mutagenesis was achieved
XX CC by incubating pso-AG10 with supF DNA in vitro to form a triplex at
XX CC positions 167-176 of the supF gene and bring the tethered psoralen into
XX CC proximity with the targeted base pair 167 (see also AAT70008). This
XX CC method of site- directed mutagenesis can be used for gene therapy, to
XX CC inactivate oncogenes or viral genes, to study DNA repair mechanisms and
XX CC to produce transmutated plants and animals
XX SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db |||||
6 GGGGG 10

RESULT 37
AAT70007
ID AAT70007 standard; DNA; 10 BP.
XX AC AAT70007;
XX DT 25-AUG-1997 (first entry)
XX XX Oligonucleotide GA10.
XX KW Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;
XX KW oncogene inactivation; supF gene; ss.
XX OS Synthetic.
XX PN WO9639195-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-US008883.
XX PR 06-JUN-1995; 95US-00463519.
XX PA (UYYA ) UNIV YALE.
XX PI Glazer PM, Havre PA;
XX DR WPI; 1997-042873/04.
XX XX Triple-helix forming oligo:nucleotide linked to a mutagen - useful for
XX PT site-specific mutagenesis of target gene, e.g. for gene therapy or to
XX PT inactivate oncogene(s) or viral genes.
XX PS Example 1; Page 15; 68pp; English.
XX CC Oligonucleotide GA10 (AAT70007), the reverse of oligonucleotide AG10
```

CC (AAT70006), was used in assays for triplex formation with the supF gene  
CC target (see also AAT70005). AG10 failed to bind to supF or to compete with  
CC AG10 for binding. AG10 bound specifically to the supF gene  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 1 GGGGG 5  
RESULT 38  
AAT80370  
ID AAT80370 standard; DNA; 10 BP.  
XX  
AC AAT80370;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-223, multiplex forming oligomer.  
XX  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..5  
FT /\*tag= a  
FT /note= "2'-OMe RNA"  
FT modified\_base 6..10  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
PN WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 28; Page 22; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefor useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence forms multiplex binding complexes with  
CC regions of the HCV genome. This sequence forms a duplex at the region -  
CC 218 to -227 and does not form a purine strand triplex  
XX

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 1 GGGGG 5  
RESULT 39  
AAT47062  
ID AAT47062 standard; DNA; 10 BP.  
XX  
AC AAT47062;  
XX  
DT 05-SEP-1997 (first entry)  
XX  
DE Oligonucleotide AG10, which binds triplex target site in supFG1.  
XX  
KW Triplex; supFG1; forming; target site; triple stranded; induction;  
KW mutation; targetted mutagenesis; triple helix; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640898-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 03-JUN-1996; 96WO-US008392.  
XX  
PR 07-JUN-1995; 95US-00476712.  
XX  
PA (UYYA ) UNIV YALE.  
PI Glazer PM;  
XX  
DR WPI; 1997-052310/05.  
XX  
PT Oligo-nucleotide for targetted mutagenesis of double stranded nucleic  
PT acid mol. - by forming triple stranded nucleic acid mol. with target  
PT region of double stranded nucleic acid mol.  
XX  
PS Example 1; Fig 1; 29pp; English.  
XX  
CC In an example of the invention, the binding of the oligonucleotides AG10  
CC (AAT47062), AG20 (AAT47061) and AG30 (AAT47060) to the supFG1 triplex  
CC target site (AAT47059), was examined using a gel mobility shift assay.  
CC Based on the concentration dependence of the triplex formation, the  
CC equilibrium constants for AG10, AG20 and AG30 were 3x10 power -5, 3x10  
CC power -7 and 2x10 power -8. The oligonucleotides were then tested for  
CC their ability to induce mutations in the pSupFG1 SV40 vector in monkey  
CC COS cells. AG30 generated mutations in the target gene at a frequency of  
CC 0.27%, 13 fold over the spontaneous background in the assay. In contrast,  
CC AG10 and AG20, which show inferior 3rd strand binding to supFG1, were  
CC much less effective in producing mutations. Examples of some of the  
CC mutations induced in the pSupFG1 vector using the oligonucleotides are  
CC given in AAT75067-73  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 6 GGGGG 10  
RESULT 40  
AAV62570/c

ID AAV62570 standard; DNA; 10 BP.  
 XX AAV62570;  
 AC  
 XX  
 DT 17-DEC-1998 (first entry)  
 XX  
 DE Septoria nodorum species specific RAPD primer OPB-19.  
 XX  
 KW Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;  
 KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;  
 KW Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;  
 KW random amplified polymorphic DNA; PCR; nucleic acid detection; RAPD;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Phaeosphaeria nodorum.  
 XX  
 PN US5814453-A.  
 XX  
 XX 29-SEP-1998.  
 PD  
 XX  
 PF 02-JUL-1997; 97US-00887480.  
 XX  
 PR 19-APR-1995; 95WO-US004712.  
 PR 15-OCT-1996; 96US-00722187.  
 XX  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 XX  
 XX Beck JJ;  
 PI  
 XX WPI; 1998-541745/46.  
 DR  
 XX DNA isolated from fungal RNA, and its internal transcribed spacer  
 PT sequence - used for detecting fungal pathogens in plant tissue.  
 PT  
 XX Example 7; Col 19; 56pp; English.  
 PS  
 XX Sequences AAV62567 to AAV62571 represent random amplified polymorphic DNA  
 CC (RAPD) primers used in the course of the invention for detection of  
 CC Septoria species. The invention provides a DNA molecule isolated from the  
 CC ribosomal RNA gene region of a fungal pathogen, where the DNA molecule  
 CC consists of an internal transcribed spacer (ITS) sequence selected from  
 CC ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium  
 CC moniliforme, Septoria avenae or Microdochium nivale. A method for  
 CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.  
 CC avenaceum and M. nivale isolates is also provided which comprises  
 CC isolating DNA from a plant leaf infected with at least one of the above  
 CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by  
 CC PCR using specific primers from within these sequences. The pathogen(s)  
 CC are detected by visualising the amplified part of the ITS sequence  
 XX  
 SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db |||||  
 6 GGGGG 2  
 RESULT 41  
 AAV45390  
 ID AAV45390 standard; DNA; 10 BP.  
 XX  
 AC AAV45390;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Mouse CD3-epsilon enhancer binding site for Ikaros.  
 XX  
 KW Ikaros; mIK; transcription factor; mouse; lymphocyte;

KW cell differentiation; T cell; cancer; immunodeficiency;  
 KW Alzheimer's disease; therapy; diagnosis; CD3-epsilon; enhancer; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN CA2194256-A.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 02-JAN-1997; 97CA-02194256.  
 XX  
 PR 05-SEP-1996; 96US-00711417.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX Georgopoulos K;  
 PI  
 XX WPI; 1998-378292/33.  
 DR  
 XX New nucleic acid encoding Ikaros protein involved in early  
 PT differentiation of lymphocytes - existing in several isoforms, and  
 PT related products, used to treat e.g. immune diseases or cancer and to  
 PT control cell differentiation.  
 XX  
 PS Disclosure; Page 38; 158pp; English.  
 XX  
 CC This oligonucleotide from the mouse CD3-epsilon gene enhancer was  
 CC identified as a potential high affinity binding site for Ikaros proteins  
 CC (see AAW70963-71). It partially includes the core motif GGGAA found in  
 CC consensus recognition sequences for murine Ikaros isoforms mIk-1, mIk-2  
 CC and mIk-3 (see AAV52830-32). High affinity binding sites for Ikaros have  
 CC been found in enhancer and promoter regions of the regulatory domains of  
 CC the TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal  
 CC repeat and in the regulatory domains of other T cell restricted antigens  
 CC (see AAV45358-402) by gel retardation assay. Ikaros is involved in early  
 CC differentiation of lymphocytes. The invention provides Ikaros nucleic  
 CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host  
 CC cells. These are used to treat T and B cell diseases, to control  
 CC expression of heterologous genes placed under control of an Ikaros-  
 CC responsive element, to treat nervous system diseases and to modulate cell  
 CC division, amplification or differentiation, especially in haematopoietic  
 CC cells  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db |||||  
 3 GGGGG 7  
 RESULT 42  
 AAV67001  
 ID AAV67001 standard; cDNA; 10 BP.  
 XX  
 AC AAV67001;  
 XX  
 DT 14-JAN-1999 (first entry)  
 XX  
 DE CD3-epsilon enhancer oligonucleotide #3.  
 XX  
 KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;  
 KW differentiation marker; immune system; corpus striatum; AIDS;  
 KW Alzheimer's disease; ss.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN US5824770-A.  
 XX

PD 20-OCT-1998.  
XX  
PF 05-JUN-1995; 9SUS-00465590.  
XX  
PR 14-SEP-1992; 92US-00946233.  
PR 14-SEP-1993; 93US-00121438.  
PR 02-MAY-1994; 94US-00238212.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Georgopoulos K;  
XX  
DR WPI; 1998-582621/49.  
XX  
PT Ikaros poly:peptide(s) - useful for treating disorders of immune system  
PT or corpus striatum.  
XX  
PS Disclosure; Col 27; 111pp; English.  
XX  
CC The present invention describes a purified peptide having at least one of  
CC the following properties: (a) it stimulates transcription of a DNA  
CC sequence under the control of a delta A element, an NFkB element or an  
CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of  
CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide  
CC consensus sequence; (c) it competitively inhibits the binding of a  
CC naturally occurring Ikaros isoform to any of a delta A element, an NFkB  
CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it  
CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
CC (e) it inhibits protein-protein interactions of transcriptional complexes  
CC formed with naturally occurring Ikaros isoforms. The proteins, provided  
CC that they stimulate gene transcription under the control of delta A  
CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to  
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
CC inhibit protein-protein interactions of transcriptional complexes with  
CC naturally occurring Ikaros isoforms, can be used to treat immune system  
CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
CC given in the present invention  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db |||||  
3 GGGGG 7

RESULT 43  
AAZ86960  
ID AAZ86960 standard; DNA; 10 BP.  
XX  
AC AAZ86960;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE PCR primer for detection of genetic uniformity of a plant clone.  
XX  
KW PCR primer; genetic uniformity; plant clone body; detection; ss.  
XX  
OS Synthetic.  
XX  
PN JP10262667-A.  
XX  
PD 06-OCT-1998.  
XX  
PF 19-MAR-1997; 97JP-00106563.  
XX

PR 19-MAR-1997; 97JP-00106563.  
XX  
PA (SAOK ) NIPPON SEISHI KK.  
XX  
DR WPI; 1998-587287/50.  
XX  
PT New primer - used for the detection of genetic uniformity of a clone  
PT plant body.  
XX  
PS Example 1; Page 5; 7pp; Japanese.  
XX  
CC This sequence represents an example of the PCR primer of the invention.  
CC The primers of the invention consist of 10 bases and have the formula: 5'  
CC -NNNN XY XY XY-3'; where: N, X and Y = optional nucleic acid monomers;  
CC and N and X as well as N and Y may be nucleic acids having a same base  
CC but X and Y are nucleic acids having different bases. The primers are  
CC used to distinguish between plant clone bodies at the DNA level, with  
CC high sensitivity  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
Db |||||  
1 GGGGG 5

RESULT 44  
AAV32461/C  
ID AAV32461 standard; RNA; 10 BP.  
XX  
AC AAV32461;  
XX  
DT 11-SEP-1998 (first entry)  
XX  
DE Oligonucleotide (aC)9T.  
XX  
KW Phosphoramidite monomer; PM; nucleophile; coupling activator; tetrazole;  
KW phosphorodiester linkage; N-methylimidazole; NMI; 4,5-dicyanoimidazole;  
KW DNA/RNA hybrid; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..9 /\*tag= a  
FT misc\_difference 10 /note= "Each nucleotide is a 2'-Aminocytidine"  
FT /\*tag= b  
FT /\*tag= "deoxythymidine"  
XX  
PN WO9816540-A1.  
XX  
PD 23-APR-1998.  
XX  
PF 08-OCT-1997; 97WO-US015744.  
XX  
PR 15-OCT-1996; 96US-00730556.  
PR 25-SEP-1997; 97US-00937867.  
XX  
PA (NEXS-) NEXSTAR PHARM INC.  
XX  
PI Vargeese C, Pieken W, Carter JD, Yegge J;  
XX  
DR WPI; 1998-261034/23.  
XX  
PT Preparation of oligonucleotides from phosphoramidite monomers - using  
PT coupling activator which is less acidic than tetrazole, e.g., 4,5-  
PT dicyanoimidazole or 2-nitroimidazole.  
XX

PS Example 6; Page 18; 49pp; English.

XX The invention provides a method for oligonucleotide synthesis from

CC phosphoramidite monomers (PMs) which involves reacting a PM and a

CC nucleophile in the presence of a coupling activator. The coupling

CC activator chosen is less acidic than, and at least as nucleophilic as,

CC tetrazole. The present oligonucleotide (aC)9T was prepared using either

CC tetrazole, N-methylimidazole (NMI) or 4,5-dicyanoimidazole as the

CC coupling activator. The method, which claims to give improved coupling

CC efficiency may be used for the production of oligonucleotides

XX

SQ Sequence 10 BP; 0 A; 9 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db |||||

9 GGGGG 5

RESULT 45

AAV56865/c

ID AAV56865 standard; DNA; 10 BP.

XX

AC AAV56865;

XX

DT 02-DEC-1998 (first entry)

XX

DE Regulatory element containing oligonucleotide #24.

XX

XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;

KW transcriptional control; STAT protein; screening; agonist; ss.

XX

OS Synthetic.

XX

PN US5814517-A.

XX

PD 29-SEP-1998.

XX

PF 27-MAR-1995; 95US-00410779.

XX

PR 14-APR-1994; 94US-00228935.

XX

PA (LIGA-) LIGAND PHARM INC.

XX

PI Lamb IP, Seidel HM;

XX

DR WPI; 1998-541763/46.

XX

PT DNA constructs containing cytokine-responsive regulatory elements -

PT useful in assays for transcription-regulating proteins or gene

PT transcription agonists or antagonists.

XX

PS Claim 11; Col 11; 58pp; English.

XX

CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the

CC production of constructs comprising a cytokine-responsive regulatory

CC element linked to a promoter which is linked to a heterologous coding

CC sequence so that the coding sequence is under the transcriptional control

CC of the regulatory element and the promoter, where the regulatory element

CC has a nucleotide sequence selected from TTCNGAA, TTANYTAA, and TTCNYTAA

CC where N is A, T, C or G, and y = 3 or 4. The constructs can be used to

CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,

CC in a sample by contacting the sample with the construct so that the

CC protein binds to the regulatory element, and detecting or separating the

CC resulting complex. The cells can be used in screening assays for agonists

CC of gene transcription, in which the level of expression of the coding

CC sequence is measured in the presence and absence of a test compound or in

CC the presence of the corresponding cytokine

XX

SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db |||||

7 GGGGG 3

RESULT 46

AAV50112/c

ID AAV50112 standard; DNA; 10 BP.

XX

AC AAV50112;

XX

DT 21-OCT-1998 (first entry)

XX

DE Yeast tag for NORF gene locus NORF2.

XX

KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;

KW eukaryotic cell; antifungal; SAGE tag; gene expression;

KW serial analysis of gene expression; probe; ss.

XX

OS Saccharomyces cerevisiae.

OS Synthetic.

XX

PN WQ9832847-A2.

XX

PD 30-JUL-1998.

XX

PF 22-JAN-1998; 98WO-US001216.

XX

PR 23-JAN-1997; 97US-0035917P.

XX

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX

PI Velculescu VE, Vogelstein B, Kinzler KW;

XX

DR WPI; 1998-427943/36.

XX

PT Yeast transcriptome - useful for modulating eukaryotic cell, for

PT screening antifungal agents, and for identifying genes in cell cycle

PT progression.

XX

PS Claim 1; Page 23; 44pp; English.

XX

CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene

CC involved in cell cycle progression selected from the group of

CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)

CC tags for highly expressed genes and NORF genes are given in AAV50051 to

CC AAV50345. The present invention describes: (1) a method of using yeast

CC genes to modulate the cell cycle which comprises administering to a cell

CC an isolated DNA molecule comprising a yeast gene which is involved in

CC cell cycle progression selected from differentially expressed genes (SAGE

CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate

CC antifungal drugs which comprises contacting a test substance with a yeast

CC cell and monitoring expression of a yeast gene which is involved in cell

CC cycle progression; (3) a method of identifying human genes which are

CC involved in cell cycle progression which comprises hybridizing a probe

CC comprising at least 10 contiguous nucleotides of a yeast gene which is

CC differentially expressed between at least 2 phases selected from the log

CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining

CC the phase in the cell cycle, where the probe comprises at least 14

CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to

CC AAV50345), or as an array of probes on a solid support

XX

SQ Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 GGGG 5
Db      10 GGGG 6

RESULT 47
AAV50068/c
ID  AAV50068 standard; DNA; 10 BP.
XX
AC  AAV50068;
XX
DT  21-OCT-1998  (first entry)
XX
DE  Yeast tag for highly expressed gene locus NORF2.
XX
KW  Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW  eukaryotic cell; antifungal; SAGE tag; gene expression;
KW  serial analysis of gene expression; probe; ss.
XX
OS  Saccharomyces cerevisiae.
OS  Synthetic.
XX
PN  WO9832847-A2.
XX
PD  30-JUL-1998.
XX
PF  22-JAN-1998;  98WO-US001216.
XX
PR  23-JAN-1997;  97US-0035917P.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI  Velulescu VE,  Vogelstein B,  Kinzler KW;
XX  WPI; 1998-427943/36.
XX
PT  Yeast transcriptome - useful for modulating eukaryotic cell, for
PT  screening antifungal agents, and for identifying genes in cell cycle
PT  progression.
XX
PS  Claim 11; Page 21; 44pp; English.
XX
CC  Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC  involved in cell cycle progression selected from the group of
CC  nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC  tags for highly expressed genes and NORF genes are given in AAV50051 to
CC  AAV50345. The present invention describes: (1) a method of using yeast
CC  genes to modulate the cell cycle which comprises administering to a cell
CC  an isolated DNA molecule comprising a yeast gene which is involved in
CC  cell cycle progression selected from differentially expressed genes (SAGE
CC  tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC  antifungal drugs which comprises contacting a test substance with a yeast
CC  cell and monitoring expression of a yeast gene which is involved in cell
CC  cycle progression; (3) a method of identifying human genes which are
CC  involved in cell cycle progression which comprises hybridizing a probe
CC  comprising at least 10 contiguous nucleotides of a yeast gene which is
CC  differentially expressed between at least 2 phases selected from the log
CC  phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC  the phase in the cell cycle, where the probe comprises at least 14
CC  contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC  AAV50345), or as an array of probes on a solid support
XX
SQ  Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No.1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGG 5
Db      10 GGGG 6

RESULT 48
AAV35941/c
ID  AAV35941 standard; DNA; 10 BP.
XX
AC  AAV35941;
XX
DT  26-AUG-1998  (first entry)
XX
DE  Primer used in RAPD assay of the invention.
XX
KW  Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW  muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS  Synthetic.
OS  Sus sp.
XX
PN  WO9815837-A1.
XX
PD  16-APR-1998.
XX
PF  07-OCT-1997;  97WO-GB002741.
XX
PR  07-OCT-1996;  96GB-00020904.
PR  18-FEB-1997;  97GB-00003350.
PR  20-MAR-1997;  97GB-00005796.
PR  09-SEP-1997;  97GB-00019002.
XX
PA  (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
PI  Maltin CA,  Steven J,  Warkup CC;
XX  WPI; 1998-240968/21.
XX
PT  Assay for alleles or muscle fibre composition characteristic of Duroc
PT  type pigs - comprises determination of genotype or muscle fibre
PT  properties, used to identify animals for breeding programs and to assess
PT  meat quality.
XX
PS  Example 3; Page 33; 56pp; English.
XX
CC  PCR primers AAV35877-996 were used in a rapid amplification of
CC  polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC  is used to determine if an animal has an allele for, or muscle fibre
CC  composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC  meat of superior quality (particularly tenderness) but are normally less
CC  efficient feed converters and fatter than other types. The assay
CC  comprises analysing a tissue sample to determine if the genotype
CC  comprises the allele, and genetic features typical of animals with Duroc-
CC  type MFC are present. The method is used to select animals that have
CC  Duroc characteristics for use in breeding programmes (to develop the
CC  animals with Duroc pig characteristics), and to assess meat quality
XX
SQ  Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No.1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 49
AAV04582
ID  AAV04582 standard; DNA; 10 BP.
XX
AC  AAV04582;
XX
DT  07-APR-1999  (first entry)
XX
DE  Inverted repeat from snRNA forming a stem structure.
XX
```

```
RESULT 48
AAV35941/c
ID  AAV35941 standard; DNA; 10 BP.
XX
AC  AAV35941;
XX
DT  26-AUG-1998  (first entry)
XX
DE  Primer used in RAPD assay of the invention.
XX
KW  Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW  muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS  Synthetic.
OS  Sus sp.
XX
PN  WO9815837-A1.
XX
PD  16-APR-1998.
XX
PF  07-OCT-1997;  97WO-GB002741.
XX
PR  07-OCT-1996;  96GB-00020904.
PR  18-FEB-1997;  97GB-00003350.
PR  20-MAR-1997;  97GB-00005796.
PR  09-SEP-1997;  97GB-00019002.
XX
PA  (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
PI  Maltin CA,  Steven J,  Warkup CC;
XX  WPI; 1998-240968/21.
XX
PT  Assay for alleles or muscle fibre composition characteristic of Duroc
PT  type pigs - comprises determination of genotype or muscle fibre
PT  properties, used to identify animals for breeding programs and to assess
PT  meat quality.
XX
PS  Example 3; Page 33; 56pp; English.
XX
CC  PCR primers AAV35877-996 were used in a rapid amplification of
CC  polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC  is used to determine if an animal has an allele for, or muscle fibre
CC  composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC  meat of superior quality (particularly tenderness) but are normally less
CC  efficient feed converters and fatter than other types. The assay
CC  comprises analysing a tissue sample to determine if the genotype
CC  comprises the allele, and genetic features typical of animals with Duroc-
CC  type MFC are present. The method is used to select animals that have
CC  Duroc characteristics for use in breeding programmes (to develop the
CC  animals with Duroc pig characteristics), and to assess meat quality
XX
SQ  Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No.1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 49
AAV04582
ID  AAV04582 standard; DNA; 10 BP.
XX
AC  AAV04582;
XX
DT  07-APR-1999  (first entry)
XX
DE  Inverted repeat from snRNA forming a stem structure.
XX
```

KW Small nucleolar RNA gene; snRNA; maize; promoter; RNA production;  
KW RNA stability; small non-translated RNA; intergenic region;  
KW inverted repeat; ds.  
XX  
OS Unidentified.  
XX  
PN EP887405-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 25-JUN-1997; 97EP-00401480.  
XX  
PR 25-JUN-1997; 97EP-00401480.  
XX  
PA (GENE-) GENE SHEARS PTY LTD.  
XX  
PI Brown JWS, Leader DJ;  
XX  
DR WPI; 1999-047872/05.  
XX  
XX Producing stabilised RNA molecules - using a DNA precursor comprising  
PT plant small nucleolar RNA stabilising sequences.  
XX  
PS Disclosure; Page 6; 98pp; English.  
XX  
CC The present sequence represents an inverted repeat from small nucleolar  
CC RNA (snRNA) sequences. The present sequence forms a stem structure in  
CC the protein binding sites of SnRNAs, and prevents overdigestion by 3'  
CC and 5' exonucleases. Plant snRNA genes enable production of multiple  
CC stabilised RNA from a single promoter in a splicing-independent manner,  
CC and allow the production of RNA from intron or non-intron sequences. The  
CC present sequence is used in the method of the invention. The  
CC specification describes a method for producing small non-translated RNA  
CC molecules, which comprises introducing a precursor DNA containing one or  
CC a cluster of coding sequences into a plant or yeast cell. Each coding  
CC sequence comprises a non-translated RNA sequence to be stabilised, which  
CC is capable of functionally interacting with a cellular component and  
CC stabilising sequences comprising at least one protein binding site. The  
CC stabilised RNA units are transcribed by the cell's endogenous processing  
CC machinery. The process is useful for qualitatively and quantitatively  
CC enhancing the production and stability of RNA molecules, especially non-  
CC translated RNA e.g. ribozymes and antisense RNA. The nucleic acid  
CC molecules are useful as probes or primers for identification of snRNA  
CC sequences and intergenic regions  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
3 GGGGG 7  
  
RESULT 50  
AAX04583/c  
ID AAX04583 standard; DNA; 10 BP.  
XX  
AC AAX04583;  
XX  
DT 07-APR-1999 (first entry)  
XX  
DE Inverted repeat from snRNA forming a stem structure.  
XX  
KW Small nucleolar RNA gene; snRNA; maize; promoter; RNA production;  
KW RNA stability; small non-translated RNA; intergenic region;  
KW inverted repeat; ds.  
XX  
OS Unidentified.  
XX  
PN EP887405-A1.

XX 30-DEC-1998.  
XX  
PF 25-JUN-1997; 97EP-00401480.  
XX  
PR 25-JUN-1997; 97EP-00401480.  
XX  
PA (GENE-) GENE SHEARS PTY LTD.  
XX  
PI Brown JWS, Leader DJ;  
XX  
DR WPI; 1999-047872/05.  
XX  
PT Producing stabilised RNA molecules - using a DNA precursor comprising  
PT plant small nucleolar RNA stabilising sequences.  
XX  
PS Disclosure; Page 6; 98pp; English.  
XX  
CC The present sequence represents an inverted repeat from small nucleolar  
CC RNA (snRNA) sequences. The present sequence forms a stem structure in  
CC the protein binding sites of SnRNAs, and prevents overdigestion by 3'  
CC and 5' exonucleases. Plant snRNA genes enable production of multiple  
CC stabilised RNA from a single promoter in a splicing-independent manner,  
CC and allow the production of RNA from intron or non-intron sequences. The  
CC present sequence is used in the method of the invention. The  
CC specification describes a method for producing small non-translated RNA  
CC molecules, which comprises introducing a precursor DNA containing one or  
CC a cluster of coding sequences into a plant or yeast cell. Each coding  
CC sequence comprises a non-translated RNA sequence to be stabilised, which  
CC is capable of functionally interacting with a cellular component and  
CC stabilising sequences comprising at least one protein binding site. The  
CC stabilised RNA units are transcribed by the cell's endogenous processing  
CC machinery. The process is useful for qualitatively and quantitatively  
CC enhancing the production and stability of RNA molecules, especially non-  
CC translated RNA e.g. ribozymes and antisense RNA. The nucleic acid  
CC molecules are useful as probes or primers for identification of snRNA  
CC sequences and intergenic regions  
XX  
SQ Sequence 10 BP; 4 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
Db |||||  
8 GGGGG 4  
  
Search completed: January 7, 2005, 07:12:13  
Job time : 258.4 secs



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GGGGG  
Perfect score: 5  
Sequence: 1 ggggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gss1:  
9: gb\_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	10	4	BM393918 50072-2-1
C 2	5	100.0	10	4	BM396043 5009-0-15
C 3	5	100.0	10	9	CL435808 PST1453-N
C 4	5	100.0	10	9	CL436345 PST2785-N
C 5	5	100.0	10	9	CL438120 PST6843-N
C 6	5	100.0	10	9	CL439043 PST8576-N
C 7	5	100.0	11	1	AJ657108 AJ657108
C 8	5	100.0	11	4	BM395228 50072-2-8
C 9	5	100.0	11	7	CF543031 S015532-0
C 10	5	100.0	12	5	BQ585390 S011420-0
C 11	5	100.0	12	6	CA851641 D15H12_O2
C 12	5	100.0	12	6	CA851649 D16A08_B2
C 13	5	100.0	12	8	AQ074231 17 pUC8 P
C 14	5	100.0	12	9	AJ600541 Arabidops
C 15	5	100.0	12	9	AJ600549 Arabidops
C 16	5	100.0	13	4	BG810452 mgct006xc
C 17	5	100.0	13	4	BG926067 HNC23-1-E
C 18	5	100.0	13	4	BM394028 50072-2-1
C 19	5	100.0	13	4	BM395265 50072-2-8
C 20	5	100.0	13	4	BM395395 50072-2-8
C 21	5	100.0	13	5	BQ595080 E012709-0
C 22	5	100.0	13	9	AJ587920 Arabidops
C 23	5	100.0	14	4	BM392794 50071-2-1
C 24	5	100.0	14	4	BM394089 50072-2-1

25	5	100.0	14	4	BM395308 50072-2-8
C 26	5	100.0	14	4	BM395363 50072-2-8
27	5	100.0	14	5	BQ585808 S014470-0
28	5	100.0	14	5	BQ593114 E012797-0
C 29	5	100.0	14	5	BX679320 BX679320
30	5	100.0	14	6	CA850835 D07A10_A2
31	5	100.0	14	7	CK258733 EST742370
C 32	5	100.0	14	7	CK258733 EST742370
33	5	100.0	14	9	AJ587271 Arabidops
34	5	100.0	15	2	AW248644 2820747.3
35	5	100.0	15	4	BM395188 50072-2-7
C 36	5	100.0	15	4	BM395189 50072-2-7
37	5	100.0	15	5	BQ588758 E012534-0
38	5	100.0	15	5	BQ590018 E012843-0
39	5	100.0	15	6	CA794555 CAC BL_14
40	5	100.0	15	6	CA850964 D08F09_L2
41	5	100.0	15	7	CK283790 EST746512
C 42	5	100.0	15	7	CK283790 EST746512
43	5	100.0	16	1	AA937364 OJ08f10.8
C 44	5	100.0	16	1	AA939272 OQ31b06.8
45	5	100.0	16	1	AA968729 OX69h11.8
C 46	5	100.0	16	1	AI075064 OX69h11.8
C 47	5	100.0	16	1	AI094839 GA22C08.X
48	5	100.0	16	1	AI209036 QG18g10.X
49	5	100.0	16	1	AI262040 QK24h08.X
C 50	5	100.0	16	1	AI274782 QV67h03.X
51	5	100.0	16	1	AI290907 QM09a04.X
C 52	5	100.0	16	1	AI290907 QM09a04.X
53	5	100.0	16	1	AI357296 QX15h01.X
C 54	5	100.0	16	1	AI357296 QX15h01.X
C 55	5	100.0	16	1	AI446372 TJ10C06.X
56	5	100.0	16	1	AI560058 TQ38h11.X
C 57	5	100.0	16	1	AI564478 TQ57g09.X
C 58	5	100.0	16	1	AI564678 TQ78g03.X
C 59	5	100.0	16	1	AI569544 TC28d10.X
C 60	5	100.0	16	1	AI590540 TW11C02.X
C 61	5	100.0	16	1	AI648507 TZ54C09.X
C 62	5	100.0	16	1	AI684114 TX79d02.X
C 63	5	100.0	16	1	AI721735 FC31g08.X
C 64	5	100.0	16	1	AI735054 AS88b02.X
65	5	100.0	16	1	AI741762 WG22f06.X
C 66	5	100.0	16	1	AI749229 AT41a02.X
C 67	5	100.0	16	1	AI758574 TY07g05.X
68	5	100.0	16	1	AJ679356 AJ679356
C 69	5	100.0	16	4	BM395110 50072-2-7
70	5	100.0	16	4	BM396717 5009-0-24
71	5	100.0	16	4	BM396718 5009-0-24
72	5	100.0	16	4	BM398398 5009-0-45
73	5	100.0	16	4	BM399771 5009-0-61
C 74	5	100.0	16	4	BM817126 HC02D04.T
75	5	100.0	16	5	BQ583458 E011979-0
C 76	5	100.0	16	5	BQ590688 S013717-0
C 77	5	100.0	16	6	CF317464 HD--07-C1
C 78	5	100.0	16	7	CK255349 EST738986
79	5	100.0	16	9	AJ596548 Arabidops
C 80	5	100.0	17	4	BM395525 50072-2-9
81	5	100.0	17	4	BM397652 5009-0-35
82	5	100.0	17	4	BM398023 5009-0-4-
83	5	100.0	17	4	BM398024 5009-0-4-
84	5	100.0	17	4	BM399768 5009-0-61
85	5	100.0	17	9	AJ599163 Arabidops
C 86	5	100.0	17	9	CL437974 PST6607-N
C 87	5	100.0	18	1	AJ648240 AJ648240
C 88	5	100.0	18	4	BM395123 50072-2-7
C 89	5	100.0	18	4	BM395302 50072-2-8
C 90	5	100.0	18	4	BM395336 50072-2-8
91	5	100.0	18	4	BM397093 5009-0-28
92	5	100.0	18	4	BM397132 5009-0-29
93	5	100.0	18	5	BQ901245 HARP002XJ
94	5	100.0	18	7	CR555236 DKFZp468N
95	5	100.0	18	9	AJ587621 Arabidops
C 96	5	100.0	19	1	AA878744 OF85a08.8
97	5	100.0	19	1	AA918795 OL69C05.8

98	5	100.0	19	1	AA928040	AA928040	oi58g09.s
c 99	5	100.0	19	1	AA953971	AA953971	oo88h01.s
100	5	100.0	19	1	AA954509	AA954509	on81d05.s
101	5	100.0	19	1	AI142547	AI142547	qb47b08.x
102	5	100.0	19	1	AI149192	AI149192	qc76d09.x
c 103	5	100.0	19	1	AI174345	AI174345	an17f09.s
c 104	5	100.0	19	1	AI251781	AI251781	qu76g01.x
105	5	100.0	19	1	AI252235	AI252235	qu78h03.x
c 106	5	100.0	19	1	AI252235	AI252235	qu78h03.x
c 107	5	100.0	19	1	AI360784	AI360784	qx98g07.x
108	5	100.0	19	1	AI363303	AI363303	qy57b09.x
c 109	5	100.0	19	1	AI363303	AI363303	qy57b09.x
c 110	5	100.0	19	1	AI364573	AI364573	qw37g03.x
111	5	100.0	19	1	AI383415	AI383415	tc97d11.x
c 112	5	100.0	19	1	AI383415	AI383415	tc97d11.x
c 113	5	100.0	19	1	AI431460	AI431460	ti53a06.x
c 114	5	100.0	19	1	AI433480	AI433480	ti53a06.x
c 115	5	100.0	19	1	AI443363	AI443363	sa31a08.x
c 116	5	100.0	19	1	AI471695	AI471695	tl99f04.x
117	5	100.0	19	1	AI476315	AI476315	ta15c09.x
c 118	5	100.0	19	1	AI476315	AI476315	ta15c09.x
c 119	5	100.0	19	1	AI500684	AI500684	tn99c01.x
c 120	5	100.0	19	1	AI5337209	AI5337209	tp06f07.x
121	5	100.0	19	1	AI570374	AI570374	to78f07.x
c 122	5	100.0	19	1	AI581717	AI581717	ar74d08.x
c 123	5	100.0	19	1	AI624451	AI624451	ts29h11.x
c 124	5	100.0	19	1	AI625518	AI625518	ty56d06.x
c 125	5	100.0	19	1	AI635491	AI635491	tb65g09.x
126	5	100.0	19	1	AI648553	AI648553	tz55e07.x
c 127	5	100.0	19	1	AI678558	AI678558	tu83h07.x
c 128	5	100.0	19	1	AI686814	AI686814	tp79f06.x
c 129	5	100.0	19	1	AI690354	AI690354	tx14f06.x
130	5	100.0	19	1	AI695637	AI695637	we51g07.x
131	5	100.0	19	1	AI696833	AI696833	wc74e09.x
132	5	100.0	19	1	AI702520	AI702520	tz67g05.x
c 133	5	100.0	19	1	AI718147	AI718147	as42f11.x
c 134	5	100.0	19	1	AI719958	AI719958	as41d06.x
c 135	5	100.0	19	1	AI758301	AI758301	ty06a07.x
c 136	5	100.0	19	1	AI802578	AI802578	tp09c11.x
c 137	5	100.0	19	1	AI807936	AI807936	wf52e09.x
c 138	5	100.0	19	1	AI810128	AI810128	wf65g12.x
139	5	100.0	19	1	AI811474	AI811474	tw43c04.x
140	5	100.0	19	1	AI918188	AI918188	tn08c09.x
141	5	100.0	19	1	AJ659543	AJ659543	AJ659543
c 142	5	100.0	19	1	AJ666284	AJ666284	AJ666284
143	5	100.0	19	1	AJ666296	AJ666296	AJ666296
144	5	100.0	19	1	AJ666299	AJ666299	AJ666299
145	5	100.0	19	1	AJ696991	AJ696991	AJ696991
c 146	5	100.0	19	1	AJ747090	AJ747090	AJ747090
147	5	100.0	19	1	AJ747498	AJ747498	AJ747498
148	5	100.0	19	1	AJ747576	AJ747576	AJ747576
c 149	5	100.0	19	1	AJ747576	AJ747576	AJ747576
c 150	5	100.0	19	3	CNS09MAX	BX064981	Single re
c 151	5	100.0	19	4	BG925619	BG925619	HNC5-1-E5
c 152	5	100.0	19	4	BM394390	BM394390	50072-2-3
153	5	100.0	19	4	BM395127	BM395127	50072-2-7
154	5	100.0	19	4	BM395903	BM395903	5009-0-13
155	5	100.0	19	4	BM396129	BM396129	5009-0-17
156	5	100.0	19	5	BQ593604	BQ593604	E012766-0
157	5	100.0	19	6	CA794263	CA794263	Cac_BL_12
158	5	100.0	19	6	CA967213	CA967213	CcLL01a03
159	5	100.0	19	6	CF280692	CF280692	14ETL--07
160	5	100.0	19	6	CF282240	CF282240	14ETL--09
c 161	5	100.0	19	6	CF282240	CF282240	14ETL--09
162	5	100.0	19	6	CF282249	CF282249	14ETL--09
c 163	5	100.0	19	6	CF295184	CF295184	30DGS--05
c 164	5	100.0	19	6	CF303019	CF303019	ABF1--01-
165	5	100.0	19	6	CF306280	CF306280	HDA1--03-
c 166	5	100.0	19	6	CF306280	CF306280	HDA1--03-
c 167	5	100.0	19	6	CF306449	CF306449	HDA1--04-I
168	5	100.0	19	6	CF310063	CF310063	ABF--04-I
c 169	5	100.0	19	6	CF310063	CF310063	ABF--04-I
c 170	5	100.0	19	6	CF310821	CF310821	ABF--05-L

c 171	5	100.0	19	6	CF312583	CF312583	ABF--08-G
c 172	5	100.0	19	6	CF314442	CF314442	HD--02-P1
173	5	100.0	19	6	CF316012	CF316012	HD--05-C0
c 174	5	100.0	19	6	CF316012	CF316012	HD--05-C0
175	5	100.0	19	6	CF323353	CF323353	HDN--03-K
176	5	100.0	19	6	CF324209	CF324209	HDN--05-O
c 177	5	100.0	19	6	CF324209	CF324209	HDN--05-O
178	5	100.0	19	6	CF324303	CF324303	HDN--06-C
c 179	5	100.0	19	6	CF324303	CF324303	HDN--06-C
c 180	5	100.0	19	6	CF331492	CF331492	NACL--07-
c 181	5	100.0	19	6	CF332005	CF332005	NACL--08-
c 182	5	100.0	19	7	CF542982	CF542982	S014680w-
c 183	5	100.0	19	7	CF848480	CF848480	p8MA006xH
184	5	100.0	19	7	CO578459	CO578459	TVEST093E
c 185	5	100.0	19	8	AZ305212	AZ305212	1M0005115
186	5	100.0	19	8	AZ309972	AZ309972	1M0018D05
c 187	5	100.0	19	8	AZ309972	AZ309972	1M0018D05
188	5	100.0	19	8	AZ310299	AZ310299	1M0025O11
189	5	100.0	19	8	AZ313207	AZ313207	1M0029A13
190	5	100.0	19	8	AZ314181	AZ314181	1M0030B22
191	5	100.0	19	8	AZ314511	AZ314511	1M0031B20
192	5	100.0	19	8	AZ316997	AZ316997	1M0035O05
193	5	100.0	19	8	AZ324165	AZ324165	1M0046C06
194	5	100.0	19	8	AZ324865	AZ324865	1M0047G10
195	5	100.0	19	8	AZ326174	AZ326174	1M0048A07
c 196	5	100.0	19	8	AZ328696	AZ328696	1M0052O06
197	5	100.0	19	8	AZ328727	AZ328727	1M0052F10
198	5	100.0	19	8	AZ330766	AZ330766	1M0056N07
c 199	5	100.0	19	8	AZ331974	AZ331974	1M0060O05
200	5	100.0	19	8	AZ338927	AZ338927	1M0070N07
c 201	5	100.0	19	8	AZ340158	AZ340158	1M0072I16
202	5	100.0	19	8	AZ342171	AZ342171	1M0075P01
203	5	100.0	19	8	AZ345792	AZ345792	1M0080G12
204	5	100.0	19	8	AZ345861	AZ345861	1M0080H18
c 205	5	100.0	19	8	AZ345894	AZ345894	1M0080C24
206	5	100.0	19	8	AZ345903	AZ345903	1M0080E23
207	5	100.0	19	8	AZ369361	AZ369361	1M0119I23
208	5	100.0	19	8	AZ369369	AZ369369	1M0119K19
209	5	100.0	19	8	AZ381798	AZ381798	1M0138G01
210	5	100.0	19	8	AZ390115	AZ390115	1M0151L15
c 211	5	100.0	19	8	AZ408199	AZ408199	1M0179I15
212	5	100.0	19	8	AZ412494	AZ412494	1M0186A06
213	5	100.0	19	8	AZ422163	AZ422163	1M0200B22
c 214	5	100.0	19	8	AZ423757	AZ423757	1M0203D19
c 215	5	100.0	19	8	AZ427731	AZ427731	1M0209G19
c 216	5	100.0	19	8	AZ427750	AZ427750	1M0209N19
c 217	5	100.0	19	8	AZ430028	AZ430028	1M0214L16
218	5	100.0	19	8	AZ435252	AZ435252	1M0222D11
c 219	5	100.0	19	8	AZ439205	AZ439205	1M0229B15
c 220	5	100.0	19	8	AZ442378	AZ442378	1M0236K18
c 221	5	100.0	19	8	AZ444563	AZ444563	1M0241P18
222	5	100.0	19	8	AZ447197	AZ447197	1M0244A08
c 223	5	100.0	19	8	AZ447198	AZ447198	1M0244A10
c 224	5	100.0	19	8	AZ447234	AZ447234	1M0244L16
c 225	5	100.0	19	8	AZ447245	AZ447245	1M0244A22
c 226	5	100.0	19	8	AZ447248	AZ447248	1M0244H23
c 227	5	100.0	19	8	AZ447936	AZ447936	1M0245O18
c 228	5	100.0	19	8	AZ453412	AZ453412	1M0254I10
c 229	5	100.0	19	8	AZ465954	AZ465954	1M0276E16
c 230	5	100.0	19	8	AZ466785	AZ466785	1M0277A16
c 231	5	100.0	19	8	AZ468226	AZ468226	1M0281D10
c 232	5	100.0	19	8	AZ474038	AZ474038	1M0290G15
233	5	100.0	19	8	AZ476952	AZ476952	1M0296J10
234	5	100.0	19	8	AZ477353	AZ477353	1M0296K16
c 235	5	100.0	19	8	AZ480415	AZ480415	1M0301K24
236	5	100.0	19	8	AZ480905	AZ480905	1M0302N22
c 237	5	100.0	19	8	AZ481469	AZ481469	1M0303B15
238	5	100.0	19	8	AZ482050	AZ482050	1M0306H20
c 239	5	100.0	19	8	AZ489350	AZ489350	1M0321K14
c 240	5	100.0	19	8	AZ490174	AZ490174	1M0323B05
c 241	5	100.0	19	8	AZ493581	AZ493581	1M0328A24
242	5	100.0	19	8	AZ493833	AZ493833	1M0328P11
c 243	5	100.0	19	8	AZ499200	AZ499200	1M0336O22

C 244	5	100.0	19	8	AZ510143	1M0354P21	AZ510143	1M0354P21	C 317	5	100.0	19	8	AZ864599	2M0174G17
C 245	5	100.0	19	8	AZ579189	1M0363I12	AZ579189	1M0363I12	C 318	5	100.0	19	8	AZ941561	AZ941561 2M0201B19
246	5	100.0	19	8	AZ585820	1M0391I15	AZ585820	1M0391I15	C 319	5	100.0	19	8	AZ949057	2M0212A20
247	5	100.0	19	8	AZ587841	1M0395J14	AZ587841	1M0395J14	320	5	100.0	19	8	AZ949434	2M0212K23
C 248	5	100.0	19	8	AZ597219	1M0411K23	AZ597219	1M0411K23	321	5	100.0	19	8	AZ950028	2M0213L19
C 249	5	100.0	19	8	AZ611179	1M0436B01	AZ611179	1M0436B01	C 322	5	100.0	19	8	AZ962769	2M0231P08
C 250	5	100.0	19	8	AZ611509	1M0437E21	AZ611509	1M0437E21	C 323	5	100.0	19	8	AZ969354	2M0242A07
C 251	5	100.0	19	8	AZ615843	1M0445E23	AZ615843	1M0445E23	324	5	100.0	19	9	CL657666	PR1012a H
C 252	5	100.0	19	8	AZ618258	1M0449G23	AZ618258	1M0449G23	C 325	5	100.0	19	9	CL665369	PR10149C
C 253	5	100.0	19	8	AZ625211	1M0464P22	AZ625211	1M0464P22	326	5	100.0	19	9	CL693170	PR10160B
C 254	5	100.0	19	8	AZ625605	1M0465D17	AZ625605	1M0465D17	C 327	5	100.0	20	1	AJ683352	AJ683352
255	5	100.0	19	8	AZ626573	1M0466J24	AZ626573	1M0466J24	C 328	5	100.0	20	1	AL695159	AL695159
C 256	5	100.0	19	8	AZ634205	1M0489D09	AZ634205	1M0489D09	C 329	5	100.0	20	4	BM393606	50072-2-1
257	5	100.0	19	8	AZ634666	1M0490P13	AZ634666	1M0490P13	C 330	5	100.0	20	4	BM393608	50072-2-1
258	5	100.0	19	8	AZ644418	1M0508B20	AZ644418	1M0508B20	C 331	5	100.0	20	4	BM394340	50072-2-3
C 259	5	100.0	19	8	AZ646713	1M0512D20	AZ646713	1M0512D20	C 332	5	100.0	20	4	BM395053	50072-2-7
C 260	5	100.0	19	8	AZ648703	1M0517A20	AZ648703	1M0517A20	333	5	100.0	20	4	BM395330	50072-2-8
C 261	5	100.0	19	8	AZ649856	1M0520G13	AZ649856	1M0520G13	C 334	5	100.0	20	4	BM395527	50072-2-9
C 262	5	100.0	19	8	AZ651069	1M0521L06	AZ651069	1M0521L06	C 335	5	100.0	20	5	BQ590446	E012839-0
C 263	5	100.0	19	8	AZ654214	1M0528H13	AZ654214	1M0528H13	336	5	100.0	20	6	CF279207	14ETL--05
C 265	5	100.0	19	8	AZ654733	1M0529A09	AZ654733	1M0529A09	C 337	5	100.0	20	6	CF280828	14ETL--07
C 266	5	100.0	19	8	AZ654842	1M0529A20	AZ654842	1M0529A20	C 338	5	100.0	20	6	CF302797	7LEAF--08
C 267	5	100.0	19	8	AZ657564	1M0533P18	AZ657564	1M0533P18	C 339	5	100.0	20	6	CF307519	HDAL--06-
C 268	5	100.0	19	8	AZ760597	1M0554N21	AZ760597	1M0554N21	C 340	5	100.0	20	6	CF309954	ABF--04-F
269	5	100.0	19	8	AZ761834	1M0556E19	AZ761834	1M0556E19	341	5	100.0	20	6	CF310673	ABF--05-H
C 270	5	100.0	19	8	AZ764495	1M0560G06	AZ764495	1M0560G06	C 342	5	100.0	20	6	CF310673	ABF--05-H
C 271	5	100.0	19	8	AZ764500	1M0560K06	AZ764500	1M0560K06	C 343	5	100.0	20	6	CF311285	ABF--06-H
C 272	5	100.0	19	8	AZ764521	1M0560C17	AZ764521	1M0560C17	C 344	5	100.0	20	6	CF312611	ABF--08-H
273	5	100.0	19	8	AZ764526	1M0560J15	AZ764526	1M0560J15	345	5	100.0	20	6	CF316000	HD--05-C0
274	5	100.0	19	8	AZ768918	1M0569F08	AZ768918	1M0569F08	C 346	5	100.0	20	6	CF316000	HD--05-C0
C 275	5	100.0	19	8	AZ769239	1M0569K09	AZ769239	1M0569K09	C 347	5	100.0	20	6	CF317375	HD--07-A1
C 276	5	100.0	19	8	AZ769242	1M0569L12	AZ769242	1M0569L12	C 348	5	100.0	20	6	CF322590	HDN--01-I
277	5	100.0	19	8	AZ771304	1M0573D22	AZ771304	1M0573D22	C 349	5	100.0	20	6	CF326591	JMT1--06-
278	5	100.0	19	8	AZ775541	2M0008H17	AZ775541	2M0008H17	C 350	5	100.0	20	6	CF327699	NACL--02-
279	5	100.0	19	8	AZ777642	2M0012M20	AZ777642	2M0012M20	C 351	5	100.0	20	6	CF331733	NACL--07-
280	5	100.0	19	8	AZ780591	2M0018B09	AZ780591	2M0018B09	352	5	100.0	20	6	CF337475	JMT--07-O
281	5	100.0	19	8	AZ781461	2M0019E20	AZ781461	2M0019E20	C 353	5	100.0	20	6	CF338875	RCL1--03-
C 282	5	100.0	19	8	AZ783420	2M0025D07	AZ783420	2M0025D07	C 354	5	100.0	20	7	CF932153	SPI-A4 (P6
283	5	100.0	19	8	AZ786308	2M0031B17	AZ786308	2M0031B17	C 355	5	100.0	20	7	CF932153	SPI-A4 (P6
C 284	5	100.0	19	8	AZ786434	2M0031M24	AZ786434	2M0031M24	C 356	5	100.0	20	7	D19156	MUSGS01378
285	5	100.0	19	8	AZ787717	2M0034A21	AZ787717	2M0034A21	C 357	5	100.0	20	7	D20001	HUMGS00971
286	5	100.0	19	8	AZ794440	2M0048A15	AZ794440	2M0048A15	358	5	100.0	20	8	AZ307491	1M0009C13
C 287	5	100.0	19	8	AZ795057	2M0049B08	AZ795057	2M0049B08	C 359	5	100.0	20	8	AZ308179	1M0010K19
288	5	100.0	19	8	AZ796963	2M0052K24	AZ796963	2M0052K24	359	5	100.0	20	8	AZ308410	1M0011A24
C 289	5	100.0	19	8	AZ798934	2M0056F01	AZ798934	2M0056F01	C 360	5	100.0	20	8	AZ309156	1M0013B09
290	5	100.0	19	8	AZ799886	2M0057C12	AZ799886	2M0057C12	361	5	100.0	20	8	AZ310481	1M0025O23
291	5	100.0	19	8	AZ802234	2M0060M21	AZ802234	2M0060M21	C 362	5	100.0	20	8	AZ310481	1M0025O23
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293	5	100.0	19	8	AZ808220	2M0071E06	AZ808220	2M0071E06	364	5	100.0	20	8	AZ314450	1M0031G14
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295	5	100.0	19	8	AZ809734	2M0073D19	AZ809734	2M0073D19	366	5	100.0	20	8	AZ317019	1M0035P14
C 296	5	100.0	19	8	AZ810082	2M0074K21	AZ810082	2M0074K21	367	5	100.0	20	8	AZ321845	1M0042A07
297	5	100.0	19	8	AZ813861	2M0081A01	AZ813861	2M0081A01	368	5	100.0	20	8	AZ328703	1M0052A07
298	5	100.0	19	8	AZ819339	2M0089I19	AZ819339	2M0089I19	C 369	5	100.0	20	8	AZ335199	1M0064K22
299	5	100.0	19	8	AZ819494	2M0091I10	AZ819494	2M0091I10	C 370	5	100.0	20	8	AZ339988	1M0071A13
C 300	5	100.0	19	8	AZ819620	2M0091A23	AZ819620	2M0091A23	371	5	100.0	20	8	AZ342269	1M0075F13
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302	5	100.0	19	8	AZ828849	2M0106C11	AZ828849	2M0106C11	C 373	5	100.0	20	8	AZ345548	1M0080D13
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304	5	100.0	19	8	AZ830469	2M0109C14	AZ830469	2M0109C14	375	5	100.0	20	8	AZ348201	1M0084F13
305	5	100.0	19	8	AZ833844	2M0116O07	AZ833844	2M0116O07	C 376	5	100.0	20	8	AZ358156	1M0100M22
306	5	100.0	19	8	AZ840418	2M0136P21	AZ840418	2M0136P21	C 377	5	100.0	20	8	AZ360709	1M0104N05
C 307	5	100.0	19	8	AZ842379	2M0140N17	AZ842379	2M0140N17	378	5	100.0	20	8	AZ388212	1M0148A10
C 308	5	100.0	19	8	AZ843215	2M0142B06	AZ843215	2M0142B06	379	5	100.0	20	8	AZ391065	1M0152H20
C 309	5	100.0	19	8	AZ845178	2M0144P16	AZ845178	2M0144P16	380	5	100.0	20	8	AZ395013	1M0158M18
C 310	5	100.0	19	8	AZ849133	2M0150L21	AZ849133	2M0150L21	381	5	100.0	20	8	AZ396417	1M0160P20
311	5	100.0	19	8	AZ853395	2M0156M04	AZ853395	2M0156M04	C 382	5	100.0	20	8	AZ403367	1M0171O11
C 312	5	100.0	19	8	AZ854647	2M0158P15	AZ854647	2M0158P15	C 383	5	100.0	20	8	AZ403941	1M0171H06
C 313	5	100.0	19	8	AZ856873	2M0161O19	AZ856873	2M0161O19	384	5	100.0	20	8	AZ405596	1M0174B06
C 314	5	100.0	19	8	AZ861541	2M0168F19	AZ861541	2M0168F19	C 385	5	100.0	20	8	AZ426899	1M0208A08
315	5	100.0	19	8	AZ861832	2M0168H21	AZ861832	2M0168H21	386	5	100.0	20	8	AZ430735	1M0215A22
316	5	100.0	19	8	AZ861876	2M0168F22	AZ861876	2M0168F22	387	5	100.0	20	8	AZ432681	1M0218N11
									388	5	100.0	20	8	AZ436223	1M0233B21
									C 389	5	100.0	20	8	AZ437804	1M0226F18

C 390	5	100.0	20	8	AZ441557	1M0233G21
C 391	5	100.0	20	8	AZ445158	1M0240H15
C 392	5	100.0	20	8	AZ447205	1M0244I07
C 393	5	100.0	20	8	AZ447706	1M0245C06
C 394	5	100.0	20	8	AZ448206	1M0245E15
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C 403	5	100.0	20	8	AZ470070	1M0283P24
C 404	5	100.0	20	8	AZ473415	1M0289K14
C 405	5	100.0	20	8	AZ475834	1M0294N10
C 406	5	100.0	20	8	AZ475852	1M0294A18
C 407	5	100.0	20	8	AZ478639	1M0298C20
C 408	5	100.0	20	8	AZ479732	1M0300A09
C 409	5	100.0	20	8	AZ486866	1M0315P24
C 410	5	100.0	20	8	AZ489864	1M0322I01
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C 455	5	100.0	20	8	AZ780925	2M0018A16
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C 457	5	100.0	20	8	AZ782243	2M0022B21
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C 473	5	100.0	20	8	AZ826426	2M0102H10
C 474	5	100.0	20	8	AZ829314	2M0106I22
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C 478	5	100.0	20	8	AZ848532	2M0149M01
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C 480	5	100.0	20	8	AZ852569	2M0155O20
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C 496	5	100.0	20	8	AZ957966	2M0225I01
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C 498	5	100.0	20	8	AZ969440	2M0242O12
C 499	5	100.0	20	8	AZ981429	2M0258B20
500	5	100.0	20	9	AG202644	Pan trogl

ALIGNMENTS

RESULT 1	BM393918/c	10 bp	mrna	linear	EST 17-JAN-2002
BM393918/c	50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)				
LOCUS	Tetrahymena thermophila cDNA, mRNA sequence.				
DEFINITION	BM393918				
ACCESSION	BM393918.1	GI:18193971			
VERSION	EST.				
KEYWORDS	Tetrahymena thermophila				
SOURCE	Tetrahymena thermophila				
ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.				
REFERENCE	1 (bases 1 to 10)				
AUTHORS	Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.				
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu				
Seq primer:	T3.				
FEATURES	Location/Qualifiers				
source	1. .10				
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	/strain="CU428.1"				

/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 10 GGGGG 6

## RESULT 2

BM396043

LOCUS

DEFINITION BM396043 10 bp mRNA linear EST 17-JAN-2002  
Tetrahymena thermophila cDNA (large fraction)

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BM396043.1 GI:18196096  
EST.

Tetrahymena thermophila  
Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 10)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

## FEATURES

source

1..10  
/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 5 GGGGG 9

## RESULT 3

CL435808/c

LOCUS

DEFINITION CL435808 10 bp DNA linear GSS 18-MAR-2004  
PST1453-NR.seq MICB1 Mus musculus genomic clone PST1453-NR.seq  
similar to Racgap1, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CL435808.1 GI:45569874  
GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 10)  
AUTHORS Hicks, G.G.  
TITLE www.EScells.ca  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hicks GG

Mammalian Functional Genomics Centre  
Manitoba Institute of Cell Biology, University of Manitoba  
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada  
Tel: 204 787 2133  
Fax: 204 787 2190

Email: hicksgg@cc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional  
sequence information and target gene cloning can be generated. ES  
cell line harboring insertion mutation of target gene is available.  
Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST1453-NR.se

g

Class: Gene Trap.

Location/Qualifiers

source

1..10  
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/mol\_type="genomic DNA"

/strain="129 sv"

/db\_xref="taxon:10090"

/clone="PST1453-NR.seq"

/sex="Male"

/cell\_type="Embryonic stem cell"

/cell\_line="D3H (J1 subclone)"

/clone\_lib="MICB1"

/note="Vector: U3NeosV1"

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 8 GGGGG 4

## RESULT 4

CL436345

LOCUS

DEFINITION

CL436345 10 bp DNA linear GSS 18-MAR-2004  
PST2785-NR.Seq MICB1 Mus musculus genomic clone PST2785-NR.Seq  
similar to Sfrs1, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CL436345.1 GI:45571051  
GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 10)

Hicks, G.G.

www.EScells.ca

Unpublished (2002)

Contact: Hicks GG

Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicksgg@cc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional

sequence information and target gene cloning can be generated. ES

cell line harboring insertion mutation of target gene is available.

Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST2785-NR.Se

g

Class: Gene Trap.

Location/Qualifiers

source

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source
1. .10
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/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
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/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 5
CL438120/c
LOCUS
DEFINITION
CL438120
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hicks,G.G.
www.EScells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST6843-NL.Se
q
Class: Gene Trap.
Location/Qualifiers
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST6843-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

FEATURES
source
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST6843-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      10 GGGGG 6
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source
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST2785-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 7
AJ657108
LOCUS
DEFINITION
AJ657108
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
```

```
RESULT 6
CL439043
LOCUS
DEFINITION
PST8576-NR.Seq MICB1 Mus musculus genomic clone PST8576-NR.Seq,
genomic survey sequence.
CL439043
VERSION
CL439043.1 GI:45576187
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hicks,G.G.
1 (bases 1 to 10)
Hicks,G.G.
www.EScells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST8576-NR.Se
q
Class: Gene Trap.
Location/Qualifiers
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST8576-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

FEATURES
source
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST8576-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
```

```
RESULT 7
AJ657108
LOCUS
DEFINITION
AJ657108
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
```



Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled early embryos, from 8- cell stage to blastocysts.  
Clones available from UK Centre for Functional Genomics in Farm  
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
www.arkgenomics.org.

FEATURES

source  
1. .11  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005196.K06"  
/tissue\_type="embryo"  
/clone\_lib="KN277"  
/note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pooled early embryos, from 8-cell stage  
to blastocysts."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

RESULT 8

BM395228/c  
LOCUS 11 bp mRNA linear EST 17-JAN-2002  
DEFINITION 50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction).  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395228  
VERSION BM395228.1 GI:18195281  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES

source  
1. .11  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 9 GGGGG 5

RESULT 9  
CF543031  
LOCUS 11 bp mRNA linear EST 22-SEP-2003  
DEFINITION CF543031  
S015532-024-030-P02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-030-P02 5-PRIME, mRNA sequence.

ACCESSION CF543031  
VERSION CF543031.1 GI:34891471  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 11)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PubMed 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 11 Std Error: 0.00  
Plate: 30 row: P column: 02  
Seq primer: SP6.

FEATURES

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1. .11  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:936732"  
/db\_xref="taxon:161934"  
/clone="024-030-P02"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

RESULT 10

BQ585390/c  
LOCUS 12 bp mRNA linear EST 06-DEC-2002  
BQ585390

DEFINITION S011420-024-001-G08-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris  
CDNA clone 024-001-G08 5-PRIME, mRNA sequence.

ACCESSION BQ585390  
VERSION BQ585390.1 GI:26114972  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 12)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissha@mpiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 1 row: G column: 08  
Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.

FEATURES  
source  
1. .12  
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/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:181317"  
/db\_xref="taxon:161934"  
/clone="024-001-G08"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 12 GGGGG 8

RESULT 11  
CA851641/c  
LOCUS D15H12 024\_16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
DEFINITION cDNA clone D15H12 5', mRNA sequence.  
CA851641  
ACCESSION CA851641.1 GI:33388434  
VERSION CA851641  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@ba.ars.usda.gov.

FEATURES  
source  
1. .12  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
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/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA  
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
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Db 11 GGGGG 7

RESULT 12  
CA851649/c  
LOCUS D16A08 B20\_02.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
DEFINITION cDNA clone D16A08 5', mRNA sequence.  
CA851649  
ACCESSION CA851649.1 GI:33388442  
VERSION CA851649  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@ba.ars.usda.gov.

FEATURES  
source  
1. .12  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="D16A08"  
/tissue\_type="Roots"

/dev\_stage="Seedlings"  
/clone\_lib="CDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA  
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|  
|  
|  
|  
Db 12 GGGGG 8

RESULT 13

AQ074231  
LOCUS 17 pUC8 PstI Rice Etiolated Leaf Genomic Library Oryza sativa  
DEFINITION (indica cultivar-group) genomic clone RG143, genomic survey  
sequence.  
ACCESSION AQ074231  
VERSION AQ074231.1 GI:3435350  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 12)  
McCouch, S.R., Kochert, G., Yu, Z.H., Wang, Z.Y., Khush, G.S.,  
Coffman, W.R., and Tanksley, S.D.  
Molecular mapping of rice chromosomes  
Theor. Appl. Genet. 76, 815-829 (1988)  
Contact: Susan R. McCouch  
Cornell University  
Dept. Plant Breeding, Ithaca, NY 14853-1901, USA  
Tel: 607 255 0420  
Fax: 607 255 6683  
Email: srm4@cornell.edu

TITLE

JOURNAL

COMMENT

For mapping information, additional citations and other related  
information concerning this probe, please refer to the RiceGenes  
database at  
http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes&  
class=Marker&object=RG143 DNA Sequencing was done by the DOE Plant  
Research Lab, Michigan State University. Informatics was done at  
the Computational Biology Centers, University of Minnesota.  
PCR Primers  
FORWARD: M13 Forward  
BACKWARD: M13 Reverse  
Insert length: 1 Std Error: 0.00  
Seq primer: M13 -21 dtd primer  
Class: RFLP probe.  
Location/Qualifiers  
1..12  
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/mol\_type="genomic DNA"  
/cultivar="IR36"  
/db\_xref="RiceGenes:RG143"  
/db\_xref="taxon:39946"  
/clone="RG143"  
/clone\_lib="pUC8 PstI Rice Etiolated Leaf Genomic Library"  
/note="Vector: pUC8; Total leaf DNA was digested with the  
restriction enzyme PstI. DHS-alpha bacterial cells were  
then transformed with ligated plasmid. Random genomic  
clones were given consecutive numbers (RG-#) as they were  
prepared. The same numbers were then used to designate  
loci in the genome as detected by genetic mapping."

FEATURES

Source

Query Match 100.0%; Score 5; DB 8; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 GGGGG 5  
|  
|  
|  
|  
Db 12 GGGGG 8

QY

1 GGGGG 5  
|  
|  
|  
|  
Db 7 GGGGG 11

RESULT 14

AJ600541  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
DEFINITION 508E06, genomic survey sequence.  
ACCESSION AJ600541  
VERSION AJ600541.1 GI:37950169  
KEYWORDS GSS; right border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 12)  
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
22363535  
12446565  
REFERENCE 2 (bases 1 to 12)  
Balzergue, S.  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.inbioigen.fr).

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Location/Qualifiers  
1..12  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="508E06"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1..12  
/note="T-DNA flanking sequence  
right border"

FEATURES

Source

Query Match 100.0%; Score 5; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 GGGGG 5  
|  
|  
|  
|  
Db 5 GGGGG 9

RESULT 15

AJ600549  
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone  
DEFINITION 508F08, genomic survey sequence.  
ACCESSION AJ600549  
VERSION AJ600549.1 GI:37950177

KEYWORDS GSS; right border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 12)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source Location/Qualifiers  
1. .12  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="508F08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1. .12  
/note="T-DNA flanking sequence  
right border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 5 GGGGG 9

RESULT 16  
BG810452/c  
LOCUS BG810452 13 bp mRNA linear EST 22-MAY-2001  
DEFINITION mgct006xc07f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea cDNA clone mgct006xc07f 5', mRNA sequence.  
ACCESSION BG810452  
VERSION BG810452.1 GI:14181432  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Choi,W. and Dean,R.A.  
TITLE Construction and sequence analysis of an appressorium stage cDNA library in the rice blast fungus, Magnaporthe grisea  
JOURNAL Unpublished (2001)  
COMMENT Contact: Ralph A. Dean  
Fungal Genomics Laboratory  
North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: [ralph.dean@ncsu.edu](mailto:ralph.dean@ncsu.edu)  
Seq primer: T3 primer (AATTAACCTCACTAAAGG).

FEATURES  
source Location/Qualifiers  
1. .13  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone="mgct006xc07f"  
/dev\_stage="Germinated conidia on appressorium-inductive surface"  
/clone\_lib="Magnaporthe grisea Appressorium Stage cDNA"  
/note="Vector: pBluescript SK(+) Vector; Site\_1: EcoRI; Site\_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."

ORIGIN  
Query Match 100.0%; Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 11 GGGGG 7

RESULT 17  
BG926067/c  
LOCUS BG926067 13 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC23-1-B8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG926067  
VERSION BG926067.1 GI:14320590  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PUBMED 11597177  
COMMENT Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: [sanjay.kumar-l@gsk.com](mailto:sanjay.kumar-l@gsk.com)  
Seq primer: T7.

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

ORIGIN

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Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 3

RESULT 18
BM394028/c
LOCUS
DEFINITION      13 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION      BM394028
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 3

RESULT 19
BM395265/c
LOCUS
DEFINITION      13 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION      BM395265
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      11 GGGGG 7

RESULT 20
BM395395/c
LOCUS
DEFINITION      13 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      12 GGGGG 8

RESULT 21
BM395395/c
LOCUS
DEFINITION      13 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9
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FEATURES
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Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      12 GGGGG 8

RESULT 20
BM395395/c
LOCUS
DEFINITION      13 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA (large fraction)
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT      Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9
```

```
FEATURES
source
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9
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RESULT 21  
BQ595080  
LOCUS  
DEFINITION  
BQ595080 13 bp mRNA linear EST 06-DEC-2002  
E012709-024-023-M14-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-023-M14 5-PRIME, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
Plate: 23 row: M column: 14  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:191776"  
/db\_xref="taxon:161934"  
/clone="024-023-M14"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 100.0%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
|  
|  
|  
|  
Db 1 GGGGG 5

RESULT 22  
AJ587920  
LOCUS  
DEFINITION  
AJ587920 13 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
340A06, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.

SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
22363535  
12446565  
2 (bases 1 to 13)  
Balzergue, S.  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment(s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).  
Location/Qualifiers  
1. .13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="340A06"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature  
1. .13  
/note="T-DNA flanking sequence  
left border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
|  
|  
|  
|  
Db 4 GGGGG 8

RESULT 23  
BM392794  
LOCUS  
DEFINITION  
BM392794 14 bp mRNA linear EST 17-JAN-2002  
50071-2-12-H08.f.1 Chilcoat/Turkewitz cDNA (small fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 14)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA







/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
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Db 14 GGGGG 10

RESULT 27  
BQ585808 14 bp mRNA linear EST 06-DEC-2002  
LOCUS S01470-024-014-A01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
DEFINITION 024-014-A01 5-PRIME, mRNA sequence.  
ACCESSION BQ585808  
VERSION BQ585808.1 GI:26115390  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 14 row: A column: 01  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1..14  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:187232"  
/db\_xref="taxon:161934"  
/clone="024-014-A01"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

RESULT 29

Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 5 GGGGG 9

RESULT 28  
BQ593114 14 bp mRNA linear EST 06-DEC-2002  
LOCUS E012797-024-027-N23-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
DEFINITION cDNA clone 024-027-N23 5-PRIME, mRNA sequence.  
ACCESSION BQ593114  
VERSION BQ593114.1 GI:26122697  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 27 row: N column: 23  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1..14  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:193738"  
/db\_xref="taxon:161934"  
/clone="024-027-N23"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

BX679320/c  
LOCUS BX679320 14 bp mRNA linear EST 28-OCT-2003  
DEFINITION BX679320 RS Pinus pinaster cDNA clone RS22H11, mRNA sequence.  
ACCESSION BX679320  
VERSION BX679320.1 GI:38013250  
KEYWORDS EST.  
SOURCE Pinus pinaster  
ORGANISM Pinus pinaster  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 14)  
REFERENCE Frigerio, J. and Plomion, C.  
AUTHORS Identification of water-deficit responsive genes in Maritime pine  
TITLE (Pinus pinaster Ait.) using an EST approach  
JOURNAL Unpublished (2002)  
COMMENT Contact: Frigerio JM  
Genetique et Amelioration 69  
INRA  
route d'Arcachon 33612 Cestas CEDEX France  
Email: Frigerio@pierrotton.inra.fr  
Email: Frigerio@pierrotton.inra.fr  
Seq primer: T3.

FEATURES  
source  
1. .14  
/organism="Pinus pinaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:71647"  
/clone="RS22H11"  
/tissue\_type="root"  
/dev\_stage="6 weeks old seedling"  
/lab\_host="SOLR"  
/clone\_lib="RS"  
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 14 GGGGG 10

RESULT 30  
CA850835  
LOCUS CA850835 14 bp mRNA linear EST 01-AUG-2003  
DEFINITION D07A10 A22\_01.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D07A10 5', mRNA sequence.  
ACCESSION CA850835  
VERSION CA850835.1 GI:33387628  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 14)  
REFERENCE Alkharouf, N.W., Khan, R. and Matthews, B.F.  
AUTHORS Analysis of expressed sequence tags from roots of resistant soybean  
TITLE infected by the soybean cyst nematode  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharouf@ba.ars.usda.gov.  
FEATURES  
source  
1. .14  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:3847"  
/clone="D07A10"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 8 GGGGG 12

RESULT 31  
CK258733  
LOCUS CK258733 14 bp mRNA linear EST 30-JUL-2004  
DEFINITION EST742370 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCDF73 5' end, mRNA sequence.  
ACCESSION CK258733  
VERSION CK258733.1 GI:39815713  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 14)  
REFERENCE Buell, C.R., Hart, A., Ziemann, V., Karamycheva, S.A. and Baker, B.  
AUTHORS Generation of ESTs from potato callus tissue  
TITLE Unpublished (2003)  
JOURNAL Contact: Robin Buell  
COMMENT The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/.

FEATURES  
source  
1. .14  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="POCDF73"  
/tissue\_type="callus"  
/lab\_host="DH10B-Tona"  
/clone\_lib="potato callus cDNA library, normalized and full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN  
Query Match 100.0%; Score 5; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LCM5 row: A column: 4  
High quality sequence stop: 6.

FEATURES

source

1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820747"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 5; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 11 GGGGG 15

RESULT 35

BM395188

LOCUS

DEFINITION 50072-2-7-H12.f.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395188

VERSION BM395188.1

KEYWORDS GI:18195241

SOURCE EST.

ORGANISM

Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES

source

1. .15  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 1 GGGGG 5

RESULT 36

BM395189/c

LOCUS

DEFINITION 50072-2-7-H12.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395189

VERSION BM395189.1

KEYWORDS GI:18195242

SOURCE EST.

ORGANISM

Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 15)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES

source

1. .15  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 12 GGGGG 8

RESULT 37

BQ588758

LOCUS

DEFINITION E012534-024-014-P24-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-014-P24 5-PRIME, mRNA sequence.

ACCESSION BQ588758

VERSION BQ588758.1

KEYWORDS GI:26118341

SOURCE EST.

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

22362189

MEDLINE

PUBMED

COMMENT

12472698

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 14 row: P column: 24

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1. .15

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187217"

/db\_xref="taxon:161934"

/clone="024-014-P24"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES

source

Query Match

Best Local Similarity

100.0%;

Score 5;

DB 5;

Length 15;

Matches

5;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGG

5

Db

5

GGGGG

9

ORIGIN

Query Match

Best Local Similarity

100.0%;

Score 5;

DB 5;

Length 15;

Matches

5;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGG

5

Db

5

GGGGG

9

RESULT 38

BQ590018

LOCUS

DEFINITION

BQ590018

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

15 bp

mRNA

linear

EST 06-DEC-2002

012843-024-019-G23-T7 MPIZ-ADIS-024-storage root Beta vulgaris

cDNA clone 024-019-G23 3-PRIME, mRNA sequence.

1 (bases 1 to 15)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

22362189

MEDLINE

PUBMED

COMMENT

12472698

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Location/Qualifiers

1. .15

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187217"

/db\_xref="taxon:161934"

/clone="024-014-P24"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES

source

Query Match

Best Local Similarity

100.0%;

Score 5;

DB 5;

Length 15;

Matches

5;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGG

5

Db

5

GGGGG

9

ORIGIN

Query Match

Best Local Similarity

100.0%;

Score 5;

DB 5;

Length 15;

Matches

5;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGG

5

Db

5

GGGGG

9

RESULT 39

CA794555

LOCUS

DEFINITION

CA794555

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

15 bp

mRNA

linear

EST 05-DEC-2002

1497 Cac BL (Bean and Leaf from Amelonardo type Cacao)

Theobroma cacao cDNA clone Cac\_BL\_1497 5', mRNA sequence.

1 (bases 1 to 15)

Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D., Retzel,E.R. and Jones,C.A.

Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties

Planta 216 (2), 255-264 (2002)

22337596

Contact: Jones, Paul

Masterfoods

3d Dundee Road, Slough, Berkshire, UK, SL1 4LG

Tel: +44 1664 416644

Email: Paul.Jones@eu.affem.com

22362189

MEDLINE

PUBMED

COMMENT

12472698

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Location/Qualifiers

1. .15

/organism="Beta vulgaris"

/mol\_type="mRNA"

/strain="Amelonado type"

/db\_xref="taxon:3641"

/clone="Cac\_BL\_1497"

/tissue\_type="Mature leaf and mature bean"

/cell\_type="Whole organ"

/dev\_stage="maturity"

FEATURES

source

Plate: 19

row: G

column: 23

Seq primer: T7; GTAATACGACTCACTATAGGC.

FEATURES

source

Location/Qualifiers

1. .15

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:190101"

/db\_xref="taxon:161934"

/clone="024-019-G23"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match

Best Local Similarity

100.0%;

Score 5;

DB 5;

Length 15;

Matches

5;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

GGGGG

5

Db

1

GGGGG

5

RESULT 39

CA794555

LOCUS

DEFINITION

CA794555

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

15 bp

mRNA

linear

EST 05-DEC-2002

1497 Cac BL (Bean and Leaf from Amelonardo type Cacao)

Theobroma cacao cDNA clone Cac\_BL\_1497 5', mRNA sequence.

1 (bases 1 to 15)

Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D., Retzel,E.R. and Jones,C.A.

Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties

Planta 216 (2), 255-264 (2002)

22337596

Contact: Jones, Paul

Masterfoods

3d Dundee Road, Slough, Berkshire, UK, SL1 4LG

Tel: +44 1664 416644

Email: Paul.Jones@eu.affem.com

22362189

MEDLINE

PUBMED

COMMENT

12472698

```

/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      8 GGGGG 12

RESULT 40
CA850964
LOCUS
DEFINITION
CA850964 L21.11.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08F09 5', mRNA sequence.
ACCESSION
CA850964
VERSION
CA850964.1 GI:33387757
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.

FEATURES
      source
      1..15
      /organism="Glycine max"
      /mol_type="mRNA"
      /cultiivar="Peking"
      /db_xref="taxon:3847"
      /clone="D08F09"
      /tissue_type="Roots"
      /dev_stage="Seedlings"
      /clone_lib="cDNA Peking library 2, 4 day SCN3"
      /note="Vector: pBluescript SK-; cDNA clones from mRNA
      extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 41
CK283790
LOCUS
DEFINITION
CK283790 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAJ54 3',
end, mRNA sequence.
ACCESSION
CK283790

```

```

CK283790.1 GI:39856749
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 15)
AUTHORS
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
TITLE
Generation of EST sequences from Nicotiana benthamiana
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST746511
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
      Location/Qualifiers
      1..15
      /organism="Nicotiana benthamiana"
      /mol_type="mRNA"
      /db_xref="taxon:4100"
      /clone="NEMAJ54"
      /tissue_type="abiotic and biotic stress-treated leaves,
      callus tissue and root tissue"
      /lab_host="DH10B-Tona"
      /clone_lib="Nicotiana benthamiana mixed tissue cDNA
      library, normalized, full-length"
      /note="Vector: pCMVSPORT6.1; Site.1: EcoRI; Site.2: NotI;
      supplier: RNA was isolated from Nicotiana benthamiana
      tissues that include callus, roots from liquid culture
      grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
      cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
      challenged leaves (Pseudomonas syringae pv tomato 12 hr;
      Xanthomonas campestris pv campestris 18 hr, 18hr;
      Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
      campestris pv vesicatoria 18hr). RNA was isolated from
      these tissues and pooled in approximately equal molar
      amounts."

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 11

RESULT 42
CK283790/c
LOCUS
DEFINITION
CK283790 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAJ54 3',
end, mRNA sequence.
ACCESSION
CK283790
VERSION
CK283790.1 GI:39856749
KEYWORDS
EST.
SOURCE
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 15)
AUTHORS
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
TITLE
Generation of EST sequences from Nicotiana benthamiana
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST746511

```



Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES  
source

1. .15  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NBMAJ54"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="DH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
Db 6 GGGGG 2

RESULT 43

AA937364

LOCUS

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AA937364

AUTHORS

NCI-CGAP

TITLE

DEFINITION  
AA937364 16 bp mRNA linear EST 19-MAY-1998  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2  
MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AA937364

VERSION

AA937364.1 GI:3095475

KEYWORDS

EST.

SOURCE



```

Db          |||||
           6 GGGG 2

RESULT 45
AA968729
LOCUS      16 bp      mRNA      linear      EST 27-AUG-1998
DEFINITION or69h11.81 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3',
            similar to SW:PRPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
            ;contains element MSRI repetitive element ;, mRNA sequence.
ACCESSION  AA968729
VERSION     AA968729.1 GI:3143909
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
FEATURES   source
            1..16
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1601157"
            /sex="female, pooled"
            /tissue_type="pooled germ cell tumors"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP GC3"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
            polylinker; 1st strand cDNA was prepared from 3 pooled
            germ cell tumors, and was then primed with a Not I -
            oligo(dT) primer. Double-stranded cDNA was ligated to Eco
            RI adaptors (Pharmacia), digested with Not I and cloned
            into the Not I and Eco RI sites of the modified pT7T3
            vector. Library is not normalized. Library was
            constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 2 GGGGG 6

RESULT 46
AI075064/c
LOCUS      16 bp      mRNA      linear      EST 27-AUG-1998
DEFINITION ou61g11.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632356 3',
            similar to TR:Q24348 Q24348 FIBRILLARIN ;, mRNA sequence.
ACCESSION  AI075064
VERSION     AI075064.1 GI:3399844
KEYWORDS   EST.

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 712 Std Error: 0.00
            Seq primer: -40ml3 fwd. ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
            1..16
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1632356"
            /sex="female, pooled"
            /tissue_type="breast"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Br2"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
            polylinker; 1st strand cDNA was prepared from pooled bulk
            breast tumor tissue, and was then primed with a Not I -
            oligo(dT) primer. Double-stranded cDNA was ligated to Eco
            RI adaptors (Pharmacia), digested with Not I and cloned
            into the Not I and Eco RI sites of the modified pT7T3
            vector. This library is the normalized version of
            NCI CGAP Br1.1. Library was constructed by Bento Soares
            and M. Fatima Bonaldo. "
ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 10 GGGGG 6

RESULT 47
AI094839/c
LOCUS      16 bp      mRNA      linear      EST 18-AUG-1998
DEFINITION ga22c08.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:1687502 3',
            similar to TR:O00599 O00599 CON1.;contains element MSRI repetitive
            element ;, mRNA sequence.
ACCESSION  AI094839
VERSION     AI094839.1 GI:3433815
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
JOURNAL   Unpublished (1998)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

```

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1687502"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Brn23"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 6 GGGGG 2

RESULT 48

AI209036

LOCUS

DEFINITION

qg18g10.x1 Soares\_placenta\_8to9weeks\_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759938 3', similar to TR:Q64371 Q64371 PR-VBETA1. ;contains element MER22 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 16)  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers  
1. .16  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1759938"

/dev stage="two placentae: one from 8 weeks and another from 9 weeks post conception"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_placenta\_8to9weeks\_2NbHP8to9W"  
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 5 GGGGG 9

RESULT 49

AI262040

LOCUS

DEFINITION

AI262040 16 bp mRNA linear EST 28-JAN-1999  
qk24h08.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1869951 3', similar to SW:CA11\_BOVIN P02453 COLLAGEN ALPHA 1(I) CHAIN ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1352 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES

source

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ORIGIN

M. Fatima Bonaldo. "

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 50

AI274782/c

LOCUS

DEFINITION

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similar to WP:F59E12.9 CE11534 ;contains element MSR1 repetitive  
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ACCESSION

AI274782

VERSION

AI274782.1 GI:3897056

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

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AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GGGGG  
Perfect score: 5  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 402 US-08-871-678C-9 Sequence 9, Appli  
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C 407 US-09-242-632A-10 Sequence 10, Appl  
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C 434 US-09-401-063-1766 Sequence 1766, Ap  
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C 450 US-09-269-576G-17 Sequence 17, Appl  
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455 US-10-059-877-18 Sequence 18, Appl  
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457 PCT-US95-12880-2 Sequence 2, Appli  
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C 459 US-09-716-319-7 Sequence 7, Appli  
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C 466 US-08-455-627-15 Sequence 15, Appl  
467 US-08-260-202A-12 Sequence 12, Appl  
468 US-08-452-196A-8 Sequence 8, Appli  
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C 470 US-08-182-968A-3 Sequence 3, Appli  
471 US-08-182-968A-53 Sequence 53, Appl  
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C 475 US-08-182-968A-162 Sequence 162, App  
C 476 US-08-182-968A-163 Sequence 163, App  
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C 478 US-08-182-968A-193 Sequence 193, App  
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C 481 US-08-182-968A-218 Sequence 218, App  
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C 489 US-08-182-968A-363 Sequence 363, App  
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C 493 US-08-182-968A-438 Sequence 438, App  
C 494 US-08-182-968A-449 Sequence 449, App  
C 495 US-08-182-968A-454 Sequence 454, App  
C 496 US-07-971-978-19 Sequence 19, Appl  
497 US-08-319-492B-53 Sequence 53, Appl  
498 US-08-319-492B-398 Sequence 398, App  
C 499 US-08-319-492B-436 Sequence 436, App  
C 500 US-08-319-492B-437 Sequence 437, App

ALIGNMENTS

RESULT 1  
US-08-151-574-51  
; Sequence 51, Application US/08151574  
; Patent No. 5436156  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Selten  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phytase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025-3471  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,574  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/688,578



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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-08-229-515A-17
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; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
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; QY 1 GGGGG 5
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; RESULT 5
; US-08-229-515A-18
; Sequence 18, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
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; INFORMATION FOR SEQ ID NO: 18:
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; LENGTH: 10 base pairs
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; US-08-128-011-3
; Sequence 3, Application US/08128011
; Patent No. 5523389
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Imbach, Jean Louis
; TITLE OF INVENTION: Inhibitors of Human Immunodeficiency
; TITLE OF INVENTION: Virus
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5523389ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/128,011
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaumont, Rebecca R.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; RESULT 7
; US-08-335-565A-6
; Sequence 6, Application US/08335565A
; Patent No. 5527671
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;/ GENERAL INFORMATION:  
;/ APPLICANT: Li, Kening  
;/ APPLICANT: Rouse, Douglas I.  
;/ APPLICANT: Gertman, Thomas L.  
;/ TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE  
;/ NUMBER OF SEQUENCES: 33  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Quarles and Brady  
;/ STREET: 1 South Pinckney St., PO BOX 2113  
;/ CITY: Madison  
;/ STATE: WI  
;/ COUNTRY: USA  
;/ ZIP: 53701-2113  
;/ COMPUTER READABLE FORM:  
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;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/335,565A  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Seay, Nicholas J  
;/ REGISTRATION NUMBER: 27,386  
;/ REFERENCE/DOCKET NUMBER: 960296,93065  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 608-251-5000  
;/ TELEFAX: 608-251-9166  
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;/ Sequence 12, Application US/08235503B  
;/ Patent No. 5563036  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Peterson, Michael G  
;/ APPLICANT: Baichwal, Vijay R  
;/ APPLICANT: Strulovici, Berta  
;/ TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
;/ NUMBER OF SEQUENCES: 75  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
;/ STREET: 4 Embarcadero Center, Suite 3400  
;/ CITY: San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94111-4187  
;/ COMPUTER READABLE FORM:  
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;/ COMPUTER: IBM PC compatible  
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;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/235,503B  
;/ FILING DATE: 29-APR-1994  
;/ CLASSIFICATION: 435

;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Osman, Richard A  
;/ REGISTRATION NUMBER: 36,627  
;/ REFERENCE/DOCKET NUMBER: A-59332/RAO  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 781-1989  
;/ TELEFAX: (415) 398-3249  
;/ TELEX: 910 277299  
;/ INFORMATION FOR SEQ ID NO: 12:  
;/ SEQUENCE CHARACTERISTICS:  
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;/ TYPE: nucleic acid  
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;/ TOPOLOGY: linear  
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;/ US-08-235-503B-12

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Db 8 GGGGG 4

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;/ Sequence 18, Application US/07860445  
;/ Patent No. 5573905  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Lerner, Richard  
;/ APPLICANT: Janda, Kim  
;/ APPLICANT: Brenner, Sydney  
;/ TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES  
;/ NUMBER OF SEQUENCES: 22  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: The Scripps Research Institute, Office of  
;/ ADDRESSEE: Patent Counsel  
;/ STREET: 10666 No. 5573905th Torrey Pines Road, TPC 8  
;/ CITY: La Jolla  
;/ STATE: CA  
;/ COUNTRY: USA  
;/ ZIP: 92037  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/07/860,445  
;/ FILING DATE: 19920330  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Fitting, Thomas  
;/ REGISTRATION NUMBER: 34,163  
;/ REFERENCE/DOCKET NUMBER: TSR5023P  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 619-554-2937  
;/ TELEFAX: 619-554-6312  
;/ INFORMATION FOR SEQ ID NO: 18:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: NUCLEIC ACID  
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;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
;/ HYPOTHETICAL: NO  
;/ ANTI-SENSE: NO  
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; OTHER INFORMATION: indicated position"
US-07-860-445-18

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      4 GGGGG 8

RESULT 10
US-08-233-608-45/c
; Sequence 45, Application US/082333608
; Patent No. 5585238
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-19
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-233-608-45

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      6 GGGGG 2

RESULT 11
US-08-307-713-18
; Sequence 18, Application US/08307713
; Patent No. 5604122
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO DNA CLONING

;
; TITLE OF INVENTION: TECHNIQUES AND PRODUCTS FOR USE THEREWITH
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: 180 No. 5604122th Stetson, Two Prudential Plaza,
; STREET: Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,713
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00584
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206210.8
; FILING DATE: 21-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 62920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: YES
; HYPOTHETICAL: YES
US-08-307-713-18

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      1 GGGGG 5

RESULT 12
US-08-197-463-4/c
; Sequence 4, Application US/08197463
; Patent No. 5627047
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael
; APPLICANT: Besnard, Francois
; APPLICANT: Nakatani, Yoshihiro
; TITLE OF INVENTION: Astrocyte-Specific Transcription
; TITLE OF INVENTION: of Human Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Koslasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/769,626  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-362P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: protein\_bind  
LOCATION: 1..10  
OTHER INFORMATION: /function= "transcription enhancer"  
OTHER INFORMATION: /bound\_moiety= "AP-2"  
OTHER INFORMATION: /standard\_name= "AP-2 site"  
US-08-197-463-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 10 GGGGG 6

## RESULT 13

US-08-202-927-16  
Sequence 16, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pal, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675

REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
OTHER INFORMATION: formula 3)."  
US-08-202-927-16

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 6 GGGGG 10

## RESULT 14

US-08-335-354A-3/c  
Sequence 3, Application US/08335354A  
Patent No. 5652358  
GENERAL INFORMATION:  
APPLICANT: Pfeleiderer, Wolfgang  
APPLICANT: Schnell, Ralf  
APPLICANT: Matysiak, Stephan  
TITLE OF INVENTION: Solid-Phase Synthesis Of  
TITLE OF INVENTION: Oligoribonucleotides.  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,354A  
FILING DATE: 03-NOV-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GR P 43 43 126.7  
FILING DATE: 17-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Horton, Ken  
REGISTRATION NUMBER: 39,481  
REFERENCE/DOCKET NUMBER: 02481.1413-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-335-354A-3

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 15
US-08-335-354A-4
; Sequence 4, Application US/08335354A
; Patent No. 5652358
; GENERAL INFORMATION:
; APPLICANT: Pfeleiderer, Wolfgang
; APPLICANT: Schnell, Ralf
; APPLICANT: Matysiak, Stephan
; TITLE OF INVENTION: Solid-Phase Synthesis Of
; TITLE OF INVENTION: Oligoribonucleotides.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,354A
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GR P 43 43 126.7
; FILING DATE: 17-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Horton, Ken
; REGISTRATION NUMBER: 39,481
; REFERENCE/DOCKET NUMBER: 02481.1413-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-335-354A-4

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      1 GGGGG 5

RESULT 16
US-08-645-865-17
; Sequence 17, Application US/08645865
```

```
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-17

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      4 GGGGG 8

RESULT 17
US-08-645-865-18
; Sequence 18, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
```





```
RESULT 20
US-08-467-126-2
; Sequence 2, Application US/08467126
; Patent No. 5776744
; GENERAL INFORMATION:
; APPLICANT: GLAZER, PETER M.
; APPLICANT: GEORGE, JAY
; APPLICANT: LIN, L. MICHAEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: EFFECTING HOMOLOGOUS RECOMBINATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORPHARM, INC.
; STREET: 200 PERRY PARKWAY
; CITY: GAITHERSBURG
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE-3.50 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: APPLE MACINTOSH POWERBOOK 520
; OPERATING SYSTEM: MACINTOSH
; SOFTWARE: WORD PERFECT 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,126
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KARTA, GLENN E.
; REGISTRATION NUMBER: 30,649
; REFERENCE/DOCKET NUMBER: PA-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2058
; TELEFAX: 301-208-6997
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-126-2

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 10

RESULT 21
US-08-887-480-45/c
; Sequence 45, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 581453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-19
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-887-480-45

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 2

RESULT 22
US-08-410-779B-24/c
; Sequence 24, Application US/08410779B
; Patent No. 5814517
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, H. MARTI
; APPLICANT: LAMB, I. PETER
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED
; STREET: 9393 TOWNE CENTRE DRIVE
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,779B
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,935
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JURGENSEN, THOMAS E
; REGISTRATION NUMBER: 34,195
; REFERENCE/DOCKET NUMBER: 016-0013A.US
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
DESCRIPTION: SYNTHETIC DNA"  
US-08-410-779B-24

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 7 GGGGG 3

RESULT 23

US-08-465-590-35  
Sequence 35, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/238,212  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,438  
FILING DATE: 14-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MPG-006C2DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-465-590-35

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 3 GGGGG 7

RESULT 24

US-08-441-887A-40  
Sequence 40, Application US/08441887A  
Patent No. 5837832  
GENERAL INFORMATION:  
APPLICANT: Chee, Mark  
APPLICANT: Cronin, Maureen T.  
APPLICANT: Fodor, Stephen P.A.  
APPLICANT: Huang, Xiaohua X.  
APPLICANT: Hubbell, Earl A.  
APPLICANT: Lipshutz, Robert J.  
APPLICANT: Lobban, Peter E.  
APPLICANT: Morris, Macdonald S.  
APPLICANT: Sheldon, Edward L.  
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
TITLE OF INVENTION: Biological Chips  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,887A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,312  
FILING DATE: 26-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,937  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joseph O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-004160US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-326-2400  
TELEFAX: 650-326-2422  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
US-08-441-887A-40

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5

Db 4 GGGGG 8

RESULT 25

US-08-441-887A-64

; Sequence 64, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
; US-08-441-887A-64

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
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|  
|  
|  
|  
Db 3 GGGGG 7

RESULT 26  
US-08-441-887A-96  
; Sequence 96, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.

; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
; US-08-441-887A-96

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|  
|  
|  
|  
|  
Db 3 GGGGG 7

RESULT 27  
US-08-173-489C-223  
; Sequence 223, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:

;/ MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
;/ COMPUTER: IBM PC/XT/AT  
;/ OPERATING SYSTEM: MS-DOS version 6.2  
;/ SOFTWARE: Wordperfect Version 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/173,489C  
;/ FILING DATE: 22 DEC 1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/968,436  
;/ FILING DATE: 29 OCT 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Handelman, Joseph H.  
;/ REGISTRATION NUMBER: 26,179  
;/ REFERENCE/DOCKET NUMBER: U9518-6  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (attorney) (212) 708-1880  
;/ TELEFAX: (attorney) (212) 246-8959  
;/ INFORMATION FOR SEQ ID NO: 223:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: double stranded  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: genomic DNA  
;/ DESCRIPTION: 238 rRNA gene from Escherichia coli  
;/ DESCRIPTION: (Accession # M25458) nucleotides 1410 to 1419  
;/ HYPOTHETICAL: no  
;/ ANTI-SENSE: no  
;/ ORIGINAL SOURCE:  
;/ ORGANISM: Escherichia coli  
;/ STRAIN: MRE600  
;/ PUBLICATION INFORMATION:  
;/ AUTHORS: Branlant, C, Krol, A, Machatt, M, A,  
;/ AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,  
;/ AUTHORS: H.  
;/ TITLE: Primary and secondary  
;/ TITLE: structures of Escherichia coli MRE 600 23S  
;/ TITLE: ribosomal RNA Comparison with models of  
;/ TITLE: secondary structure for maize chloroplast 23S  
;/ TITLE: rRNA and for large portions of mouse and human  
;/ TITLE: 16S mitochondrial rRNAs  
;/ JOURNAL: Nucleic Acids Research  
;/ VOLUME: 9  
;/ PAGES: 4303-4324  
;/ DATE: 1981  
;/ RELEVANT RESIDUES IN SEQ ID NO: 223 :FROM 1 TO 10  
US-08-173-489C-223

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 4 GGGGG 8

RESULT 28  
US-08-173-489C-224/c  
; Sequence 224, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK

;/ COUNTRY: USA  
;/ ZIP: 10021.  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
;/ COMPUTER: IBM PC/XT/AT  
;/ OPERATING SYSTEM: MS-DOS version 6.2  
;/ SOFTWARE: Wordperfect Version 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/173,489C  
;/ FILING DATE: 22 DEC 1993  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: US 07/968,436  
;/ FILING DATE: 29 OCT 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Handelman, Joseph H.  
;/ REGISTRATION NUMBER: 26,179  
;/ REFERENCE/DOCKET NUMBER: U9518-6  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (attorney) (212) 708-1880  
;/ TELEFAX: (attorney) (212) 246-8959  
;/ INFORMATION FOR SEQ ID NO: 224:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 bases  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single stranded  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: other nucleic acid  
;/ DESCRIPTION: third strand derived from E. coli 23s  
;/ DESCRIPTION: region in Seq ID No. 5861244223  
;/ HYPOTHETICAL: yes  
;/ ANTI-SENSE: no  
;/ PUBLICATION INFORMATION:  
;/ RELEVANT RESIDUES IN SEQ ID NO: 224 :FROM 1 TO 10  
US-08-173-489C-224

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 9 GGGGG 5

RESULT 29  
US-08-590-571-28  
; Sequence 28, Application US/08590571  
; Patent No. 5861246  
; GENERAL INFORMATION:  
; APPLICANT: Sherman Weissman and Girish N. Nallur  
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Yahwak & Associates  
; STREET: 25 Skytop Drive  
; CITY: Trumbull  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06611  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,571  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: George M. Yahwak  
; REGISTRATION NUMBER: 26,824  
; REFERENCE/DOCKET NUMBER: Yale

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-28

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
       |||||
Db      3 GGGGG 7

RESULT 30
US-08-590-571-33
; Sequence 33, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-33

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
       |||||
Db      1 GGGGG 5

RESULT 31
US-08-590-571-44
; Sequence 44, Application US/08590571
```

```
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-44

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
       |||||
Db      4 GGGGG 8

RESULT 32
US-08-590-571-47
; Sequence 47, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
```

```
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-47

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      5 GGGGG 9

RESULT 33
US-08-590-571-49
; Sequence 49, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-49

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      3 GGGGG 7

RESULT 34
US-08-419-448-51
```

```
; Sequence 51, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
US-08-419-448-51

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 35
US-08-419-448-52/c
; Sequence 52, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
```



; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,448  
; FILING DATE: 10-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20026.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
; HYPOTHETICAL: NO  
US-08-419-448-52

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||  
Db 9 GGGGG 5

RESULT 36  
US-08-821-205-3/c  
; Sequence 3, Application US/08821205  
; Patent No. 5866700  
; GENERAL INFORMATION:  
; APPLICANT: Pfeiderer, Wolfgang  
; APPLICANT: Schnell, Ralf  
; APPLICANT: Matysiak, Stephan  
; TITLE OF INVENTION: Solid-Phase Synthesis Of  
; TITLE OF INVENTION: Oligoribonucleotides.  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,205  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,354  
; FILING DATE: 03-NOV-1994  
; APPLICATION NUMBER: GR P 43 43 126.7  
; FILING DATE: 17-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Horton, Ken  
; REGISTRATION NUMBER: 39,481  
; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-4

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-3

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||  
Db 10 GGGGG 6

RESULT 37  
US-08-821-205-4  
; Sequence 4, Application US/08821205  
; Patent No. 5866700  
; GENERAL INFORMATION:  
; APPLICANT: Pfeiderer, Wolfgang  
; APPLICANT: Schnell, Ralf  
; APPLICANT: Matysiak, Stephan  
; TITLE OF INVENTION: Solid-Phase Synthesis Of  
; TITLE OF INVENTION: Oligoribonucleotides.  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,205  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,354  
; FILING DATE: 03-NOV-1994  
; APPLICATION NUMBER: GR P 43 43 126.7  
; FILING DATE: 17-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Horton, Ken  
; REGISTRATION NUMBER: 39,481  
; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-4

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 1 GGGGG 5

RESULT 38  
US-08-482-651-57/c  
; Sequence 57, Application US/08482651  
; Patent No. 5874409  
; GENERAL INFORMATION:  
; APPLICANT: Victoria, Edward J.  
; APPLICANT: Marquis, David M.  
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED  
; TITLE OF INVENTION: PATHOLOGIES  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,651  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Park, Freddie K.  
; REGISTRATION NUMBER: 35,636  
; REFERENCE/DOCKET NUMBER: 25231-20061.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-482-651-57

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 8 GGGGG 4

RESULT 39  
US-08-595-043A-66/c  
; Sequence 66, Application US/08595043A  
; Patent No. 5935824  
; GENERAL INFORMATION:  
; APPLICANT: SGARLATO, GREGORY D.  
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/595,043A  
; FILING DATE: 31-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: SGAR-00371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-595-043A-66

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||

Db 10 GGGGG 6

RESULT 40  
US-08-595-043A-67  
; Sequence 67, Application US/08595043A  
; Patent No. 5935824  
; GENERAL INFORMATION:  
; APPLICANT: SGARLATO, GREGORY D.  
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/595,043A  
; FILING DATE: 31-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: SGAR-00371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

```
US-08-595-043A-67
;
; Query Match          100.0%; Score 5; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 GGGGG 5
      |||||
Db      5 GGGGG 9

RESULT 41
US-08-403-888A-145
; Sequence 145, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-403-888A-145
;
; Query Match          100.0%; Score 5; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 42
US-08-481-658B-19/c
; Sequence 19, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
;
US-08-481-658B-19
;
; Query Match          100.0%; Score 5; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY      1 GGGGG 5
      |||||
Db      6 GGGGG 2

RESULT 43
US-08-481-658B-20/c
; Sequence 20, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
```

```
/ FILING DATE: 15-JUN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lauder, Leona L.
/ REGISTRATION NUMBER: 30,863
/ REFERENCE/DOCKET NUMBER: D-0021.3E
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-435-2034
/ TELEFAX: 415-435-0727
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ DESCRIPTION: initiator (Inr) element
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-08-481-658B-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 8 GGGGG 4

RESULT 44
US-08-722-187-45/c
/ Sequence 45, Application US/08722187
/ Patent No. 595274
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M
/ APPLICANT: Beck, James J
/ TITLE OF INVENTION: Detection of Fungal Pathogens Using the
/ TITLE OF INVENTION: Polymerase Chain Reaction
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ciba-Geigy Corporation
/ STREET: 7 Skyline Drive
/ CITY: Hawthorne
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10532
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/722,187
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/233,608
/ FILING DATE: 04-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Walsh, Andrea C.
/ REGISTRATION NUMBER: 34,988
/ REFERENCE/DOCKET NUMBER: CGC 1739
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8666
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Other nucleic acid
/ DESCRIPTION: Oligonucleotide primer OPE-19
```

```
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-08-722-187-45

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 2

RESULT 45
US-08-476-712-1
/ Sequence 1, Application US/08476712
/ Patent No. 5962426
/ GENERAL INFORMATION:
/ APPLICANT: Glazer, Peter, M.
/ TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
/ TITLE OF INVENTION: Targeted Mutagenesis
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: 2800 One Atlantic Center
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/476,712
/ FILING DATE: 7-JUNE-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabat, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: YU114
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-873-8794
/ TELEFAX: (404)-873-8795
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-476-712-1

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 10

RESULT 46
US-08-477-504A-19/c
/ Sequence 19, Application US/08477504A
/ Patent No. 5972353
/ GENERAL INFORMATION:
/ APPLICANT: Zavada, Jan
/ APPLICANT: Pastorekova, Silvia
/ APPLICANT: Pastorek, Jaromir
/ TITLE OF INVENTION: MN Gene and Protein
```

```
;
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
;
; US-08-477-504A-19
;
; Query Match 100.0%; Score 5; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGGGG 5
; Db 6 GGGGG 2
;
; RESULT 47
; US-08-477-504A-20/c
; Sequence 20, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
```

```
;
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: initiator (Inr) element
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
; US-08-477-504A-20
;
; Query Match 100.0%; Score 5; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGGGG 5
; Db 8 GGGGG 4
;
; RESULT 48
; US-08-486-756A-19/c
; Sequence 19, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```

; DESCRIPTION: AP-2 transcription factor
US-08-486-756A-19
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

RESULT 49
US-08-486-756A-20/c
; Sequence 20, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: initiator (Inr) element
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-486-756A-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 8 GGGGG 4

RESULT 50
US-08-485-862B-19/c
; Sequence 19, Application US/08485862B
; Patent No. 5989838
```

```

; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-485-862B-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

Search completed: January 7, 2005, 11:05:47
Job time : 61 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
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Title: GGGGG

Perfect score: 5

Sequence: 1 ggggg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10

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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1  
US-08-887-505-160  
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; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
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; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
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STREET: 60 State Street  
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ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
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INFORMATION FOR SEQ ID NO: 160:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-160

Query Match 100.0%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
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Db 1 GGGGG 5

RESULT 2  
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Sequence 31, Application US/09005243  
Patent No. US20020018763A1  
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TITLE OF INVENTION: Stem Cell Factor  
NUMBER OF SEQUENCES: 104  
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CITY: Chicago  
STATE: Illinois  
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ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,243  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/449,653

FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
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TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
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MOLECULE TYPE: DNA  
US-09-005-243-31

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Db 7 GGGGG 3

RESULT 3  
US-09-783-338A-2  
Sequence 2, Application US/09783338A  
Patent No. US20020028922A1  
GENERAL INFORMATION:  
APPLICANT: Glazer, Peter M.  
Havre, Pamela A.  
TITLE OF INVENTION: Chemically Modified Oligonucleotide for  
Site-Directed Mutagenesis  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/783,338A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/083,088  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:

```
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-338A-2

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 4
US-09-783-338A-3
; Sequence 3, Application US/09783338A
; Patent No. US2002028922A1
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
;           Havre, Pamela A.
; TITLE OF INVENTION: Chemically Modified Oligonucleotide for
;                   Site-Directed Mutagenesis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,338A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,088
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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US-09-783-338A-3

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 5
US-09-224-683-31/c
; Sequence 31, Application US/09224683
; Patent No. US20020031491A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor: Composition Claims
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-224-683-31

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 7 GGGGG 3

RESULT 6
US-09-989-789-96
; Sequence 96, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-989-789-96

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 10

RESULT 7
US-09-989-789-97
; Sequence 97, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-989-789-97

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 1 GGGGG 5

RESULT 8
US-09-989-789-604
; Sequence 604, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-989-789-604

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 1 GGGGG 5

RESULT 9
US-09-989-789-634
; Sequence 634, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; US-09-989-789-634

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 1 GGGGG 5

RESULT 10
US-09-989-789-635
; Sequence 635, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
```



```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-635

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 11
US-09-989-789-1271
; Sequence 1271, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1271

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 12
US-09-989-789-1272
; Sequence 1272, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1272
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1271

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 13
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 14
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
```

```
; OTHER INFORMATION: DNA
US-09-989-789-1272

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 13
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 14
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
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RESULT 15  
US-09-989-789-1637  
; Sequence 1637, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1637  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1637

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

RESULT 16  
US-09-989-789-1660  
; Sequence 1660, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1660  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1660

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
|||||  
Db 3 GGGGG 7

RESULT 17  
US-09-989-789-1668  
; Sequence 1668, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1668  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1668

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
|||||  
Db 3 GGGGG 7

RESULT 18  
US-09-852-261-8/c  
; Sequence 8, Application US/09852261  
; Patent No. US20020083477A1  
; GENERAL INFORMATION:  
; APPLICANT: GOLDSPIK, GEOFFREY  
; APPLICANT: TRENCHI, GIORGIO  
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE  
; FILE REFERENCE: 117-351  
; CURRENT APPLICATION NUMBER: US/09/852,261  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: GB 0011278.9  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-09-852-261-8

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGG 5  
|||||  
Db 6 GGGGG 2

RESULT 19  
US-09-816-763-28/c  
; Sequence 28, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28

; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: EGR-2  
US-09-816-763-28

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 8 GGGGG 4

RESULT 20  
US-09-772-719-19/c  
; Sequence 19, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: AP-2 transcription factor  
US-09-772-719-19

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 6 GGGGG 2

RESULT 21  
US-09-772-719-20/c  
; Sequence 20, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: initiator (Inr) element  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-772-719-20

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 8 GGGGG 4

RESULT 22  
US-09-846-033B-139  
; Sequence 139, Application US/09846033B  
; Publication No. US20030044404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.

```
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; TITLE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-139
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGG 5
        |||||
Db       1 GGGGG 5
```

```
RESULT 23
US-09-846-033B-141
; Sequence 141, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-141
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGG 5
        |||||
Db       6 GGGGG 10
```

```
RESULT 24
US-09-846-033B-143
; Sequence 143, Application US/09846033B
; Publication No. US2003004404A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; TITLE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-143
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGG 5
        |||||
Db       4 GGGGG 8
```

```
RESULT 25
US-09-846-033B-144
; Sequence 144, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; TITLE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-144
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 26
US-09-846-033B-145
; Sequence 145, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 145
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-145

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 27
US-09-846-033B-146
; Sequence 146, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-146

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      3 GGGGG 7

RESULT 28
US-09-846-033B-240
; Sequence 240, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-240

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      4 GGGGG 8

RESULT 29
US-09-971-894-39
; Sequence 39, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kashi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerman, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
; PRIOR FILING DATE: 1999-12-27
```

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-971-894-39

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 30
US-09-967-237-20/c
; Sequence 20, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
US-09-967-237-20

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      8 GGGGG 4

RESULT 31
US-09-990-186-96
; Sequence 96, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-96

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      8 GGGGG 4

RESULT 32
US-09-990-186-97
; Sequence 97, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-97

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      3 GGGGG 7

RESULT 33
US-09-990-186-604
; Sequence 604, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-604

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 34
US-09-990-186-634
; Sequence 634, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
QY      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 32
US-09-990-186-97
; Sequence 97, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-97

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      3 GGGGG 7

RESULT 33
US-09-990-186-604
; Sequence 604, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-604

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 34
US-09-990-186-634
; Sequence 634, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
```

```
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-634

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 35
US-09-990-186-635
; Sequence 635, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-635

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 36
US-09-990-186-1271
; Sequence 1271, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1271

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 37
US-09-990-186-1272
; Sequence 1272, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1272
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1272

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 38
US-09-990-186-1317
; Sequence 1317, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1317

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
```



```
Db          |||||
            1 GGGGG 5

RESULT 39
US-09-990-186-1345
; Sequence 1345, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1345

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      1 GGGGG 5

RESULT 40
US-09-990-186-1637
; Sequence 1637, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1637
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1637

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      1 GGGGG 5

RESULT 41
US-09-990-186-1660
; Sequence 1660, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
```

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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1660

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      3 GGGGG 7

RESULT 42
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1668

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      3 GGGGG 7

RESULT 43
US-09-979-593-43
; Sequence 43, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MWH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
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; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-43

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 44
US-09-989-994-96
; Sequence 96, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-96

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      6 GGGGG 10

RESULT 45
US-09-989-994-97
; Sequence 97, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-97

Query Match      100.0%; Score 5; DB 10; Length 10;
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```
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      3 GGGGG 7

RESULT 46
US-09-989-994-604
; Sequence 604, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-604
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
```

```
RESULT 47
US-09-989-994-634
; Sequence 634, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-634
```

```
Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5
```

```
RESULT 48
US-09-989-994-635
; Sequence 635, Application US/09989994
```

```

; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-635

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 49
US-09-989-994-1271
; Sequence 1271, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1271

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

RESULT 50
US-09-989-994-1272
; Sequence 1272, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1272
```

```

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1272

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      1 GGGGG 5

Search completed: January 7, 2005, 11:31:30
Job time : 272.2 secs
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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGCTG  
Perfect score: 5  
Sequence: 1 gggtg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

- GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	100.0	10	6	A52270
2	5	100.0	10	6	A52271
3	5	100.0	10	6	A98816
4	5	100.0	10	6	AR013952
5	5	100.0	10	6	AR016043
6	5	100.0	10	6	AR016245
7	5	100.0	10	6	AR017948
8	5	100.0	10	6	AR020527
9	5	100.0	10	6	AR030206
10	5	100.0	10	6	AR030234
11	5	100.0	10	6	AR035526
12	5	100.0	10	6	AR050986
13	5	100.0	10	6	AR059204
14	5	100.0	10	6	AR069288
15	5	100.0	10	6	AR069301
16	5	100.0	10	6	AR074300
17	5	100.0	10	6	AR074448
18	5	100.0	10	6	AR074449
19	5	100.0	10	6	AR075515
					A52270 Sequence 60
					A52271 Sequence 61
					A98816 Sequence 16
					AR013952 Sequence
					AR016043 Sequence
					AR016245 Sequence
					AR017948 Sequence
					AR020527 Sequence
					AR030206 Sequence
					AR030234 Sequence
					AR035526 Sequence
					AR050986 Sequence
					AR059204 Sequence
					AR069288 Sequence
					AR069301 Sequence
					AR074300 Sequence
					AR074448 Sequence
					AR074449 Sequence
					AR075515 Sequence

C	20	5	100.0	10	6	AR081128	Sequence
C	21	5	100.0	10	6	AR081129	Sequence
C	22	5	100.0	10	6	AR085325	Sequence
C	23	5	100.0	10	6	AR085326	Sequence
C	24	5	100.0	10	6	AR088073	Sequence
C	25	5	100.0	10	6	AR088074	Sequence
C	26	5	100.0	10	6	AR092704	Sequence
C	27	5	100.0	10	6	AR096109	Sequence
C	28	5	100.0	10	6	AR100871	Sequence
C	29	5	100.0	10	6	AR104232	Sequence
C	30	5	100.0	10	6	AR104233	Sequence
C	31	5	100.0	10	6	AR106688	Sequence
C	32	5	100.0	10	6	AR107848	Sequence
C	33	5	100.0	10	6	AR143496	Sequence
C	34	5	100.0	10	6	AR143497	Sequence
C	35	5	100.0	10	6	AR161913	Sequence
C	36	5	100.0	10	6	AR161930	Sequence
C	37	5	100.0	10	6	AR168826	Sequence
C	38	5	100.0	10	6	AR171402	Sequence
C	39	5	100.0	10	6	AR171573	Sequence
C	40	5	100.0	10	6	BD175929	Paramyxov
C	41	5	100.0	10	6	BD176154	Mammalian
C	42	5	100.0	10	6	BD181867	Polypepti
C	43	5	100.0	10	6	BD238590	Preparati
C	44	5	100.0	10	6	BD238595	Preparati
C	45	5	100.0	10	6	BD238645	Preparati
C	46	5	100.0	10	6	BD238727	Preparati
C	47	5	100.0	10	6	BD238770	Preparati
C	48	5	100.0	10	6	BD238804	Preparati
C	49	5	100.0	10	6	BD238817	Preparati
C	50	5	100.0	10	6	BD238821	Preparati
C	51	5	100.0	10	6	BD238826	Preparati
C	52	5	100.0	10	6	BD238834	Preparati
C	53	5	100.0	10	6	BD238859	Preparati
C	54	5	100.0	10	6	BD238969	Preparati
C	55	5	100.0	10	6	BD239005	Preparati
C	56	5	100.0	10	6	BD239106	Preparati
C	57	5	100.0	10	6	BD239126	Preparati
C	58	5	100.0	10	6	BD239160	Preparati
C	59	5	100.0	10	6	BD239179	Preparati
C	60	5	100.0	10	6	BD239241	Preparati
C	61	5	100.0	10	6	BD239308	Preparati
C	62	5	100.0	10	6	BD239338	Preparati
C	63	5	100.0	10	6	BD239342	Preparati
C	64	5	100.0	10	6	BD239409	Preparati
C	65	5	100.0	10	6	BD239419	Preparati
C	66	5	100.0	10	6	BD239473	Preparati
C	67	5	100.0	10	6	BD239501	Preparati
C	68	5	100.0	10	6	BD239661	Preparati
C	69	5	100.0	10	6	BD239664	Preparati
C	70	5	100.0	10	6	BD239800	Preparati
C	71	5	100.0	10	6	BD239802	Preparati
C	72	5	100.0	10	6	BD239820	Preparati
C	73	5	100.0	10	6	BD239823	Preparati
C	74	5	100.0	10	6	BD239831	Preparati
C	75	5	100.0	10	6	BD239871	Preparati
C	76	5	100.0	10	6	BD239878	Preparati
C	77	5	100.0	10	6	BD239902	Preparati
C	78	5	100.0	10	6	BD239987	Preparati
C	79	5	100.0	10	6	BD240044	Preparati
C	80	5	100.0	10	6	BD240445	Preparati
C	81	5	100.0	10	6	BD240663	Preparati
C	82	5	100.0	10	6	BD240687	Preparati
C	83	5	100.0	10	6	BD240708	Preparati
C	84	5	100.0	10	6	BD243162	MN gene a
C	85	5	100.0	10	6	CQ766681	Sequence
C	86	5	100.0	10	6	CQ766684	Sequence
C	87	5	100.0	10	6	CQ772479	Sequence
C	88	5	100.0	10	6	CQ832318	Sequence
C	89	5	100.0	10	6	E08985	PCR primer
C	90	5	100.0	10	6	E16981	PCR primer
C	91	5	100.0	10	6	E39488	Genes with
C	92	5	100.0	10	6	E39565	Genes with

93		5	100.0	10	6	E39635	E39635 Genes with
c 94		5	100.0	10	6	E54679	E54679 Human norma
c 95		5	100.0	10	6	E54735	E54735 Human norma
96		5	100.0	10	6	E54765	E54765 Human norma
97		5	100.0	10	6	E54796	E54796 Human norma
98		5	100.0	10	6	E54840	E54840 Human norma
c 99		5	100.0	10	6	I18846	I18846 Sequence 27
c 100		5	100.0	10	6	I22300	I22300 Sequence 27
101		5	100.0	10	6	I22313	I22313 Sequence 43
c 102		5	100.0	10	6	I35483	I35483 Sequence 34
c 103		5	100.0	10	6	I48951	I48951 Sequence 4
104		5	100.0	10	6	I51787	I51787 Sequence 55
105		5	100.0	10	6	I54915	I54915 Sequence 5
106		5	100.0	10	6	I54917	I54917 Sequence 7
107		5	100.0	10	6	I54921	I54921 Sequence 11
108		5	100.0	10	6	I54922	I54922 Sequence 12
109		5	100.0	10	6	I54923	I54923 Sequence 13
110		5	100.0	10	6	I54930	I54930 Sequence 20
111		5	100.0	10	6	I54931	I54931 Sequence 21
112		5	100.0	10	6	I54932	I54932 Sequence 22
113		5	100.0	10	6	I54933	I54933 Sequence 23
114		5	100.0	10	6	I54934	I54934 Sequence 24
115		5	100.0	10	6	I54935	I54935 Sequence 25
116		5	100.0	10	6	I54936	I54936 Sequence 26
c 117		5	100.0	10	6	I54937	I54937 Sequence 27
118		5	100.0	10	6	I54938	I54938 Sequence 28
119		5	100.0	10	6	I54939	I54939 Sequence 29
120		5	100.0	10	6	I54940	I54940 Sequence 30
121		5	100.0	10	6	I54941	I54941 Sequence 31
122		5	100.0	10	6	I54953	I54953 Sequence 43
c 123		5	100.0	10	6	I79680	I79680 Sequence 7
c 124		5	100.0	10	6	I81499	I81499 Sequence 6
c 125		5	100.0	10	6	I81499	I81499 Sequence 6
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c 138		5	100.0	10	6	AR234504	AR234504 Sequence
c 139		5	100.0	10	6	AR234506	AR234506 Sequence
c 140		5	100.0	10	6	AR234508	AR234508 Sequence
c 141		5	100.0	10	6	AR234510	AR234510 Sequence
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c 147		5	100.0	10	6	AR266609	AR266609 Sequence
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c 149		5	100.0	10	6	AR267970	AR267970 Sequence
c 150		5	100.0	10	6	AR285615	AR285615 Sequence
c 151		5	100.0	10	6	AR303518	AR303518 Sequence
c 152		5	100.0	10	6	AR303525	AR303525 Sequence
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c 154		5	100.0	10	6	AR306461	AR306461 Sequence
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c 173	5	100.0	10	6	AX152090	AX152090 Sequence
c 174	5	100.0	10	6	AX152154	AX152154 Sequence
c 175	5	100.0	10	6	AX152199	AX152199 Sequence
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182	5	100.0	10	6	AX152387	AX152387 Sequence
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185	5	100.0	10	6	AX152501	AX152501 Sequence
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c 196	5	100.0	10	6	AX152857	AX152857 Sequence
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c 200	5	100.0	10	6	AX153053	AX153053 Sequence
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c 219	5	100.0	10	6	AX153635	AX153635 Sequence
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261	5	100.0	10	6	BD014515	Remedy ut
262	5	100.0	10	6	BD064779	A novel a
263	5	100.0	10	6	BD064782	A novel a
264	5	100.0	10	6	BD065112	Character
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266	5	100.0	10	6	BD073892	Isolation
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269	5	100.0	10	6	BD083302	Human mat
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271	5	100.0	10	6	BD091188	P53-induc
272	5	100.0	10	6	BD097103	Paramyxov
273	5	100.0	10	6	BD102510	Aids viru
274	5	100.0	10	6	BD135461	Fatty aci
275	5	100.0	10	6	BD141036	Virus vec
276	5	100.0	10	6	BD143888	Paramyxov
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C 493	5	100.0	11	6	AX626981	Sequence
C 494	5	100.0	11	6	AX627050	Sequence
C 495	5	100.0	11	6	AX627072	Sequence
C 496	5	100.0	11	6	AX627085	Sequence
C 497	5	100.0	11	6	AX627151	Sequence
C 498	5	100.0	11	6	AX627180	Sequence
C 499	5	100.0	11	6	AX627213	Sequence
C 500	5	100.0	11	6	AX627293	Sequence

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RESULT 1						
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LOCUS	DEFINITION	Sequence 60 from Patent EP0705842.				
ACCESSION	A52270					
VERSION	A52270.1	GI:2852042				
KEYWORDS	.					
SOURCE	unidentified					
ORGANISM	unidentified					
	unclassified.					
REFERENCE	1					
AUTHORS	Bartnik,E.D. and Margerie,D.D.					
TITLE	Regulated genes by stimulation of chondrocytes with 1L-1beta					
JOURNAL	Patent: EP 0705842-A 60 10-APR-1996;					
	HOECHST AG (DE)					
COMMENT	Other publication ZA 9508381 960424					
	Other publication JP 8191693 960730					
	Other publication CA 2159957 960407					
	Other publication AU 3308695 960418.					
FEATURES	Location/Qualifiers					
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
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Db 6 GGGTG 10

RESULT 2  
A52271  
LOCUS A52271 10 bp DNA linear PAT 12-DEC-1997  
DEFINITION Sequence 61 from Patent EP0705842.  
ACCESSION A52271  
VERSION A52271.1 GI:2852041  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1  
AUTHORS Bartnik, E.D. and Margerie, D.D.  
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta  
JOURNAL Patent: EP 0705842-A 61 10-APR-1996;  
HOECHST AG (DE)  
COMMENT Other publication ZA 9508381 960424  
Other publication JP 8191693 960730  
Other publication CA 2159957 960407  
Other publication AU 3308695 960418.  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 3  
A98816  
LOCUS A98816 10 bp DNA linear PAT 26-JAN-2000  
DEFINITION Sequence 16 from Patent WO9909817.  
ACCESSION A98816  
VERSION A98816.1 GI:6781837  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Finnegan, D.J. and Sang, H.  
TITLE USE OF MARINER TRANSPOSAN IN THE PRODUCTION OF TRANSGENIC ANIMALS  
JOURNAL Patent: WO 9909817-A 16 04-MAR-1999;  
FINNEGAN DAVID JOHN (GB); SANG HELEN (GB)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

Db 4 GGGTG 8  
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RESULT 4  
AR013952/c  
LOCUS AR013952 10 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 7 from patent US 5773226.  
ACCESSION AR013952  
VERSION AR013952.1 GI:3971406  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Millan, J.L.  
TITLE Recombinant calf intestinal alkaline phosphatase  
JOURNAL Patent: US 5773226-A 7 30-JUN-1998;  
FEATURES  
source Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
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Db 10 GGGTG 6

RESULT 5  
AR016043/c  
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DEFINITION Sequence 11 from patent US 5776679.  
ACCESSION AR016043  
VERSION AR016043.1 GI:3972320  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.  
TITLE Assays for the DNA component of human telomerase  
JOURNAL Patent: US 5776679-A 11 07-JUL-1998;  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
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Db 7 GGGTG 3

RESULT 6  
AR016245/c  
LOCUS AR016245 10 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 13 from patent US 5776683.  
ACCESSION AR016245  
VERSION AR016245.1 GI:3972522  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Smith,H.S. and Chen,L.-C.  
TITLE Methods for identifying genes amplified in cancer cells  
JOURNAL Patent: US 5776683-A 13 07-JUL-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 8 GGGTG 4  
RESULT 7  
AR017948  
LOCUS AR017948 10 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 13 from patent US 5780273.  
ACCESSION AR017948  
VERSION AR017948.1 GI:3973551  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Burg,J.Lawrence.  
TITLE Insertion elements and amplifiable nucleic acids  
JOURNAL Patent: US 5780273-A 13 14-JUL-1998;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 8  
AR020527/c  
LOCUS AR020527 10 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 3 from patent US 5789174.  
ACCESSION AR020527  
VERSION AR020527.1 GI:3975142  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Mouton,C., Guillot,E. and Menard,C.  
TITLE Detection of periodontal pathogens including bacteroides forsythus, porphyromonas gingivalis, prevotella intermedia and prevotella nigrescens  
JOURNAL Patent: US 5789174-A 3 04-AUG-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 8 GGGTG 4  
RESULT 9  
AR030206  
LOCUS AR030206 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 17 from patent US 5861246.  
ACCESSION AR030206  
VERSION AR030206.1 GI:5943420  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 17 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 10  
AR030234  
LOCUS AR030234 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 45 from patent US 5861246.  
ACCESSION AR030234  
VERSION AR030234.1 GI:5943448  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 45 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 3 GGGTG 7  
RESULT 11  
AR035526  
LOCUS AR035526 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 52 from patent US 5871910.  
ACCESSION AR035526  
VERSION AR035526.1 GI:5952194  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.  
TITLE Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria  
JOURNAL Patent: US 5871910-A 52 16-FEB-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 12  
AR050986  
LOCUS AR050986 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 55 from patent US 5830644.  
ACCESSION AR050986  
VERSION AR050986.1 GI:5974350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS West,M.D., Shay,J. and Wright,W.E.  
TITLE Method for screening for agents which increase telomerase activity in a cell  
JOURNAL Patent: US 5830644-A 55 03-NOV-1998;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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Db 2 GGGTG 6

RESULT 13  
AR059204/c  
LOCUS AR059204 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5837857.  
ACCESSION AR059204  
VERSION AR059204.1 GI:5984781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Peng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5837857-A 11 17-NOV-1998;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 14  
AR069288/c  
LOCUS AR069288 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 27 from patent US 5891631.  
ACCESSION AR069288  
VERSION AR069288.1 GI:7220176  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.  
TITLE Methods relating tosterol regulatory element binding proteins  
JOURNAL Patent: US 5891631-A 27 06-APR-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 15  
AR069301  
LOCUS AR069301 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 43 from patent US 5891631.  
ACCESSION AR069301  
VERSION AR069301.1 GI:7220189  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.  
TITLE Methods relating tosterol regulatory element binding proteins  
JOURNAL Patent: US 5891631-A 43 06-APR-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 16  
AR074300  
LOCUS AR074300 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 108 from patent US 5952490.  
ACCESSION AR074300  
VERSION AR074300.1 GI:10001055

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KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
              Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
              Imbach,J.Louis.
TITLE        Oligonucleotides having a conserved G4 core sequence
JOURNAL      Patent: US 5952490-A 108 14-SEP-1999;
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      1 GGGTG 5

RESULT 17
AR074448/c
LOCUS      AR074448
DEFINITION Sequence 19 from patent US 5955075.
ACCESSION  AR074448
VERSION     AR074448.1 GI:10001203
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL      Patent: US 5955075-A 19 21-SEP-1999;
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      10 GGGTG 6

RESULT 18
AR074449/c
LOCUS      AR074449
DEFINITION Sequence 20 from patent US 5955075.
ACCESSION  AR074449
VERSION     AR074449.1 GI:10001204
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL      Patent: US 5955075-A 20 21-SEP-1999;
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"
ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db      10 GGGTG 6

RESULT 19
AR075515/c
LOCUS      AR075515
DEFINITION Sequence 12 from patent US 5958680.
ACCESSION  AR075515
VERSION     AR075515.1 GI:10002263
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE        Mammalian telomerase
JOURNAL      Patent: US 5958680-A 12 28-SEP-1999;
FEATURES     Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      7 GGGTG 3

RESULT 20
AR081128/c
LOCUS      AR081128
DEFINITION Sequence 19 from patent US 5972353.
ACCESSION  AR081128
VERSION     AR081128.1 GI:10007856
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL      Patent: US 5972353-A 19 26-OCT-1999;
FEATURES     Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      10 GGGTG 6

RESULT 21
AR081129/c
LOCUS      AR081129
DEFINITION Sequence 20 from patent US 5972353.
ACCESSION  AR081129
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      6 GGGTG 2

RESULT 19
AR075515/c
LOCUS      AR075515
DEFINITION Sequence 12 from patent US 5958680.
ACCESSION  AR075515
VERSION     AR075515.1 GI:10002263
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE        Mammalian telomerase
JOURNAL      Patent: US 5958680-A 12 28-SEP-1999;
FEATURES     Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db      7 GGGTG 3

RESULT 20
AR081128/c
LOCUS      AR081128
DEFINITION Sequence 19 from patent US 5972353.
ACCESSION  AR081128
VERSION     AR081128.1 GI:10007856
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL      Patent: US 5972353-A 19 26-OCT-1999;
FEATURES     Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db      10 GGGTG 6

RESULT 21
AR081129/c
LOCUS      AR081129
DEFINITION Sequence 20 from patent US 5972353.
ACCESSION  AR081129
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VERSION AR081129.1 GI:10007857  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 20 26-OCT-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 2  
RESULT 22  
AR085325/c  
LOCUS AR085325 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 19 from patent US 5981711.  
ACCESSION AR085325  
VERSION AR085325.1 GI:10012094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 19 09-NOV-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 2  
RESULT 23  
AR085326/c  
LOCUS AR085326 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 20 from patent US 5981711.  
ACCESSION AR085326  
VERSION AR085326.1 GI:10012095  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 20 09-NOV-1999;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 2  
RESULT 24  
AR088073/c  
LOCUS AR088073 10 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 19 from patent US 5989838.  
ACCESSION AR088073  
VERSION AR088073.1 GI:10014836  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 19 23-NOV-1999;  
FEATURES Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
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Db 10 GGGTG 6  
RESULT 25  
AR088074/c  
LOCUS AR088074 10 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 20 from patent US 5989838.  
ACCESSION AR088074  
VERSION AR088074.1 GI:10014837  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 20 23-NOV-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 2  
RESULT 26  
AR092704  
LOCUS AR092704 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 16 from patent US 5998193.  
ACCESSION AR092704  
VERSION AR092704.1 GI:10019456





KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Periman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 16 22-AUG-2000;  
source Location/Qualifiers  
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QY 1 GGGTG 5  
Db |||||  
4 GGGTG 8  
RESULT 32  
AR107848  
LOCUS AR107848 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 94 from patent US 6110667.  
ACCESSION AR107848  
VERSION AR107848.1 GI:12823335  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 10)  
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.  
TITLE Processes, apparatus and compositions for characterizing nucleotide  
JOURNAL sequences based on K-tuple analysis  
FEATURES Patent: US 6110667-A 94 29-AUG-2000;  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
4 GGGTG 8  
RESULT 33  
AR143496/c  
LOCUS AR143496 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 19 from patent US 6204370.  
ACCESSION AR143496  
VERSION AR143496.1 GI:15104782  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6204370-A 19 20-MAR-2001;  
FEATURES Patent: US 6204370-A 19 20-MAR-2001;  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
10 GGGTG 6  
RESULT 34  
AR143497/c  
LOCUS AR143497 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 20 from patent US 6204370.  
ACCESSION AR143497  
VERSION AR143497.1 GI:15104783  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6204370-A 20 20-MAR-2001;  
FEATURES Patent: US 6204370-A 20 20-MAR-2001;  
source Location/Qualifiers  
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QY 1 GGGTG 5  
Db |||||  
6 GGGTG 2  
RESULT 35  
AR161913/c  
LOCUS AR161913 10 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 11 from patent US 6258535.  
ACCESSION AR161913  
VERSION AR161913.1 GI:16228931  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 6258535-A 11 10-JUL-2001;  
FEATURES Patent: US 6258535-A 11 10-JUL-2001;  
source Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
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RESULT 36  
AR161930  
LOCUS AR161930 10 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 3 from patent US 6258537.  
ACCESSION AR161930

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VERSION      AR161930.1  GI:16228961
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Keinath,A.P., Somai,B.M. and Dean,R.A.
TITLE        Method of diagnosing gummy stem blight in plants using a polymerase
              chain reaction assay
JOURNAL      Patent: US 6258537-A 3 10-JUL-2001;
FEATURES     Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db      1 GGGTG 5

RESULT 37
AR168826
LOCUS      AR168826               10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 52 from patent US 6288042.
ACCESSION  AR168826
VERSION     AR168826.1  GI:17904948
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE        Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL      Patent: US 6288042-A 52 11-SEP-2001;
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db      1 GGGTG 5

RESULT 38
AR171402/c
LOCUS      AR171402               10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 20 from patent US 6297041.
ACCESSION  AR171402
VERSION     AR171402.1  GI:17910352
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        MN gene and protein
JOURNAL      Patent: US 6297041-A 20 02-OCT-2001;
FEATURES     Location/Qualifiers
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QY      1 GGGTG 5
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Db      6 GGGTG 2

RESULT 39
AR171573/c
LOCUS      AR171573               10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 20 from patent US 6297051.
ACCESSION  AR171573
VERSION     AR171573.1  GI:17910523
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE        MN gene and protein
JOURNAL      Patent: US 6297051-A 20 02-OCT-2001;
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db      6 GGGTG 2

RESULT 40
BD175929/c
LOCUS      BD175929               10 bp      DNA      linear      PAT 18-MAR-2003
DEFINITION Paramyxovirus vectors used for transduction of foreign genes.
ACCESSION  BD175929
VERSION     BD175929.1  GI:29121633
KEYWORDS    JP 2002272465-A/1.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Tokusumi,T., Iida,A. and Hasegawa,M.
TITLE        Paramyxovirus vectors used for transduction of foreign genes
JOURNAL      Patent: JP 2002272465-A 1 24-SEP-2002;
COMMENT     Dनावेक RESEARCH INC
              OS Artificial Sequence
              PN JP 2002272465-A/1
              PD 24-SEP-2002
              PF 16-MAY-2001 JP 2001145935
              PR 27-OCT-2000 CA 2322057
              PI TSUYOSHI TOKUSUMI,AKIHIRO IIDA,MAMORU HASEGAWA PC
              CI2N15/09//A61K35/76,A61K48/00,A61P29/00,A61P31/16,A61P35/00, PC
              CI2N15/00
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              CC sequence
              FH Key Location/Qualifiers
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              FT Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 9 GGGTG 5

RESULT 41  
BD176154/c

LOCUS BD176154 DNA linear PAT 18-MAR-2003  
DEFINITION Mammalian telomerase.  
ACCESSION BD176154  
VERSION BD176154.1 GI:29121858  
KEYWORDS JP 2002272489-A/13.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: JP 2002272489-A 13 24-SEP-2002;  
GERON CORP

COMMENT OS Unidentified  
PN JP 2002272489-A/13  
PD 24-SEP-2002  
PF 06-MAR-2002 JP 2002061125  
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR  
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 PI BRYANT  
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC  
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC  
Strandedness: Single;  
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QY 1 GGGTG 5  
Db 7 GGGTG 3

RESULT 42  
BD181867

LOCUS BD181867 DNA linear PAT 15-MAY-2003  
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis.

ACCESSION BD181867  
VERSION BD181867.1 GI:30792785  
KEYWORDS JP 2002320494-A/23.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Arthur,M., Duktamalen,S., Molinas,C. and Courvalin,P.  
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis  
JOURNAL Patent: JP 2002320494-A 23 05-NOV-2002;

INSTITUT PASTEUR  
OS Bacteria  
PN JP 2002320494-A/23  
PD 05-NOV-2002  
PF 21-FEB-2002 JP 2002045484  
PR 31-OCT-1990 FR 90/13579  
PI MICHEL ARTHUR,SYLVIE DUKTA-MALEN,CATHERINE MOLINAS,PATRICE PI  
COURVALIN  
PC C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,  
PC (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC  
Polypeptides implicated in the expression of resistance to CC  
glycopeptides,  
CC in particular in gram-positive bacteria, nucleotide sequence  
CC cod ing for  
CC these polypeptides and use for diagnosis  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 43  
BD238590

LOCUS BD238590 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238590  
VERSION BD238590.1 GI:33048360  
KEYWORDS JP 2002534056-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 8 15-OCT-2002;  
GENZYME CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/8  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR  
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR  
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR  
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR  
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC

C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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PC C12N15/00,C12N5/00,C12N15/00  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
3 GGGTG 7  
RESULT 44  
BD238595  
LOCUS BD238595 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238595  
VERSION BD238595.1 GI:33048365  
KEYWORDS JP 2002534056-A/13.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 13 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/13  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
3 GGGTG 7  
RESULT 45  
BD238645/c  
LOCUS BD238645 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238645  
VERSION BD238645.1 GI:33048415  
KEYWORDS JP 2002534056-A/63.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 63 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/63  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
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C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
FH Key Location/Qualifiers  
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FEATURES  
source  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238727  
VERSION BD238727.1 GI:33048497  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
Roberts,B.L. and Shankara,S.  
AUTHORS Preparation and use of superior vaccines  
TITLE Patent: JP 2002534056-A 145 15-OCT-2002;  
JOURNAL GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/145  
PD 15-OCT-2002  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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ACCESSION BD238770  
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KEYWORDS JP 2002534056-A/188.  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)

AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 188 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/188  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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ACCESSION BD238804  
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ORGANISM Homo sapiens  
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1 (bases 1 to 10)  
Roberts,B.L. and Shankara,S.  
AUTHORS Preparation and use of superior vaccines  
TITLE Patent: JP 2002534056-A 222 15-OCT-2002;  
JOURNAL GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/222  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238817  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 235 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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ACCESSION BD238821  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 239 15-OCT-2002;  
GENZYME CORP  
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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GenCore version 5.1.6  
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94	5	100.0	10	3 AAZ78169	Aaz78169 Human den

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c 96	5	100.0	10	3	AAZ78810	Aaz78810	Human	den
c 97	5	100.0	10	3	AAZ78654	Aaz78654	Human	den
c 98	5	100.0	10	3	AAZ79034	Aaz79034	Human	den
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101	5	100.0	10	3	AAZ77995	Aaz77995	Human	den
102	5	100.0	10	3	AAZ78790	Aaz78790	Human	den
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105	5	100.0	10	3	AAZ78868	Aaz78868	Human	den
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c 113	5	100.0	10	3	AAZ79698	Aaz79698	Human	den
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C 416	5	100.0	5	AAF38128	Aaf38128	Yeast	NOR
C 417	5	100.0	5	AAF43380	Aaf43380	Yeast	NOR
C 418	5	100.0	5	AAF33972	Aaf33972	Yeast	NOR
C 419	5	100.0	5	AAF38024	Aaf38024	Yeast	NOR
C 420	5	100.0	5	AAF38450	Aaf38450	Yeast	NOR
C 421	5	100.0	5	AAF34328	Aaf34328	Yeast	NOR
C 422	5	100.0	5	AAF34421	Aaf34421	Yeast	NOR
C 423	5	100.0	5	AAF35620	Aaf35620	Yeast	NOR
C 424	5	100.0	5	AAF36334	Aaf36334	Yeast	NOR
C 425	5	100.0	5	AAF37182	Aaf37182	Yeast	NOR
C 426	5	100.0	5	AAF37611	Aaf37611	Yeast	NOR
C 427	5	100.0	5	AAF37836	Aaf37836	Yeast	NOR
C 428	5	100.0	5	AAF40577	Aaf40577	Yeast	NOR
C 429	5	100.0	5	AAF43541	Aaf43541	Yeast	NOR
C 430	5	100.0	5	AAF36354	Aaf36354	Yeast	NOR
C 431	5	100.0	5	AAF39165	Aaf39165	Yeast	NOR
C 432	5	100.0	5	AAF40017	Aaf40017	Yeast	NOR
C 433	5	100.0	5	AAF40556	Aaf40556	Yeast	NOR
C 434	5	100.0	5	AAF36335	Aaf36335	Yeast	NOR
C 435	5	100.0	5	AAF34600	Aaf34600	Yeast	NOR
C 436	5	100.0	5	AAF43574	Aaf43574	Yeast	NOR
C 437	5	100.0	5	AAF35219	Aaf35219	Yeast	NOR
C 438	5	100.0	5	AAF37063	Aaf37063	Yeast	NOR
C 439	5	100.0	5	AAF37745	Aaf37745	Yeast	NOR
C 440	5	100.0	5	AAF38236	Aaf38236	Yeast	NOR
C 441	5	100.0	5	AAF41499	Aaf41499	Yeast	NOR
C 442	5	100.0	5	AAF42059	Aaf42059	Yeast	NOR
C 443	5	100.0	5	AAF35014	Aaf35014	Yeast	NOR
C 444	5	100.0	5	AAF36705	Aaf36705	Yeast	NOR
C 445	5	100.0	5	AAF37893	Aaf37893	Yeast	NOR
C 446	5	100.0	5	AAF38031	Aaf38031	Yeast	NOR
C 447	5	100.0	5	AAF38496	Aaf38496	Yeast	NOR
C 448	5	100.0	5	AAF40349	Aaf40349	Yeast	NOR
C 449	5	100.0	5	AAF40576	Aaf40576	Yeast	NOR
C 450	5	100.0	5	AAF42263	Aaf42263	Yeast	NOR
C 451	5	100.0	5	AAF43277	Aaf43277	Yeast	NOR
C 452	5	100.0	5	AAS19599	Aas19599	Primer-ex	
C 453	5	100.0	5	AAS19657	Aas19657	Primer-ex	
C 454	5	100.0	5	AAS19649	Aas19649	Primer-ex	
C 455	5	100.0	5	AAS19665	Aas19665	Primer-ex	
C 456	5	100.0	5	ABS64901	Abs64901	Primer-ex	
C 457	5	100.0	5	AAD26711	Aad26711	Human GPR	
C 458	5	100.0	5	AAD26716	Aad26716	Human GPR	
C 459	5	100.0	5	ABK24237	Abk24237	Retinalde	

460	5	100.0	10	6	ABK46595	Abk46595	EDG4 gene
C 461	5	100.0	10	6	ABK51085	Abk51085	Human CCR
C 462	5	100.0	10	6	AAS99288	Aas99288	Human F12
C 463	5	100.0	10	6	ABL88326	AbL88326	Human CHR
C 464	5	100.0	10	6	ABL88335	AbL88335	Human CHR
C 465	5	100.0	10	6	ABL52185	AbL52185	Human PER
C 466	5	100.0	10	6	AAL39611	Aal39611	SSTR4 gen
C 467	5	100.0	10	6	AAL38369	Aal38369	Oligonucl
C 468	5	100.0	10	6	ABK81958	Abk81958	Human CYP
C 469	5	100.0	10	6	AAS98913	Aas98913	Colony st
C 470	5	100.0	10	6	AAS98911	Aas98911	Colony st
C 471	5	100.0	10	6	ABL01297	AbL01297	Human MMP
C 472	5	100.0	10	6	AAD25890	Aad25890	Primer #1
C 473	5	100.0	10	6	ABL42694	AbL42694	Human mat
C 474	5	100.0	10	6	ABL42849	AbL42849	Human mat
C 475	5	100.0	10	6	ABL42683	AbL42683	Human mat
C 476	5	100.0	10	6	ABK70547	Abk70547	Human G p
C 477	5	100.0	10	6	ABN84300	Abn84300	RP primer
C 478	5	100.0	10	6	ABS51974	Abs51974	Human FMO
C 479	5	100.0	10	6	ABS51962	Abs51962	Human FMO
C 480	5	100.0	10	6	ABS53693	Abs53693	Mint RAPD
C 481	5	100.0	10	6	ABN81489	Abn81489	Human HTA
C 482	5	100.0	10	6	ABN81496	Abn81496	Human HTA
C 483	5	100.0	10	6	ABK81400	Abk81400	SCYA21 ge
C 484	5	100.0	10	6	AAL47265	Aal47265	Sendai vi
C 485	5	100.0	10	6	ABK96075	Abk96075	Human LIP
C 486	5	100.0	10	6	ABK96047	Abk96047	Human LIP
C 487	5	100.0	10	6	ABK96083	Abk96083	Human LIP
C 488	5	100.0	10	6	AAS96201	Aas96201	Human Ace
C 489	5	100.0	10	6	AAS96199	Aas96199	Human Ace
C 490	5	100.0	10	6	AAS96210	Aas96210	Human Ace
C 491	5	100.0	10	6	AAS96188	Aas96188	Human Ace
C 492	5	100.0	10	6	ABA97031	Aba97031	ZFP36 ext
C 493	5	100.0	10	6	ABA97043	Aba97043	ZFP36 ext
C 494	5	100.0	10	6	AAD25919	Aad25919	Human MC4
C 495	5	100.0	10	6	AAD26188	Aad26188	Human end
C 496	5	100.0	10	6	ABL39904	AbL39904	Sendai vi
C 497	5	100.0	10	6	ABK96383	Abk96383	Human SA
C 498	5	100.0	10	6	AAL48059	Aal48059	Human CSF
C 499	5	100.0	10	6	AAS95402	Aas95402	Human ICA
C 500	5	100.0	10	12	ADN12444	Adn12444	Synthetic

ALIGNMENTS

RESULT 1	
AAN82154	
ID	AAN82154 standard; DNA; 10 BP.
XX	
AC	AAN82154;
XX	
DT	25-MAR-2003 (revised)
DT	12-DEC-1990 (first entry)
XX	
DE	Sequence #12 recognised by probe for 16S RNA gene.
XX	
KW	Mollicutes.
XX	
OS	Mycoplasma.
XX	
PN	EP250662-A.
XX	
PD	07-JAN-1988.
XX	
PF	25-JUN-1986; 86EP-00304919.
XX	
PR	25-JUN-1986; 86EP-00304919.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Gobel U, Stanbridge EJ;
XX	



```
RESULT 4
AAQ79359/c
ID AAQ79359 standard; DNA; 10 BP.
XX
AC AAQ79359;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
DE Sequence of AP2 regulatory sequence located at posn. 2621 in hEpsLH.
XX
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
XX
OS Synthetic.
XX
PN WO9423570-A1.
XX
PD 27-OCT-1994.
XX
PF 15-APR-1994; 94WO-US004141.
XX
PR 15-APR-1993; 93US-00046295.
PR 23-JUN-1993; 93US-00082850.
XX
PA (UUNY ) UNIV NEW YORK STATE.
XX
PI Lee-Huang S;
XX
DR WPI; 1994-341353/42.
XX
PT New regulatory regions of human erythropoietin gene - used for studying
PT and treating diseases and for prodn. of transgenic animal models (Eng).
XX
PS Disclosure; Table I, p. 12; 81pp; English.
XX
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'
CC flanking region contg. multiple regulatory elements and a 3' flanking
CC region contg. multiple regulatory elements. AAQ79354 shows the extended
CC 5' flanking region and includes all the 5' regulatory elements. This
CC region, consisting of the first 3892 of AAQ79353, was not found in the
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362
CC show several of these elements and their positions. The nucleotide
CC position of these elements is measured from the BamHI site at the 5' end
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 BP; 1 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 10 GGGTG 6

RESULT 5
AAQ61967
ID AAQ61967 standard; DNA; 10 BP.
XX
AC AAQ61967;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
DE Phospholipase A2 inhibiting oligomer, ISIS no 4962.
XX
KW Inhibition; replication; herpes simplex virus; HSV; HIV; aging;
KW human cytomegalovirus; influenza virus; inflammation; telomere length;
```

```
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..10
FT /*tag= a
FT /note= "Phosphorothioate intersugar linkages"
XX
PN WO9408053-A1.
XX
PD 14-APR-1994.
XX
PF 29-SEP-1993; 93WO-US009297.
XX
PR 29-SEP-1992; 92US-00954185.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX
DR WPI; 1994-135613/16.
XX
PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT of chromosomes.
XX
PS Disclosure; Page 29; 144pp; English.
XX
CC The sequences given in AAQ61956-67 are oligonucleotides which represent
CC the core sequences of G4 containing oligos which may be used for
CC inhibiting phospholipase A2 enzyme activity. Oligonucleotides such as
CC these may also be used for inhibiting activity of HSV, HIV, human
CC cytomegalovirus or influenza virus, or for treating inflammatory and
CC neurological disorders caused by phospholipase A2 activity in cases of
CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
CC They may also be used for inhibiting division of malignant cells by
CC modulating telomere length, which may also retard aging. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 1 GGGTG 5

RESULT 6
AAQ63553
ID AAQ63553 standard; DNA; 10 BP.
XX
AC AAQ63553;
XX
DT 25-MAR-2003 (revised)
DT 21-DEC-1994 (first entry)
XX
DE C22 5' spacer element.
XX
KW Insertion element; junk DNA; spacer element; functional DNA sequence;
KW primer binding site; reaction product; binding specificity; primer;
KW recombinant molecule; structural stress; hybridisation assay; ss.
XX
OS Synthetic.
XX
PN WO9409159-A2.
XX
PD 28-APR-1994.
```



XX 08-OCT-1993; 93WO-US009702.  
XX 09-OCT-1992; 92US-00959939.  
PR 09-APR-1993; 93US-00045587.  
XX (STAD ) AMOCO CORP.  
XX Burg J;  
PI WPI; 1994-151343/18.  
DR  
XX  
XX Insertion elements an amplifiable nucleic acids - for use as probes in  
PT hybridisation assays and for the prepn. of libraries used to identify  
PT preferred insertion elements.  
XX  
XX Disclosure; Page 23; 39pp; English.  
XX  
XX The sequences given in AAQ63549-60 are spacer elements used within the  
CC insertion elements of the invention. These insertion elements contain  
CC junk DNA, two spacer elements, a functional DNA sequence and a primer  
CC binding site. They also contain an MluI site, an MluI/NheI site and a  
CC NheI site. The junk DNA serves to keep the MluI site from being at the  
CC extreme end of the molecule and also allows determination that the MluI  
CC cleavage has occurred because the extended DNA will be reduced in size by  
CC the length of the junk sequence and the junk sequence will appear as a  
CC reaction product. The nucleotides making up the spacer elements are  
CC chosen randomly and the functional nucleotide sequence is chosen to  
CC achieve the binding specificity required of the amplifiable nucleic acid.  
CC The primer binding site can be any nucleotide sequence for which a  
CC complementary primer is available or can be synthesised. However, the  
CC primer and primer binding site are chosen such that the primer itself  
CC does not bind to any other portion of the insertion element under  
CC construction. Insertion sequences such as these can be used to insert a  
CC functional molecule into a host molecule to form a recombinant molecule.  
CC The spacer elements are thought to relieve structural stresses imposed on  
CC the host by addition of the functional nucleotide sequence. The insertion  
CC elements can be used with nucleic acid hybridisation assays. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 7  
AAQ79252  
ID AAQ79252 standard; DNA; 10 BP.  
XX  
AC AAQ79252;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-JUL-1995 (first entry)  
XX  
DE Guanosine rich oligonucleotide used to treat viral infection.  
XX  
KW Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;  
KW infection; herpes simplex virus; human papilloma virus;  
KW Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;  
KW hepatitis B virus; human cytomegalovirus; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 10  
FT /\*tag= a  
FT /mod\_base

FT /note= "Propanolamine group attached to this base."  
XX  
PN WO9425037-A1.  
XX  
PD 10-NOV-1994.  
XX  
PF 25-APR-1994; 94WO-US004529.  
XX  
PR 23-APR-1993; 93US-00053027.  
PR 28-OCT-1993; 93US-00145704.  
XX  
PA (TRIP-) TRIPLEX PHARM CORP.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Rando RF, Fennwald S, Zendegui JG, Ojwang JO, Hogan ME;  
XX  
XX WPI; 1994-357890/44.  
XX  
XX Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used  
PT to treat viral infections, e.g. herpes-virus and HIV.  
PT  
XX Claim 41; Page 71; 101pp; English.  
XX  
CC The oligonucleotides (See AAQ79201-52) can be used to treat viral  
CC infections. The oligonucleotides inhibit viral replication by forming  
CC guanosine tetrads which form a stabilised 3D structure. Preferred  
CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases  
CC and may be capped at the 3' terminus with a modifier selected from  
CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also  
CC have a modified phosphodiester linkage or be modified to contain a  
CC phosphorothioate linkage. They are used to treat infections with viruses  
CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,  
CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human  
CC cytomegalovirus. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 3 GGGTG 7  
RESULT 8  
AAQ81904/c  
ID AAQ81904 standard; RNA; 10 BP.  
XX  
AC AAQ81904;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-SEP-1995 (first entry)  
XX  
DE Interferon-gamma binding oligonucleotide 34.  
XX  
KW Interferon gamma; IFN-gamma; inhibition; binding; immunomodulation;  
KW septic shock; rheumatoid arthritis; HIV infection; ss.  
XX  
OS Synthetic.  
XX  
PN WO9500529-A1.  
XX  
PD 05-JAN-1995.  
XX  
PF 17-JUN-1994; 94WO-US006897.  
XX  
PR 18-JUN-1993; 93US-00079677.  
PR 17-MAR-1994; 94US-00210222.  
XX  
PA (PHAR-) PHARMAGENICS INC.  
XX

PI Coppola GR, Beutel BA, Bertelsen AH;  
XX WPI; 1995-051993/07.  
XX Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating,  
PT inhibiting or enhancing the activity or function of interferon-gamma.  
XX  
XX Claim 4; Page 32; 43pp; English.  
XX Oligonucleotides which bind to interferon-gamma are useful for  
CC modulating, inhibiting or enhancing the activity or function of the IFN.  
CC Particularly, they are useful for treatment of septic shock, rheumatoid  
CC arthritis and HIV infection. Preferred oligonucleotides are given in  
CC AAQ81894-Q81909 and AAQ81913-Q81932; esp. the oligo- nucleotides comprise  
CC at least one of the sequences AAGUUG, UGANGCUC, GCACCNC, AAQ81903 or  
CC AAQ81904. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 0 T; 1 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
7 GGGTG 3  
  
RESULT 9  
AAX32613  
ID AAX32613 standard; DNA; 10 BP.  
XX AAX32613;  
AC  
XX 23-JUN-1999 (first entry)  
XX Anticancer duplex forming oligonucleotide SEQ ID #13.  
DE  
XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX Synthetic.  
OS  
XX WO9523162-A1.  
PN  
XX 31-AUG-1995.  
PD  
XX 27-FEB-1995; 95WO-US002419.  
PF  
XX 28-FEB-1994; 94US-00202927.  
PR  
XX (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
DR  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 49; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance

XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 10  
AAX32607  
ID AAX32607 standard; DNA; 10 BP.  
XX  
AC AAX32607;  
XX 23-JUN-1999 (first entry)  
XX Anticancer duplex forming oligonucleotide SEQ ID #7.  
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX Synthetic.  
OS  
XX WO9523162-A1.  
PN  
XX 31-AUG-1995.  
PD  
XX 27-FEB-1995; 95WO-US002419.  
PF  
XX 28-FEB-1994; 94US-00202927.  
PR  
XX (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
DR  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 47; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
4 GGGTG 8  
  
RESULT 11  
AAX32622  
ID AAX32622 standard; DNA; 10 BP.  
XX

AC AAX32622;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #22.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 53; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 12  
AAX32611  
ID AAX32611 standard; DNA; 10 BP.  
XX  
AC AAX32611;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #11.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX

XX 28-FEB-1994; 94US-00202927.  
XX  
XX (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 48; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 13  
AAX32625  
ID AAX32625 standard; DNA; 10 BP.  
XX  
AC AAX32625;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #25.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 54; 107pp; English.  
XX

CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db |||||  
6 GGGTG 10

RESULT 14  
AAX32612  
ID AAX32612 standard; DNA; 10 BP.  
XX  
AC AAX32612;  
XX 23-JUN-1999 (first entry)  
XX Anticancer duplex forming oligonucleotide SEQ ID #12.  
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
XX multiple drug resistance; MDR; ss.  
KW Synthetic.  
XX WO9523162-A1.  
XX 31-AUG-1995.  
PF 27-FEB-1995; 95WO-US002419.  
PR 28-FEB-1994; 94US-00202927.  
XX (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX Disclosure; Page 49; 107pp; English.

CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db |||||  
6 GGGTG 10

RESULT 15  
AAX32620  
ID AAX32620 standard; DNA; 10 BP.  
XX  
AC AAX32620;  
XX 23-JUN-1999 (first entry)  
XX Anticancer duplex forming oligonucleotide SEQ ID #20.  
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
XX multiple drug resistance; MDR; ss.  
KW Synthetic.  
XX WO9523162-A1.  
XX 31-AUG-1995.  
PF 27-FEB-1995; 95WO-US002419.  
PR 28-FEB-1994; 94US-00202927.  
XX (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX Disclosure; Page 52; 107pp; English.

CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db |||||  
6 GGGTG 10

RESULT 16  
AAX32624  
ID AAX32624 standard; DNA; 10 BP.  
XX  
AC AAX32624;  
XX 23-JUN-1999 (first entry)  
XX Anticancer duplex forming oligonucleotide SEQ ID #24.  
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
XX multiple drug resistance; MDR; ss.

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 53; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 17  
AAX32623  
ID AAX32623 standard; DNA; 10 BP.  
XX  
AC AAX32623;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #23.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;

KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;

XX WPI; 1995-311501/40.  
DR  
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 53; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 18  
AAX32605  
ID AAX32605 standard; DNA; 10 BP.  
XX  
AC AAX32605;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #5.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 46; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC including some with multiple drug resistance

CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 19  
AAX32626  
ID AAX32626 standard; DNA; 10 BP.  
XX  
AC AAX32626;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #26.  
XX  
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
KW  
XX Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
OS New stable oligo:nucleotide duplex with 3'-steroid gp - including  
XX intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
PT  
XX Disclosure; Page 54; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 20  
AAX32626/c

ID AAX32626 standard; DNA; 10 BP.  
XX  
AC AAX32626;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #26.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
OS New stable oligo:nucleotide duplex with 3'-steroid gp - including  
XX intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
PT  
XX Disclosure; Page 54; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
5 GGGTG 1  
  
RESULT 21  
AAX32621  
ID AAX32621 standard; DNA; 10 BP.  
XX  
AC AAX32621;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #21.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.

XX PF 27-FEB-1995; 95WO-US002419.  
XX PR 28-FEB-1994; 94US-00202927.  
XX PA (MICR-) MICROPROBE CORP.  
XX PA (UYVA ) UNIV YALE.  
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX DR WPI; 1995-311501/40.  
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
XX PT intramolecular duplex with hairpin loop region, having selective  
XX PT cytotoxicity against some tumour cells.  
XX PS Disclosure; Page 52; 107pp; English.  
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
XX CC and which have a steroid structure attached to the 3'-end through a  
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the  
XX CC present sequence has a cholesterol moiety attached by its A-ring to to  
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
XX CC oligonucleotides form stable duplexes at physiological temperature and  
XX CC have selective cytotoxic activity against certain tumour cell lines,  
XX CC including some with multiple drug resistance  
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 22  
AAX32627  
ID AAX32627 standard; DNA; 10 BP.  
XX AC AAX32627;  
XX DT 23-JUN-1999 (first entry)  
XX DE Anticancer duplex forming oligonucleotide SEQ ID #27.  
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
XX KW multiple drug resistance; MDR; ss.  
XX OS Synthetic.  
XX PN WO9523162-A1.  
XX PD 31-AUG-1995.  
XX PF 27-FEB-1995; 95WO-US002419.  
XX PR 28-FEB-1994; 94US-00202927.  
XX PA (MICR-) MICROPROBE CORP.  
XX PA (UYVA ) UNIV YALE.  
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX DR WPI; 1995-311501/40.  
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
XX PT intramolecular duplex with hairpin loop region, having selective  
XX PT cytotoxicity against some tumour cells.  
XX

PS Disclosure; Page 54; 107pp; English.  
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
XX CC and which have a steroid structure attached to the 3'-end through a  
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the  
XX CC present sequence has a cholesterol moiety attached by its A-ring to to  
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
XX CC oligonucleotides form stable duplexes at physiological temperature and  
XX CC have selective cytotoxic activity against certain tumour cell lines,  
XX CC including some with multiple drug resistance  
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
RESULT 23  
AAX32630  
ID AAX32630 standard; DNA; 10 BP.  
XX AC AAX32630;  
XX DT 23-JUN-1999 (first entry)  
XX DE Anticancer duplex forming oligonucleotide SEQ ID #30.  
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
XX KW multiple drug resistance; MDR; ss.  
XX OS Synthetic.  
XX PN WO9523162-A1.  
XX PD 31-AUG-1995.  
XX PF 27-FEB-1995; 95WO-US002419.  
XX PR 28-FEB-1994; 94US-00202927.  
XX PA (MICR-) MICROPROBE CORP.  
XX PA (UYVA ) UNIV YALE.  
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX DR WPI; 1995-311501/40.  
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
XX PT intramolecular duplex with hairpin loop region, having selective  
XX PT cytotoxicity against some tumour cells.  
XX PS Disclosure; Page 56; 107pp; English.  
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
XX CC and which have a steroid structure attached to the 3'-end through a  
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the  
XX CC present sequence has a cholesterol moiety attached by its A-ring to to  
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
XX CC oligonucleotides form stable duplexes at physiological temperature and  
XX CC have selective cytotoxic activity against certain tumour cell lines,  
XX CC including some with multiple drug resistance  
XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;



Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 24  
AAX32628  
ID AAX32628 standard; DNA; 10 BP.  
XX  
AC AAX32628;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #28.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 55; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 25  
AAX32643/c  
ID AAX32643 standard; DNA; 10 BP.  
XX  
AC AAX32643;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #43.

XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 60; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
XX  
Qy 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 26  
AAX32629  
ID AAX32629 standard; DNA; 10 BP.  
XX  
AC AAX32629;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #29.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX DR WPI; 1995-311501/40.  
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX PS Disclosure; Page 55; 107pp; English.  
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 27  
AAX32631  
ID AAX32631 standard; DNA; 10 BP.  
XX  
AC AAX32631;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #31.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYA ) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 56; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance

CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 28  
AAQ96407  
ID AAQ96407 standard; DNA; 10 BP.  
XX  
AC AAQ96407;  
XX  
DT 16-OCT-2003 (revised)  
DT 19-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 2.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 188; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
2 GGGTG 6

```
RESULT 29
AAQ96408
ID AAQ96408 standard; DNA; 10 BP.
XX
XX AAQ96408;
XX
XX 16-OCT-2003 (revised)
DT 19-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 3.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
XX
XX 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU0000063.
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 188; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db |||||
1 GGGTG 5

RESULT 30
AAQ96488
ID AAQ96488 standard; DNA; 10 BP.
XX
XX AAQ96488;
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 83.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
XX
```

```
XX WO9521912-A1.
PN
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 189; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db |||||
4 GGGTG 8

RESULT 31
AAQ96900/c
ID AAQ96900 standard; DNA; 10 BP.
XX
XX AAQ96900;
XX
XX 16-OCT-2003 (revised)
DT 26-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 495.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
```

XX WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or

PT LTR region - can be used in a vaccine to inhibit/reduce productive

PT infection in an individual by a pathogenic strain.

XX Claim 13; Page 194; 301pp; English.

PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or

XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more

CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of

CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune

CC response in humans, and enable the generation of therapeutic, diagnostic

CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to

CC standardise OS field)

XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

Db |||||

6 GGGTG 2

RESULT 32

AAQ96486

ID AAQ96486 standard; DNA; 10 BP.

XX

AC AAQ96486;

XX

DT 16-OCT-2003 (revised)

DT 20-MAR-1996 (first entry)

XX

DE HIV-1 NL4-3 nef gene nucleotide deletion 81.

XX

XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

KW Human immunodeficiency virus 1.

XX

OS W09521912-A1.

PN

XX

PD 17-AUG-1995.

XX

PF 14-FEB-1995; 95WO-AU0000063.

XX

PR 14-FEB-1994; 94AU-00003864.

PR 21-FEB-1994; 94AU-00004002.

PR 23-DEC-1994; 94AU-00000284.

XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX

PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

XX

OS Human immunodeficiency virus 1.

XX

PN W09521912-A1.

XX

PD 17-AUG-1995.

XX

PF 14-FEB-1995; 95WO-AU0000063.

XX

PR 14-FEB-1994; 94AU-00003864.

PR 21-FEB-1994; 94AU-00004002.

PR 23-DEC-1994; 94AU-00000284.

XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX

PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

XX

OS WPI; 1995-293115/38.

XX

PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or

PT LTR region - can be used in a vaccine to inhibit/reduce productive

PT infection in an individual by a pathogenic strain.

XX Claim 13; Page 189; 301pp; English.

PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or

XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more

CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of

CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune

CC response in humans, and enable the generation of therapeutic, diagnostic

CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to

CC standardise OS field)

XX

SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

Db |||||

6 GGGTG 10

RESULT 33

AAQ96896/c

ID AAQ96896 standard; DNA; 10 BP.

XX

AC AAQ96896;

XX

DT 16-OCT-2003 (revised)

DT 26-MAR-1996 (first entry)

XX

DE HIV-1 NL4-3 nef gene nucleotide deletion 491.

XX

XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

OS Human immunodeficiency virus 1.

XX

PN W09521912-A1.

XX

PD 17-AUG-1995.

XX

PF 14-FEB-1995; 95WO-AU0000063.

XX

PR 14-FEB-1994; 94AU-00003864.

PR 21-FEB-1994; 94AU-00004002.

PR 23-DEC-1994; 94AU-00000284.

XX

PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX

PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

XX

OS WPI; 1995-293115/38.

XX

PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or

PT LTR region - can be used in a vaccine to inhibit/reduce productive

PT infection in an individual by a pathogenic strain.

XX Claim 13; Page 194; 301pp; English.

PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or

XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more

CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of

CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune

CC response in humans, and enable the generation of therapeutic, diagnostic

CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to

CC standardise OS field)

XX

SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

Db |||||

10 GGGTG 6

RESULT 34

AAQ96901/c  
ID AAQ96901 standard; DNA; 10 BP.  
XX  
AC AAQ96901;  
XX  
DT 16-OCT-2003 (revised)  
DT 26-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 496.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 194; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGGTG 5  
Db |||||  
5 GGGTG 1  
XX  
RESULT 35  
AAQ96491  
ID AAQ96491 standard; DNA; 10 BP.  
XX  
AC AAQ96491;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 86.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.

XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 GGGTG 5  
Db |||||  
1 GGGTG 5  
XX  
RESULT 36  
AAQ96406  
ID AAQ96406 standard; DNA; 10 BP.  
XX  
AC AAQ96406;  
XX  
DT 16-OCT-2003 (revised)  
DT 24-FEB-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 1.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX Claim 13; Page 188; 301pp; English.  
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
3 GGGTG 7  
  
RESULT 37  
AAQ96490  
ID AAQ96490 standard; DNA; 10 BP.  
XX  
AC AAQ96490;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 85.  
DE  
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW  
XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX Claim 13; Page 189; 301pp; English.  
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
2 GGGTG 6  
  
RESULT 38  
AAQ96487  
ID AAQ96487 standard; DNA; 10 BP.  
XX  
AC AAQ96487;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 82.  
DE  
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
KW  
XX Human immunodeficiency virus 1.  
OS  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX Claim 13; Page 189; 301pp; English.  
PS Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
5 GGGTG 9  
  
RESULT 39  
AAQ96489  
ID AAQ96489 standard; DNA; 10 BP.

```
XX AC AAQ96489;
XX DT 16-OCT-2003 (revised).
XX DT 20-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 84.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
PT Query Match 100.0%; Score 5; DB 2; Length 10;
PT Best Local Similarity 100.0%; Pred. No. 1.4e+06;
PT Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX PS Claim 13; Page 189; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
PT Query Match 100.0%; Score 5; DB 2; Length 10;
PT Best Local Similarity 100.0%; Pred. No. 1.4e+06;
PT Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GGGTG 5
XX DB |||||
XX 3 GGGTG 7
XX RESULT 40
XX AAQ96897/c
XX ID AAQ96897 standard; DNA; 10 BP.
XX AC AAQ96897;
XX DT 16-OCT-2003 (revised)
XX DT 26-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 492.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
```

```
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 194; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
PT Query Match 100.0%; Score 5; DB 2; Length 10;
PT Best Local Similarity 100.0%; Pred. No. 1.4e+06;
PT Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GGGTG 5
XX DB |||||
XX 9 GGGTG 5
XX RESULT 41
XX AAQ96899/c
XX ID AAQ96899 standard; DNA; 10 BP.
XX AC AAQ96899;
XX DT 16-OCT-2003 (revised)
XX DT 26-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 494.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
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PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 194; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
7 GGGTG 3  
  
RESULT 42  
AAQ96898/c  
ID AAQ96898 standard; DNA; 10 BP.  
XX  
AC AAQ96898;  
XX  
DT 16-OCT-2003 (revised)  
DT 26-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 493.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACP-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 194; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
7 GGGTG 3  
  
RESULT 44  
AAQ29364  
ID AAT29364 standard; DNA; 10 BP.  
XX  
AC AAT29364;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JUN-1996 (first entry)  
XX  
DE 5'-primer for mammalian G-protein coupled receptor coding sequences.  
XX  
KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;  
KW characterisation; biological samples; PCR amplification; indexing;  
KW identification; cloning; analysis; genes; genome mapping;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
8 GGGTG 4  
  
RESULT 43  
AAQ88111  
ID AAQ88111 standard; DNA; 10 BP.  
XX  
AC AAQ88111;  
XX  
DT 18-DEC-1995 (first entry)  
XX  
DE PCR primer for selection of water melons with dark green peel.  
XX  
KW Watermelon; Citrullus sp; polymerase chain reaction amplification;  
KW detection; melon peel; colour; ss.  
XX  
OS Synthetic.  
XX  
PN JP07087979-A.  
XX  
PD 04-APR-1995.  
XX  
PF 27-SEP-1993; 93JP-00260415.  
XX  
PR 27-SEP-1993; 93JP-00260415.  
XX  
PA (YASA-) YASAI CHAGYO SHIKENBACHO.  
PA (HAGI-) HAGIWARA NOJO SEISAN KENKYUSHO KK.  
XX  
DR WPI; 1995-166381/22.  
XX  
PT Synthetic oligo:nucleotide used for the selection of water-melon - using  
PT PCR for the selection of water-melon seedlings which will produce fruit  
PT with dark green peel.  
XX  
PS Claim 1; Page 4; 5pp; Japanese.  
XX  
CC Three synthetic oligonucleotides (see AAQ88111-Q88113) are useful for PCR  
CC amplification of DNA from watermelons to identify seeds which will give  
CC rise to watermelons with dark green peel  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
4 GGGTG 8  
  
RESULT 44  
AAT29364  
ID AAT29364 standard; DNA; 10 BP.  
XX  
AC AAT29364;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JUN-1996 (first entry)  
XX  
DE 5'-primer for mammalian G-protein coupled receptor coding sequences.  
XX  
KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;  
KW characterisation; biological samples; PCR amplification; indexing;  
KW identification; cloning; analysis; genes; genome mapping;

KW disease diagnosis; ss.  
XX  
OS Synthetic.  
XX  
PN WO9531574-A1.  
XX  
PD 23-NOV-1995.  
XX  
XX 12-MAY-1995; 95WO-US0006032.  
PF  
XX 16-MAY-1994; 94US-00242887.  
PR  
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
PA  
XX Lopeznieto CE, Nigam SK;  
PI  
XX WPI; 1996-010958/01.  
DR  
XX Characterisation of nucleotide sequences using primer pairs - by PCR  
PT amplification and indexing of amplification prods. w.r.t. primers used  
PT for genome mapping and disease diagnosis.  
XX  
XX Claim 46; Page 55; 72pp; English.  
PS  
XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived  
CC from them, which target mammalian G-protein coupled receptor coding  
CC sequences, together comprise a PCR primer kit. The kit is used in a new  
CC method for the characterisation of nucleic acid sequences obtd. from  
CC mammalian biological samples, which comprises PCR amplification and  
CC indexing of the prods. w.r.t the primer pair that hybridised to its  
CC delineating subsequences. The method may be used in the identification,  
CC cloning and analysis of genes, e.g. in genome mapping, and disease  
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
4 GGGTG 8  
  
RESULT 45  
AAT18613  
ID AAT18613 standard; DNA; 10 BP.  
XX  
AC AAT18613;  
XX  
DT 06-NOV-1996 (first entry)  
XX  
DE Arbitrary 5' oligodecamer DDRT-PCR primer OPA 8.  
XX  
KW Differential display of mRNA; reverse transcription; DDRT-PCR; human;  
KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;  
KW IL-1beta; diagnosis; connective tissue disease; oseteoarthritis;  
KW rheumatoid arthritis; polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN EP705842-A2.  
XX  
PD 10-APR-1996.  
XX  
PF 02-OCT-1995; 95EP-00115510.  
XX  
PR 06-OCT-1994; 94EP-00115751.  
XX  
PA (FARH ) HOECHST AG.  
XX  
PI Bartnik E, Margerie D;

XX WPI; 1996-181045/19.  
DR  
XX  
PT Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
PT antibodies to them.  
XX  
PS Example; Page 15; 31pp; English.  
XX  
CC The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
CC were used along with 4 degenerate 3' oligo dT primers for the  
CC differential display of human chondrocyte mRNA by reverse transcription  
CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
CC clones, which were then searched against DNA databases for homology to  
CC known human genes. The cDNA mols. can be used for the prodn. of gene  
CC specific primers and probes to isolate genes induced by treating (esp.  
CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the  
CC diagnosis of IL-1beta related connective tissue diseases, in partic.  
CC oseteoarthritis or rheumatoid arthritis  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGTG 5  
Db |||||  
6 GGGTG 10  
  
RESULT 46  
AAT18612  
ID AAT18612 standard; DNA; 10 BP.  
XX  
AC AAT18612;  
XX  
DT 06-NOV-1996 (first entry)  
XX  
DE Arbitrary 5' oligodecamer DDRT-PCR primer OPA 7.  
XX  
KW Differential display of mRNA; reverse transcription; DDRT-PCR; human;  
KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;  
KW IL-1beta; diagnosis; connective tissue disease; oseteoarthritis;  
KW rheumatoid arthritis; polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN EP705842-A2.  
XX  
PD 10-APR-1996.  
XX  
PF 02-OCT-1995; 95EP-00115510.  
XX  
PR 06-OCT-1994; 94EP-00115751.  
XX  
PA (FARH ) HOECHST AG.  
XX  
PI Bartnik E, Margerie D;  
XX  
DR WPI; 1996-181045/19.  
XX  
PT Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
PT antibodies to them.  
XX  
PS Example; Page 15; 31pp; English.  
XX  
CC The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
CC were used along with 4 degenerate 3' oligo dT primers for the  
CC differential display of human chondrocyte mRNA by reverse transcription  
CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
CC clones, which were then searched against DNA databases for homology to  
CC known human genes. The cDNA mols. can be used for the prodn. of gene  
CC specific primers and probes to isolate genes induced by treating (esp.  
CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the  
CC diagnosis of IL-1beta related connective tissue diseases, in partic.  
CC oseteoarthritis or rheumatoid arthritis  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

```
CC known human genes. The cDNA mols. can be used for the prodn. of gene
CC specific primers and probes to isolate genes induced by treating (esp.
CC human) chondrocytes with interleukin-beta (IL-1beta), and for the
CC diagnosis of IL-1beta related connective tissue diseases, in partic.
CC oseteoarthritis or rheumatoid arthritis
XX
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
   |||||
Db 6 GGGTG 10

RESULT 47
AAQ99300/c
ID AAQ99300 standard; cDNA; 10 BP.
XX
AC AAQ99300;
XX
DT 06-SEP-1996 (first entry)
XX
DE Multi-drug resistant-1 gene antisense oligonucleotide 1114.
XX
KW Antisense oligonucleotide; nucleotides 1712-1721 and 3642-3656;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.
XX
OS Synthetic.
XX
PN WO9602556-A2.
XX
PD 01-FEB-1996.
XX
PF 18-JUL-1995; 95WO-US009011.
XX
PR 18-JUL-1994; 94US-00276567.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Smyth AP;
XX
DR WPI; 1996-105848/11.
XX
PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
PT preventing induction of multi:drug resistance or for treating multi:drug
PT resistant cancer cells.
XX
PS Disclosure; Page 14; 43pp; English.
XX
CC The present oligonucleotide is antisense to nucleotides 1712-1721 and
CC 3642-3656 of the multi-drug resistant-1 (MDR-1) gene, which encode the
CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
CC oligonucleotide inhibits the expression of P170, and can therefore be
CC used to treat MDR cancer cells, and prevent the induction of MDR in
CC cancer cells and the expression of P170 in cells
XX
SQ Sequence 10 BP; 1 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
   |||||
Db 5 GGGTG 1

RESULT 48
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```
AAT98860
ID AAT98860 standard; DNA; 10 BP.
XX
AC AAT98860;
XX
DT 20-MAR-1998 (first entry)
XX
DE Core-binding site clone 6-7-1.
XX
KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYVA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 22; 52pp; English.
XX
CC This sequence represents a core-binding site identified using the method
CC of the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
   |||||
Db 3 GGGTG 7

RESULT 49
AAT98837
ID AAT98837 standard; DNA; 10 BP.
XX
AC AAT98837;
XX
DT 20-MAR-1998 (first entry)
XX
DE Binding site BSN7 identified using the method of the invention.
XX
```

KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.  
OS Synthetic.  
XX WO9727330-A1.  
PN  
XX  
XX WO9727330-A1.  
PD  
XX 31-JUL-1997.  
PF 24-JAN-1997; 97WO-US001230.  
XX  
PR 24-JAN-1996; 96US-00590571.  
XX  
PA (UYVA ) UNIV YALE.  
XX Weissman SM, Kulkarni P, Nallur GN;  
PI WPI; 1997-393714/36.  
XX  
DR Identifying protein-binding sites for DNA-binding proteins - using  
XX duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.  
PT  
XX Example 3; Page 19; 52pp; English.  
PS This sequence represents a binding site identified using the method of  
XX the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
2 GGGTG 6  
RESULT 50  
AAT51668  
ID AAT51668 standard; DNA; 10 BP.  
XX  
AC AAT51668;  
XX  
DT 12-NOV-1997 (first entry)  
XX  
DE Viral integrase inhibiting oligonucleotide.  
XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;  
KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;  
KW respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;  
KW integrase inhibition; guanosine tetrad; ss.  
XX  
OS Synthetic.  
XX WO9703997-A1.  
PN  
XX

PD 06-FEB-1997.  
XX  
PF 17-JUL-1996; 96WO-US011786.  
XX  
PR 19-JUL-1995; 95US-0001505P.  
PR 23-OCT-1995; 95US-00535168.  
PR 19-MAR-1996; 96US-0013688P.  
PR 25-MAR-1996; 96US-0014007P.  
PR 17-APR-1996; 96US-0015714P.  
PR 23-APR-1996; 96US-0016271P.  
XX (ARON-) ARONEX PHARM INC.  
PA  
XX Rando RF, Fennewald S, Zendegui JG, Ojwang JO, Hogan ME;  
PI Pommier Y, Mazumder A;  
XX WPI; 1997-132569/12.  
DR  
XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit viral  
PT enzyme responsible for integrating viral nucleic acid into the host  
PT genome.  
XX Claim 3; Page 168; 245pp; English.  
PS AAT51619-T51698 are oligonucleotides used to inhibit the production of  
XX viruses within a host cell. The oligonucleotides may form guanosine  
CC tetrads (structures formed of eight hydrogen bonds by coordination of the  
CC four oxygen atoms of guanine with alkali cations believed to bind to the  
CC centre of a quadruplex, and by strong stacking interactions) and are used  
CC to prevent the integration of viral nucleic acid into a host genome. The  
CC oligonucleotides inhibit functioning of the integrase enzyme and hence  
CC prevent viral infection. Viral infections that may be treated include  
CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes  
CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory  
CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),  
CC especially HIV-1 infection  
XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db |||||  
3 GGGTG 7  
Search completed: January 7, 2005, 07:12:09  
Job time : 258.4 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GGCTG  
Perfect score: 5  
Sequence: 1 gggtg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues 156772

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	10	9	CL437370 PST5215-N
2	5	100.0	10	9	CL439017 PST8527-N
3	5	100.0	11	6	CF323154 HDN--03-B
C 4	5	100.0	12	6	CA851641 D15H12 O2
5	5	100.0	12	9	AJ600145 Arabidops
C 6	5	100.0	13	1	AJ647906 AJ647906
C 7	5	100.0	14	1	AJ655566 AJ655566
C 8	5	100.0	14	5	BQ605961 BRY 1556
9	5	100.0	15	7	L76129 SCMRAP0223
10	5	100.0	15	7	R41075 HK082-f Adu
11	5	100.0	16	1	AA937364 Oj08f10.s
C 12	5	100.0	16	1	AI248882 qu73e07.x
C 13	5	100.0	16	1	AI569544 to28d10.x
C 14	5	100.0	16	1	AI684114 tx79d02.x
C 15	5	100.0	16	1	AI735054 as8b02.x
C 16	5	100.0	16	1	AI741762 wg22f06.x
C 17	5	100.0	16	3	CNS08PR1 Single re
C 18	5	100.0	16	4	BM399085 5009-0-52
C 19	5	100.0	16	6	CF317464 HD--07-C1
C 20	5	100.0	16	9	AJ596548 Arabidops
C 21	5	100.0	17	1	AJ666397 AJ666397
C 22	5	100.0	17	5	BQ589968 S013719-0
C 23	5	100.0	17	9	AJ594891 Arabidops
24	5	100.0	18	4	BM395046 S0072-2-7

25	5	100.0	18	5	BQ594466
26	5	100.0	18	6	CA850820
C 27	5	100.0	18	6	CA853355
C 28	5	100.0	19	1	AA878747
29	5	100.0	19	1	AA909236
30	5	100.0	19	1	AA911671
31	5	100.0	19	1	AI077581
C 32	5	100.0	19	1	AI187072
C 33	5	100.0	19	1	AI364573
C 34	5	100.0	19	1	AI431460
C 35	5	100.0	19	1	AI584018
C 36	5	100.0	19	1	AI758301
37	5	100.0	19	1	AI804310
C 38	5	100.0	19	1	AI807936
C 39	5	100.0	19	1	AJ660078
C 40	5	100.0	19	4	BG925619
41	5	100.0	19	6	CF298891
C 42	5	100.0	19	6	CF334260
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C 44	5	100.0	19	7	CO792214
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58	5	100.0	19	8	AZ379786
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C 66	5	100.0	19	8	AZ447198
C 67	5	100.0	19	8	AZ447936
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74	5	100.0	19	8	AZ485264
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88	5	100.0	19	8	AZ768918
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91	5	100.0	19	8	AZ782026
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93	5	100.0	19	8	AZ787717
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97	5	100.0	19	8	AZ807609

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104	5	100.0	19	8	AZ842166	AZ842166	2M0140G06
105	5	100.0	19	8	AZ954606	AZ954606	2M0220B22
106	5	100.0	19	8	AZ967656	AZ967656	2M0238M09
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c 108	5	100.0	19	9	AJ600584	AJ600584	Arabidops
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c 110	5	100.0	20	4	BG896991	BG896991	HOA59-1-G
c 111	5	100.0	20	4	BG927393	BG927393	HNC1-1-F7
c 112	5	100.0	20	4	BM399070	BM399070	5009-0-52
c 113	5	100.0	20	6	CD533611	CD533611	32L6 Arab
c 114	5	100.0	20	6	CF293092	CF293092	3ODGS--02
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c 118	5	100.0	20	8	AZ308143	AZ308143	1M0010A21
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c 136	5	100.0	20	8	AZ514611	AZ514611	1M0336M20
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c 138	5	100.0	20	8	AZ592635	AZ592635	1M0403M11
139	5	100.0	20	8	AZ601843	AZ601843	1M0420M13
140	5	100.0	20	8	AZ609449	AZ609449	1M0434D20
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144	5	100.0	20	8	AZ652975	AZ652975	1M0526L20
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147	5	100.0	20	8	AZ766582	AZ766582	1M0564G16
c 148	5	100.0	20	8	AZ769146	AZ769146	1M0569C05
149	5	100.0	20	8	AZ769811	AZ769811	1M0570B23
c 150	5	100.0	20	8	AZ774978	AZ774978	2M0004C23
151	5	100.0	20	8	AZ780905	AZ780905	2M0018M12
152	5	100.0	20	8	AZ782314	AZ782314	2M0022D03
153	5	100.0	20	8	AZ784073	AZ784073	2M0026B06
154	5	100.0	20	8	AZ792281	AZ792281	2M0043F09
155	5	100.0	20	8	AZ793982	AZ793982	2M0047I05
c 156	5	100.0	20	8	AZ796123	AZ796123	2M0051O04
157	5	100.0	20	8	AZ797468	AZ797468	2M0053F09
158	5	100.0	20	8	AZ808291	AZ808291	2M0071D09
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c 160	5	100.0	20	8	AZ833695	AZ833695	2M0115N20
161	5	100.0	20	8	AZ836147	AZ836147	2M0130O14
162	5	100.0	20	8	AZ846316	AZ846316	2M0146N24
163	5	100.0	20	8	AZ846437	AZ846437	2M0146E10
164	5	100.0	20	8	AZ853944	AZ853944	2M0157B21
165	5	100.0	20	8	AZ948873	AZ948873	2M0212P02
c 166	5	100.0	20	8	AZ995803	AZ995803	2M0281G14
167	5	100.0	20	9	AJ587163	AJ587163	Arabidops
168	5	100.0	20	9	AG188183	AG188183	Pan trogl
169	5	100.0	20	9	AG197313	AG197313	Pan trogl
170	5	100.0	21	1	AU257028	AU257028	AU257028

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c 173	5	100.0	21	6	CD533377	CD533377	31H19 Ara
c 174	5	100.0	21	7	CO779017	CO779017	BL005B_G0
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c 177	5	100.0	21	8	AZ341842	AZ341842	1M0074F05
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181	5	100.0	21	8	AZ399828	AZ399828	1M0165A23
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c 187	5	100.0	21	8	AZ445481	AZ445481	1M0241P15
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212	5	100.0	21	8	AZ788269	AZ788269	2M0035D18
213	5	100.0	21	8	AZ788597	AZ788597	2M0035B19
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c 215	5	100.0	21	8	AZ812415	AZ812415	2M0079N04
c 216	5	100.0	21	8	AZ816100	AZ816100	2M0084M11
c 217	5	100.0	21	8	AZ819244	AZ819244	2M0089F14
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c 219	5	100.0	21	8	AZ830720	AZ830720	2M0110D12
220	5	100.0	21	8	AZ834643	AZ834643	2M0117N24
221	5	100.0	21	8	AZ864022	AZ864022	2M0173G22
222	5	100.0	21	8	AZ875300	AZ875300	2M0189D22
223	5	100.0	21	8	AZ978432	AZ978432	2M0254G15
224	5	100.0	21	8	AZ995847	AZ995847	2M0281N16
225	5	100.0	21	8	AZ997000	AZ997000	2M0283D24
226	5	100.0	21	9	AJ590147	AJ590147	Arabidops
227	5	100.0	21	9	CL669293	CL669293	PRI015a_B
228	5	100.0	21	9	AG190803	AG190803	Pan trogl
229	5	100.0	21	9	AG201733	AG201733	Pan trogl
c 230	5	100.0	21	9	AG202462	AG202462	Pan trogl
c 231	5	100.0	21	9	AG203513	AG203513	Pan trogl
232	5	100.0	22	1	AA908627	AA908627	og86e01.s
233	5	100.0	22	1	AA931331	AA931331	OO06C03.s
234	5	100.0	22	1	AA936651	AA936651	ol87b12.s
235	5	100.0	22	1	AA938474	AA938474	OO56h02.s
236	5	100.0	22	1	AA973612	AA973612	OO47f01.s
c 237	5	100.0	22	1	AA978171	AA978171	ny36f08.s
238	5	100.0	22	1	AA982956	AA982956	ua23g03.r
239	5	100.0	22	1	AI000026	AI000026	Ot03d12.s
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C 246	5	100.0	22	1	AI371446	AI371446	qy06b02.x
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ALIGNMENTS

RESULT 1	CL437370/c	10 bp	DNA	linear	GSS 18-MAR-2004
LOCUS	CL437370				
DEFINITION	PST5215-NR.Seq MICB1 Mus musculus genomic clone PST5215-NR.Seq similar to Q8C075, genomic survey sequence.				
ACCESSION	CL437370				
VERSION	CL437370.1				GI:45573022
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 10)				
TITLE	Hicks,G.G.				
JOURNAL	www.EScells.ca				
COMMENT	Unpublished (2002)				
	Contact: Hicks GG				
	Mammalian Functional Genomics Centre				
	Manitoba Institute of Cell Biology, University of Manitoba				
	ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada				
	Tel: 204 787 2133				
	Fax: 204 787 2190				
	Email: hicksgg@cc.umanitoba.ca				
	U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from				
	http://140.193.242.7/esdb/public_search_frame.php?PST=PST5215-NR.Seq				
	q				
	Class: Gene Trap.				



**TITLE** Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

**JOURNAL** Unpublished (2002)

**COMMENT** Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
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Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@ba.ars.usda.gov.

**FEATURES**

source

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**ORIGIN**

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Db 9 GGGTG 5

**RESULT 5**  
AJ600145

**LOCUS** AJ600145.1 GI:37949773 12 bp DNA linear GSS 15-JAN-2004

**DEFINITION** Arabidopsis thaliana T-DNA flanking sequence, right border, clone 501A06, genomic survey sequence.

**ACCESSION** AJ600145

**VERSION** AJ600145.1 GI:37949773

**KEYWORDS** GSS; right border; T-DNA flanking sequence.

**SOURCE** Arabidopsis thaliana (chale cress)

**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

**REFERENCE** 1  
**AUTHORS** Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

**TITLE** Arabidopsis thaliana T-DNA flanking sequence

**JOURNAL** EMBO Rep. 3 (12), 1152-1157 (2002)

**MEDLINE** 22363535

**PUBMED** 12446565

**REFERENCE** 2 (bases 1 to 12)  
**AUTHORS** Balzergue, S.  
**TITLE** Direct Submision  
**JOURNAL** Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

**COMMENT** PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

**FEATURES**

Location/Qualifiers

source

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**ORIGIN**

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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||

Db 7 GGGTG 11

**RESULT 6**  
AJ647906/c

**LOCUS** AJ647906 CSEQAN19 Sus scrofa cDNA clone C0003263\_A12, mRNA

**DEFINITION** AJ647906 CSEQAN19 Sus scrofa cDNA clone C0003263\_A12, mRNA sequence.

**ACCESSION** AJ647906

**VERSION** AJ647906.1 GI:49324751

**KEYWORDS** EST.

**SOURCE** Sus scrofa (pig)

**ORGANISM** Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

**REFERENCE** 1 (bases 1 to 13)  
**AUTHORS** Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
**TITLE** Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector: pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5' Seg Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, [www.ark-genomics.org](http://www.ark-genomics.org).

**FEATURES**

source

1. .13  
Location/Qualifiers

1. .13  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0003263\_A12"  
/tissue\_type="ovary"  
/clone\_lib="CSEQAN19"  
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"

**ORIGIN**

Query Match 100.0%; Score 5; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||

Db 11 GGGTG 7

**RESULT 7**  
AJ655566/c

LOCUS AJ655566 14 bp mRNA linear EST 28-JUN-2004  
 DEFINITION AJ655566 KN277 Sus scrofa cDNA clone C0005190\_P15, mRNA sequence.  
 ACCESSION AJ655566  
 VERSION AJ655566.1 GI:49339598  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 14)  
 REFERENCE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
 AUTHORS Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
 TITLE Unpublished (2004)  
 JOURNAL Contact: Anderson SI  
 COMMENT Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES  
 source Location/Qualifiers  
 1. .14  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C0005190\_P15"  
 /tissue\_type="embryo"  
 /clone\_lib="KN277"  
 /notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site\_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."  
 ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
 |||||  
 Db 9 GGGTG 5

RESULT 8  
 BQ605961/c  
 LOCUS BQ605961 14 bp mRNA linear EST 25-JUN-2002  
 DEFINITION BRY\_1556 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence.  
 ACCESSION BQ605961  
 VERSION BQ605961.1 GI:21555112  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
 1 (bases 1 to 14)

REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.  
 AUTHORS Arabidopsis genomic information for interpreting wheat EST sequences  
 TITLE Arabidopsis Integr. Genomics 3 (1-2), 33-38 (2003)  
 JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
 MEDLINE 22478026  
 PUBMED 12590341  
 COMMENT Contact: Lambrecht M  
 The Arabidopsis Information Resource  
 Carnegie Institution of Washington, Dept. of Plant Biology  
 260 Panama Street, Stanford, CA 94305, USA

Tel: 1 650 325 1521 x 251  
 Fax: 1 650 325 3748  
 Email: rheee@acoma.stanford.edu.  
 Location/Qualifiers  
 1. .14  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Wyuna"  
 /db\_xref="taxon:4565"  
 /tissue\_type="endosperm"  
 /dev\_stage="developing endosperm tissue 8, 10 and 12 DPA (days post anthesis)"  
 /clone\_lib="wheat EST endosperm library"  
 ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
 |||||  
 Db 8 GGGTG 4

RESULT 9  
 L76129  
 LOCUS L76129 15 bp mRNA linear EST 21-FEB-1996  
 DEFINITION SCMRAP0223 G2/KS adult worm mini-library Schistosoma mansoni cDNA clone SMRAP0223, mRNA sequence.  
 ACCESSION L76129  
 VERSION L76129.1 GI:1196867  
 KEYWORDS EST.  
 SOURCE Schistosoma mansoni  
 ORGANISM Schistosoma mansoni  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.  
 1 (bases 1 to 15)

REFERENCE Neto,E.D., Harrop,R, Correa-Oliveira,R, Wilson,R.A., Pena,S.D. and Simpson,A.J.G.  
 AUTHORS Minilibraries constructed from cDNA generated by arbitrarily primed RT-PCR: an alternative to normalized libraries for the generation of ESTs from nanogram quantities of mRNA  
 JOURNAL Gene 186 (1), 135-142 (1997)  
 MEDLINE 97199380  
 PUBMED 9047356  
 COMMENT Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A., Pena,S.D. and Simpson,A.J.G.  
 Location/Qualifiers  
 1. .15  
 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6183"  
 /clone="SMRAP0223"  
 /clone\_lib="G2/KS adult worm mini-library"  
 /note="A mini-library was made by cloning products derived from RNA-arbitrarily primed PCR (RAP PCR) profiles into the pUC 18 vector. Reverse transcription of adult worm mRNA was primed with G2and subsequent PCR amplification was performed in the presence of primer KS"

ORIGIN  
 Query Match 100.0%; Score 5; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
 |||||  
 Db 3 GGGTG 7

RESULT 10  
 R41075  
 LOCUS R41075 15 bp mRNA linear EST 16-MAY-1995

DEFINITION HK082-f Adult heart, Clontech Homo sapiens cDNA clone k082-f, mRNA sequence.  
ACCESSION R41075  
VERSION R41075.1 GI:798691  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Lui,V.W.Y., Luk,S.C.W., Tsui,S.K.W., Tung,C.K.C., Yam,N.Y.H., Liew,C.C. and Lee,C.Y.  
TITLE Gene expression of adult human heart as revealed by random sequencing of cDNA library  
JOURNAL Miami Winter Biotechnol. Symp. Proc. 6, 90 (1995)  
COMMENT Contact: Wayne Mary M.Y.  
Department of Biochemistry  
The Chinese University of Hong Kong  
Rm 302C, Basic Medical Science Building, The Chinese University of Hong Kong, Shatin, N.T., Hong Kong.  
Tel: 8526096874  
Fax: 8526035123  
Email: bl33723@vax.csc.cuhk.hk  
Seq primer: GGTGGCAGCAGCTCTGGAGCC.  
Location/Qualifiers  
FEATURES  
source  
1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="k082-f"  
/lab\_host="E. coli Y1090"  
/clone\_lib="Adult heart, Clontech"  
/note="Vector: Lambda gt11; Site\_1: EcoRI; Site\_2: EcoRI"  
ORIGIN  
Query Match 100.0%; Score 5; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
|||||  
Db 1 GGGTG 5  
RESULT 11  
AA937364  
LOCUS  
DEFINITION oJ08f10.s1 NCI CGAP\_Mel3 Homo sapiens cDNA clone IMAGE:1491595 3' similar to SW:ACRO\_RABIT P48038 ACROSIN PRECURSOR ;contains MSRI.b2 MSRI repetitive element ;, mRNA sequence.  
ACCESSION AA937364  
VERSION AA937364.1 GI:3095475  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Insert Length: 1265 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
FEATURES  
source  
1. .16  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1491595"  
/tissue\_type="metastatic melanoma to bowel"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Mel3"  
/note="Organ: bowel (skin primary); Vector: pCMV-SPORT4; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 0.9 kb. Life Technologies catalog #: 10981-017"  
ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10  
RESULT 12  
AI248882/c  
LOCUS  
DEFINITION AI248882 qu73e07.x1 NCI CGAP\_Brn35 Homo sapiens cDNA clone IMAGE:1977732 3' similar to SW:CAL3\_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;, mRNA sequence.  
ACCESSION AI248882  
VERSION AI248882.1 GI:3844279  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Insert Length: 1913 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
FEATURES  
source  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1977732"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Brn35"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.33 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV). Life Technologies catalog #: 11544-012"  
ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
|||||  
Db 10 GGGTG 6

RESULT 13  
AI569544/c  
LOCUS  
DEFINITION  
AI569544 16 bp mRNA linear EST 12-MAY-1999  
similar to TR:Q18444 Q18444 COSMID C34D4. ; contains MSRI.b2 MSRI  
repetitive element ;, mRNA sequence.

ACCESSION  
AI569544  
VERSION  
AI569544.1 GI:4532918  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1683 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source  
Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2180371"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 16 GGGTG 12

RESULT 14  
AI684114/c  
LOCUS  
DEFINITION  
AI684114 16 bp mRNA linear EST 16-DEC-1999  
similar to TR:Q09084 Q09084 EXTENSIN CLASS II PRECURSOR ;, mRNA  
sequence.

ACCESSION  
AI684114  
VERSION  
AI684114.1 GI:4895408  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE

AUTHORS  
TITLE  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1454 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2275779"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 15  
AI735054/c  
LOCUS  
DEFINITION  
AI735054 16 bp mRNA linear EST 14-JUN-1999  
as88b02.x1 Barstead colon HPLRB7 Homo sapiens CDNA clone  
IMAGE:2335755 3' similar to WP:T28C6.1 CE03746 ; contains MSRI.b2  
MSRI repetitive element ;, mRNA sequence.

ACCESSION  
AI735054  
VERSION  
AI735054.1 GI:5056653  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE  
AUTHORS  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality



Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2335755"  
/sex="male"  
/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCACCTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 13 GGGTG 9

RESULT 16

AI741762/c  
LOCUS  
DEFINITION  
AI741762 16 bp mRNA linear EST 19-DEC-1999  
IMAGE:2365859 3' similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH  
PROTEIN RP15 PRECURSOR. ;contains PTR5.b3 MSRI MSRI repetitive  
element ;, mRNA sequence.  
AI741762  
AI741762.1 GI:5110050  
EST.  
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert length: 630 Std Error: 0.00  
Seg primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES

Source  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2365859"  
/lab\_host="DH10B"  
/clone\_lib="Soares NSF P8 9W OT PA P S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from five normalized  
libraries were mixed, and ss circles were made in vitro.  
Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was  
PCR-amplified cDNAs from pools of 5,000 clones made from  
the same 5 libraries. The pools consisted of the following  
libraries and cloneIDs: Soares NbHSP pool 1:  
309384-310919, 323208-325895 Soares Nb2HP pool 1:  
145032-147335, 147720-148103, 148872-149255, 15002 -  
150407, 151176-152327 Soares Nb2HP8-9W pool 1:  
758280-760583, 772104-774407 Soares NbHPA pool 1:  
304776-306311, 320136-322823, 326280-326663 Soares NbHOT  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 17

CNS08PR1/c  
LOCUS  
DEFINITION  
CNS08PR1 16 bp mRNA linear HTC 07-JAN-2003  
Single read from an extremity of a full-length cDNA clone made from  
Anopheles gambiae total adult females. 3-PRIME end of clone  
FK0AAA34DD10 of strain 6-9 of Anopheles gambiae (African malaria  
mosquito).  
BX022793  
BX022793.1 GI:27572013  
HTC.

ACCESSION

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Anopheles.  
1 (bases 1 to 16)  
Genoscope.  
Direct Submission  
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

FEATURES

source  
1. .16  
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/mol\_type="mRNA"  
/strain="6-9"  
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/clone="FK0AAA34DD10"  
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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 18

BM399085  
LOCUS  
DEFINITION  
BM399085 16 bp mRNA linear EST 17-JAN-2002  
5009-0-52-G11.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Tetrahymena thermophila



```

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 16)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..16
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
|||||
Db 11 GGGTG 15

RESULT 19
CF317464/c
LOCUS
DEFINITION
HD--07-C19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-C19, mRNA sequence.
CF317464
CF317464.1 GI:33689225
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-C19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 16)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..16
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
|||||
Db 11 GGGTG 15

RESULT 19
CF317464/c
LOCUS
DEFINITION
HD--07-C19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-C19, mRNA sequence.
CF317464
CF317464.1 GI:33689225
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-C19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid

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CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
|||||
Db 15 GGGTG 11

RESULT 20
AJ596548
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
435H06, genomic survey sequence.
AJ596548
AJ596548.1 GI:37946176
VERSION
GSS; left border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
PUBMED
12446565
2 (bases 1 to 16)
Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1..16
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="435H06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..16
/note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

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Db 10 GGGTG 14

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RESULT 21  
AJ666397/c

LOCUS AJ666397 17 bp mRNA linear EST 28-JUN-2004

DEFINITION AJ666397 CSEQRAN09 Sus scrofa cDNA clone C000033\_K10, mRNA sequence.

ACCESSION AJ666397

VERSION AJ666397.1 GI:49350848

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 17)

REFERENCE Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

AUTHORS Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

TITLE Unpublished (2004)

JOURNAL Contact: Anderson SI

COMMENT Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source Location/Qualifiers

1. .17

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone="C000033\_K10"

/tissue\_type="placenta"

/clone\_lib="CSEQRAN09"

/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

|||||

Db 7 GGGTG 3

RESULT 22  
BQ589968/c

LOCUS BQ589968 17 bp mRNA linear EST 06-DEC-2002

DEFINITION S013719-024-019-B24-T7 MP12-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-B24 3-PRIME, mRNA sequence.

ACCESSION BQ589968

VERSION BQ589968.1 GI:26119551

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta. 1 (bases 1 to 17)

REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

AUTHORS Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

TITLE

JOURNAL

COMMENT

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 19 row: B column: 24

Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES

source Location/Qualifiers

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/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:190150"

/db\_xref="taxon:161934"

/clone="024-019-B24"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5

|||||

Db 7 GGGTG 3

RESULT 23  
AJ594891/c

LOCUS AJ594891 17 bp DNA linear GSS 15-JAN-2004

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 407D12, genomic survey sequence.

ACCESSION AJ594891

VERSION AJ594891.1 GI:37944515

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1

REFERENCE Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.

AUTHORS T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

TITLE EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL 22363535

MEDLINE 12446565

PUBMED 2 (bases 1 to 17)

REFERENCE Balzergue,S.

AUTHORS Direct Submission

TITLE Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

JOURNAL PCR was performed on DNA from transformants of Arabidopsis thaliana

COMMENT

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
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/organism="Arabidopsis thaliana"  
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/db\_xref="taxon:3702"  
/clone="407D12"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
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/note="T-DNA flanking sequence  
left border"

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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 14 GGGTG 10

RESULT 24  
BM395046  
LOCUS  
DEFINITION  
50072-2-7-C05.f.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
BM395046  
VERSION  
BM395046.1 GI:18195099  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 18)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
TITLE  
Molecular Genetics and Cell Biology  
JOURNAL  
University of Chicago  
COMMENT  
Contact: Turkewitz AP  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
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/organism="Tetrahymena thermophila"  
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preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Query Match 100.0%; Score 5; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
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Db 9 GGGTG 13  
RESULT 25  
BQ594466  
LOCUS  
DEFINITION  
E012442-024-024-I18-SP6 MPI2-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-024-I18 5-PRIME, mRNA sequence.  
ACCESSION  
BQ594466  
VERSION  
BQ594466.1 GI:26124049  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL  
Plant J. 32 (5), 845-857 (2002)  
MEDLINE  
22362189  
PUBMED  
12472698  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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Seq primer: SP6; CATACGATTTAGTGACACTATAG.

FEATURES  
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line)"  
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/db\_xref="taxon:161934"  
/clone="024-024-I18"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 10 GGGTG 14

RESULT 26  
CA850820  
LOCUS  
DEFINITION  
D06H05\_H05\_15.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max

ACCESSION CA850820  
VERSION CA850820.1 GI:33387613  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@ba.ars.usda.gov.

FEATURES  
source  
1. .18  
/organism="Glycine max"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3847"  
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/dev\_stage="Seedlings"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 7 GGGTG 11

RESULT 27  
CA853355/c  
LOCUS B07C12.5', mRNA sequence.  
DEFINITION CA853355 18 bp mRNA linear EST 01-AUG-2003  
ACCESSION CA853355  
VERSION CA853355.1 GI:33390148  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
JOURNAL Unpublished (2002)  
COMMENT Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharon@ba.ars.usda.gov.

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="B07C12"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 12hr SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA  
extracted from roots of soybean cv. Peking 12 hrs after  
infection by SCN race 3. These are cloned in pBluescript  
SK- phagemid."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 12 GGGTG 8

RESULT 28  
AA878747/c  
LOCUS AA878747 19 bp mRNA linear EST 25-MAR-1998  
DEFINITION of85b01.81 NCI CGAP Li5 Homo sapiens cDNA clone IMAGE:1437097 3',  
similar to TR:Q26739 Q26739 CYTOCHROME C OXIDASE III ;contains  
element MSRL repetitive element ;, mRNA sequence.  
ACCESSION AA878747  
VERSION AA878747.1 GI:2987712  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1437097"  
/tissue\_type="hepatic adenoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP\_Li5"  
/note="Organ: liver; Vector: pCMV-SPORT4; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 0.8 kb."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 9 GGGTG 5

RESULT 29

AA909236  
LOCUS  
DEFINITION  
AA909236 19 bp mRNA linear EST 09-JUN-1998  
ol08all.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1522844 3' similar to SW:EXTN\_DAUCA P06599 EXTENSIN  
PRECURSOR. ; mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 347 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1522844"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI-CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "  
ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 1 GGGTG 5  
RESULT 30  
AA911671  
LOCUS  
DEFINITION  
AA911671 19 bp mRNA linear EST 10-JUN-1998  
ol49f08.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1526823 3' similar to TR:Q18444 Q18444 COSMID C34D4.  
; contains MSR1.b2 MSR1 repetitive element ; mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 897 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1666926"  
/tissue\_type="senescent fibroblast"

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 682 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1526823"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NbHL19W, testis NHT, and B-cell  
NCI-CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "  
ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
|||||  
Db 10 GGGTG 14  
RESULT 31  
AI077581  
LOCUS  
DEFINITION  
AI077581 19 bp mRNA linear EST 24-SEP-1998  
oy26a04.s1 Soares\_senescent\_fibroblasts\_NbHSF\_Homo\_sapiens\_CDNA  
clone IMAGE:1666926 3' similar to SW:PP31\_HUMAN P48556 26S  
PROTEASOME REGULATORY SUBUNIT P31. ; mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AI077581 GI:3411989  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 897 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1666926"  
/tissue\_type="senescent fibroblast"

/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares senescent fibroblasts\_NbHSF"  
/note="Vector: pT7T3D (Pharmacia) with a modified  
polylinker V\_TYPE: phagemid; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5',  
TGTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 9 GGGTG 13

RESULT 32

AI187072/c

LOCUS

DEFINITION

AI187072 19 bp mRNA linear EST 29-OCT-1998  
qe38a01.s1 Soares fetal\_lung NbHL19W Homo sapiens cDNA clone  
IMAGE:1741224 3' similar to TR:Q07912 Q07912 TYROSINE-PROTEIN  
KINASE ACK ;contains TAR1.t1 MSRI repetitive element ;, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 2024 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1741224"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal\_lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NbHL19W."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 15 GGGTG 11

RESULT 33

AI364573/c

LOCUS

DEFINITION

AI364573 19 bp mRNA linear EST 15-FEB-1999  
qw37903.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:1993300 3'  
similar to TR:Q39835 Q39835 EXTENSIN. ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1632 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1993300"

/tissue\_type="serous papillary carcinoma, high grade, 2

pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut4"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;

Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.48 kb. Life Technologies catalog #:

11542-016"

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 10 GGGTG 6

RESULT 34

AI431460/c

LOCUS

DEFINITION

AI431460 19 bp mRNA linear EST 13-APR-1999  
th40c01.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2120736 3'  
similar to TR:Q04117 Q04117 SALIVARY PROLINE-RICH PROTEIN RP4  
PRECURSOR. ;contains element MSRI repetitive element ;, mRNA



sequence.  
ACCESSION AI431460  
VERSION AI431460.1 GI:4303341  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Life Technologies catalog #: 11547-015  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 653 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
FEATURES  
source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2120736"  
/tissue\_type="lymphoma, follicular mixed small and large cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lym12"  
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;  
QY 1 GGGTG 5  
|||||  
Db 16 GGGTG 12

RESULT 35  
AI584018/c  
LOCUS AI584018 19 bp mRNA linear EST 14-DEC-1999  
DEFINITION ts12e10.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2228394 3', similar to SW:PRPL\_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO ;, mRNA sequence.

ACCESSION AI584018  
VERSION AI584018.1 GI:4569915  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 3996 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2228394"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;  
QY 1 GGGTG 5  
|||||  
Db 9 GGGTG 5

RESULT 36  
AI758301/c  
LOCUS AI758301 19 bp mRNA linear EST 16-DEC-1999  
DEFINITION ty06a07.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278260 3', similar to SW:SP49\_HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49 ;contains MSR1.b2 MSR1 repetitive element ;, mRNA sequence.

ACCESSION AI758301  
VERSION AI758301.1 GI:5152024  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1803 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
FEATURES  
source  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2278260"  
/tissue\_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"



```

/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut3"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GGGTG 5
        |||||
Db      6 GGGTG 2

```

## RESULT 37

```

AI804310
LOCUS      tc69g08.x1 Soares NhMPu S1 Homo sapiens cDNA clone IMAGE:2069918
DEFINITION 3', similar to SW:AAC3_HUMAN Q08043 ALPHA-ACTININ 3, SKELETAL MUSCLE
            ISOFORM ; contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION  AI804310
VERSION     AI804310.1 GI:5369782
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            TRACE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 766 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES    Location/Qualifiers
             1..19
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2069918"
                /tissue_type="Pooled human melanocyte, fetal heart, and
                pregnant uterus"
                /lab_host="DH10B"
                /clone_lib="Soares NhMPu S1"
                /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                (Pharmacia) with a modified polylinker; Site 1: Not I;
                Site 2: Eco RI; Equal amounts of plasmid DNA from three
                normalized libraries (melanocyte 2NBHM, pregnant uterus
                NhMPU, and fetal heart NbHL19W) were mixed, and ss circles
                were made in vitro. Following HAP purification, this DNA
                was used as tracer in a subtractive hybridization
                reaction. The driver was PCR-amplified cDNAs from pools of
                5,000 clones made from the same 3 libraries. The pools
                consisted of I.M.A.G.E. clones 260232-265223,
                340488-345479, and 484488-489479."

```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GGGTG 5
        |||||
Db      1 GGGTG 5

```

## RESULT 38

```

AI807936/c
LOCUS      AI807936      19 bp      mRNA      linear      EST 19-DEC-1999
DEFINITION w52e09.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
            IMAGE:2359240 3', similar to TR:Q39600 Q39600 EXTENSIN. ; contains
            element MSR1 repetitive element ;, mRNA sequence.
ACCESSION  AI807936
VERSION     AI807936.1 GI:5394502
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 724 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES    Location/Qualifiers
             1..19
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2359240"
                /lab_host="DH10B"
                /clone_lib="Soares NFL T GBC_S1"
                /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                a modified polylinker; Site 1: Not I; Site 2: Eco RI;
                Equal amounts of plasmid DNA from three normalized
                libraries (fetal lung NbHL19W, testis NHT, and B-cell
                NCI_CGAP_GCB1) were mixed, and ss circles were made in
                vitro. Following HAP purification, this DNA was used as
                tracer in a subtractive hybridization reaction. The driver
                was PCR-amplified cDNAs from pools of 5,000 clones made
                from the same 3 libraries. The pools consisted of
                I.M.A.G.E. clones 297480-302087, 682632-687239,
                726408-728711, and 729096-731399. Subtraction by Bento
                Soares and M. Fatima Bonaldo."

```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 GGGTG 5
        |||||
Db      16 GGGTG 12

```

## RESULT 39

```

AJ660078/c
LOCUS      AJ660078      19 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ660078 KN277 Sus scrofa cDNA clone C0005218_I04, mRNA sequence.
ACCESSION  AJ660078
VERSION     AJ660078.1 GI:49344223
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
            Development of cDNA and EST resources for studying reproduction and
            TITLE

```



```
VERSION      CF334260.1  GI:33816853
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
             1..19
             /organism="Oryza sativa (japonica cultivar-group)"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:39947"
             /clone="JMT--03-H18"
             /tissue_type="leaf"
             /dev_stage="14 days after germination"
             /lab_host="E.coli DH10B"
             /clone_lib="AtJMT-overexpressing transgenic rice plasmid
             cDNA library (JMT)"
             /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
             was reverse transcribed and then used for PCR. mRNA was
             prepared from Arabidopsis Jasmoinate Carboxyl
             methyltransferase overexpression line."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
    |||||
Db 17 GGGTG 13

RESULT 43
CF542982
LOCUS      CF542982
DEFINITION S014680w-024-030-P12-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
clone 024-030-P12 5-PRIME, mRNA sequence.
ACCESSION  CF542982
VERSION     CF542982.1  GI:34891422
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE    12472698
PUBMED
COMMENT    Contact: Weisshaar B
             ADIS DNA core facility at MP1Z
             Max-Planck-Institute for Plant Breeding Research
             Carl-von-Linne Weg 10, 50829 Koeln, Germany
             Fax: 00492215062851

Query Match      100.0%; Score 5; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
    |||||
Db 17 GGGTG 13

RESULT 44
CO792214/c
LOCUS      CO792214
DEFINITION NT014C A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
similar to hypothetical protein, mRNA sequence.
ACCESSION  CO792214
VERSION     CO792214.1  GI:51008185
KEYWORDS   EST.
SOURCE     Ambystoma mexicanum (axolotl)
ORGANISM   Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 19)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfotenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT014C row: 10 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES     Location/Qualifiers
             1..19
             /organism="Ambystoma mexicanum"
             /mol_type="mRNA"
             /db_xref="taxon:8296"
             /tissue_type="Neural Tube, Notochord, Somites"
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 30 row: P column: 12
Seq primer: SP6.
Location/Qualifiers
1..19
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:936786"
/db_xref="taxon:161934"
/clone="024-030-P12"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
    |||||
Db 11 GGGTG 15

RESULT 44
CO792214/c
LOCUS      CO792214
DEFINITION NT014C A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
similar to hypothetical protein, mRNA sequence.
ACCESSION  CO792214
VERSION     CO792214.1  GI:51008185
KEYWORDS   EST.
SOURCE     Ambystoma mexicanum (axolotl)
ORGANISM   Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 19)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfotenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT014C row: 10 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES     Location/Qualifiers
             1..19
             /organism="Ambystoma mexicanum"
             /mol_type="mRNA"
             /db_xref="taxon:8296"
             /tissue_type="Neural Tube, Notochord, Somites"
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/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/note="vector: pCMVSPORT6; Site\_1: NotI; Site\_2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was polydT primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
EMDH108-TONA. Average insert size is 1.5 kb.  
TAG\_LIB=NT"

ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 17 GGGTG 13

RESULT 45

AZ314511  
LOCUS  
DEFINITION  
1M0031B20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0031B20 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ314511.1 GI:10360474  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

REFERENCE

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: B column: 20  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0031B20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 1 GGGTG 5

RESULT 46

AZ324865  
LOCUS  
DEFINITION  
1M0047G10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0047G10 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ324865.1 GI:10381216  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

REFERENCE

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0047 row: G column: 10  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0047G10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 4 GGGTG 8

RESULT 47  
AZ330741/c

LOCUS AZ330741 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0056G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056G11 F, genomic survey sequence.

ACCESSION AZ330741  
VERSION AZ330741.1 GI:10392745  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0056 row: G column: 11  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.  
Location/Qualifiers

FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0056G11"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 48  
AZ341989/c

LOCUS AZ341989 19 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0074H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0074H13 R, genomic survey sequence.

ACCESSION AZ341989  
VERSION AZ341989.1 GI:10418787  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0074 row: H column: 13  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 19.  
Location/Qualifiers

FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0074H13"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 11 GGGTG 7

RESULT 49  
AZ343228  
LOCUS  
DEFINITION  
1M0076M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0076M05 R, genomic survey sequence.  
ACCESSION  
AZ343228  
VERSION  
AZ343228.1 GI:10421448  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: M column: 05  
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Class: plasmid ends  
High quality sequence stop: 19.

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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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Db 1 GGGTG 5

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VERSION  
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GSS.  
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AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
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Niederhausern,A. and Wright,D.,Weiss,R.  
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Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0077 row: G column: 21  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
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Db 6 GGGTG 2

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Job time : 2234.4 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GGGTG  
Perfect score: 5  
Sequence: 1 gggtg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 7, Application US/09263790  
; Patent No. PP12997  
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; APPLICANT: Nirmal Kumar PATRA et al.  
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOGON WINTERIANUS  
; FILE REFERENCE: 2761-0120P  
; CURRENT APPLICATION NUMBER: US/09/263,790  
; CURRENT FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 38  
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; SEQ ID NO 7  
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; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.  
US-09-263-790-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: OPT 09 Primer - Used to develop the unique RAPD profiles of the
; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-29
```

```
Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGTG 5
        |||||
Db       5 GGGTG 1
```

## RESULT 3

```
US-09-263-790-31
; Sequence 31, Application US/09263790
; Patent No. PP12997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: OPT 12 Primer - Used to develop the unique RAPD profiles of the
; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-31
```

```
Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGTG 5
        |||||
Db       1 GGGTG 5
```

## RESULT 4

```
US-09-721-777-9/c
; Sequence 9, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
```

```
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-9
```

```
Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGTG 5
        |||||
Db       5 GGGTG 1
```

## RESULT 5

```
US-09-721-777-12
; Sequence 12, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-12
```

```
Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGTG 5
        |||||
Db       1 GGGTG 5
```

## RESULT 6

```
US-09-799-880-7/c
; Sequence 7, Application US/09799880
; Patent No. PP14400
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
```

; APPLICANT: Shaany, Ajit  
; APPLICANT: Darokar, Mahendra  
; APPLICANT: Khanuja, Suman  
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAPAL  
; FILE REFERENCE: 2734-102  
; CURRENT APPLICATION NUMBER: US/09/799,880  
; CURRENT FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-799-880-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 7  
US-09-482-645A-7/c  
; Sequence 7, Application US/09482645A  
; Patent No. PP14538  
; GENERAL INFORMATION:  
; APPLICANT: KHANUJA, Suman Preet Singh  
; APPLICANT: SHASANY, Ajit Kumar  
; APPLICANT: DHAWAN, Sunita  
; APPLICANT: DAROKAR, Mahendra Pandurang  
; APPLICANT: SATAPATHY, Sarita  
; APPLICANT: KUMAR, Tiruppadiripuliyur Ranganathan Santha  
; APPLICANT: SAIKIA, Dharmendra  
; APPLICANT: PATRA, Nirmal Kumar  
; APPLICANT: BAHL, Janak Raj  
; APPLICANT: TRIPATHY, Arun Kumar  
; TITLE OF INVENTION: Mint Plant Named ?Sambhav?  
; FILE REFERENCE: U 012566-4  
; CURRENT APPLICATION NUMBER: US/09/482,645A  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MAP Primer  
US-09-482-645A-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 8  
US-08-061-697-27/c  
; Sequence 27, Application US/08061697  
; Patent No. 5498696  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.; Briggs, Michael R.; Wang,  
; APPLICANT: Xiaodong; Goldstein, Joseph L.  
; TITLE OF INVENTION: Sterol Regulatory Element Binding Proteins  
; TITLE OF INVENTION: and Their Use in Screening Assays

; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/061,697  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:347/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 320-7200  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-061-697-27

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 9  
US-08-131-365B-27/c  
; Sequence 27, Application US/08131365B  
; Patent No. 5527690  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Briggs, Michael R.  
; APPLICANT: Wang, Xiaodong  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/131,365B  
; FILING DATE: 01-OCT-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.



REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-131-365B-27

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 7 GGGTG 3

RESULT 10  
US-08-131-365B-43  
Sequence 43, Application US/08131365B  
Patent No. 5527690  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/131,365B  
FILING DATE: 01-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-131-365B-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 11  
US-08-330-123A-11/c  
Sequence 11, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330,123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-123A-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 7 GGGTG 3

RESULT 12  
US-08-210-222-34/c  
Sequence 34, Application US/08210222  
Patent No. 5599917  
GENERAL INFORMATION:  
APPLICANT: Coppola, George R.  
APPLICANT: Beutel, Bruce A.  
APPLICANT: Bertelsen, Arthur H.  
TITLE OF INVENTION: Inhibition of Interferon-  
with Oligonucleotides  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,



ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,222  
FILING DATE: Unassigned  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Herron, Charles J.  
REGISTRATION NUMBER: 28,019  
REFERENCE/DOCKET NUMBER: 23550-114  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 BASES  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
HYPOTHETICAL: NO  
US-08-210-222-34

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

RESULT 13

US-08-197-463-4/c  
Sequence 4, Application US/08197463  
Patent No. 5627047  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael  
APPLICANT: Besnard, Francois  
APPLICANT: Nakatani, Yoshihiro  
TITLE OF INVENTION: Astrocyte-Specific Transcription  
TITLE OF INVENTION: of Human Genes  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Koslasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/769,626  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-362P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: protein\_bind  
LOCATION: 1..10  
OTHER INFORMATION: /function= "transcription enhancer"  
OTHER INFORMATION: /bound\_moiety= "AP-2"  
OTHER INFORMATION: /standard\_name= "AP-2 site"  
US-08-197-463-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 8 GGGTG 4

RESULT 14

US-08-153-051B-55  
Sequence 55, Application US/08153051B  
Patent No. 5645986  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,051B  
FILING DATE: No. 5645986ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-153-051B-55

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
        |||||
Db       2 GGGTG 6

RESULT 15
US-08-202-927-5
; Sequence 5, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."

```

## RESULT 17

US-08-202-927-11

; Sequence 11, Application US/08202927

; Patent No. 5646126

; GENERAL INFORMATION:

; APPLICANT: Cheng, Yung-chi

; APPLICANT: Lukhtanov, Eugeny A.

; APPLICANT: Meyer Jr., Rich B.

; APPLICANT: Pai, Balakrishna S.

; APPLICANT: Reed, Michael W.

; APPLICANT: Zhou, James H.

; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having

; TITLE OF INVENTION: Anticancer Activity

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klein &amp; Szekeres

; STREET: 4199 Campus Drive, Suite 700

; CITY: Irvine

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92715

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/202,927

; FILING DATE: 28-FEB-1994

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Szekeres, Gabor L.

; REGISTRATION NUMBER: 28,675

; REFERENCE/DOCKET NUMBER: 491-07-PA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (714) 854-5502

; TELEFAX: (714) 854-4897

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: 10

; OTHER INFORMATION: /mod\_base= OTHER

; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises

; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to

; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached

; OTHER INFORMATION: to the ring nitrogen of a moiety derived from

; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see

; OTHER INFORMATION: formula 3)."

US-08-202-927-11

Query Match

Best Local Similarity 100.0%; Score 5; DB 1; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GGGTG 5

|||||

Db 6 GGGTG 10

## RESULT 18

US-08-202-927-12

; Sequence 12, Application US/08202927

; Patent No. 5646126

; GENERAL INFORMATION:

; APPLICANT: Cheng, Yung-chi

; APPLICANT: Lukhtanov, Eugeny A.

; APPLICANT: Meyer Jr., Rich B.

; APPLICANT: Pai, Balakrishna S.

; APPLICANT: Reed, Michael W.

; APPLICANT: Zhou, James H.

; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having

; TITLE OF INVENTION: Anticancer Activity

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klein &amp; Szekeres

; STREET: 4199 Campus Drive, Suite 700

; CITY: Irvine

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92715

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/202,927

; FILING DATE: 28-FEB-1994

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Szekeres, Gabor L.

; REGISTRATION NUMBER: 28,675

; REFERENCE/DOCKET NUMBER: 491-07-PA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (714) 854-5502

; TELEFAX: (714) 854-4897

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: 10

; OTHER INFORMATION: /mod\_base= OTHER

; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises

; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to

; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached

; OTHER INFORMATION: to the ring nitrogen of a moiety derived from

; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see

; OTHER INFORMATION: formula 3)."

US-08-202-927-12

Query Match

Best Local Similarity 100.0%; Score 5; DB 1; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GGGTG 5

|||||

Db 6 GGGTG 10

## RESULT 19

US-08-202-927-13

; Sequence 13, Application US/08202927

; Patent No. 5646126

; GENERAL INFORMATION:

; APPLICANT: Cheng, Yung-chi

; APPLICANT: Lukhtanov, Eugeny A.

; APPLICANT: Meyer Jr., Rich B.

; APPLICANT: Pai, Balakrishna S.

; APPLICANT: Reed, Michael W.

; APPLICANT: Zhou, James H.

; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having

; TITLE OF INVENTION: Anticancer Activity

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klein &amp; Szekeres

```

; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-13
```

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Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GGGTG 5
        |||||
Db      6 GGGTG 10
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```

RESULT 20
US-08-202-927-20
; Sequence 20, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-20
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```

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 GGGTG 5
        |||||
Db      6 GGGTG 10
```

```

RESULT 21
US-08-202-927-21
; Sequence 21, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
; US-08-202-927-21

```

```

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGGTG 5
        |||||
Db      6 GGGTG 10

```

```

RESULT 22
US-08-202-927-22
; Sequence 22, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
; US-08-202-927-22

```

```

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGGTG 5
        |||||
Db      6 GGGTG 10

```

```

RESULT 23
US-08-202-927-23
; Sequence 23, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see

```

```
; OTHER INFORMATION: formula 3)."
US-08-202-927-23

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 24
US-08-202-927-24
; Sequence 24, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3))."
US-08-202-927-24

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

US-08-202-927-25
; Sequence 25, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3))."
US-08-202-927-25

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 26
US-08-202-927-26
; Sequence 26, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
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Db      6 GGGTG 10

RESULT 25
US-08-202-927-25
; Sequence 25, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3))."
US-08-202-927-25

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 26
US-08-202-927-26
; Sequence 26, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
```

APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
OTHER INFORMATION: formula 3)."  
US-08-202-927-26

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 10  
|||||

RESULT 27  
US-08-202-927-26/c  
Sequence 26, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
OTHER INFORMATION: formula 3)."  
US-08-202-927-26

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 5 GGGTG 1  
|||||

RESULT 28  
US-08-202-927-27  
Sequence 27, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
a cholesterol moiety which has its A ring linked to  
the 3'-phosphate through a carbonyl group attached  
to the ring nitrogen of a moiety derived from  
4-hydroxy-2-hydroxymethylpyrrolidine (see  
formula 3)."  
US-08-202-927-27

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 29  
US-08-202-927-28  
Sequence 28, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675

REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
a cholesterol moiety which has its A ring linked to  
the 3'-phosphate through a carbonyl group attached  
to the ring nitrogen of a moiety derived from  
4-hydroxy-2-hydroxymethylpyrrolidine (see  
formula 3)."  
US-08-202-927-28

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 30  
US-08-202-927-29  
Sequence 29, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

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; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-29

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 31
US-08-202-927-30
; Sequence 30, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
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; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-30

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 32
US-08-202-927-31
; Sequence 31, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-31

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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Db |||||  
6 GGTG 10

RESULT 33  
US-08-202-927-43/c  
; Sequence 43, Application US/08202927  
; Patent No. 5646126  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Yung-chi  
; APPLICANT: Lukhtanov, Eugeny A.  
; APPLICANT: Meyer Jr., Rich B.  
; APPLICANT: Pai, Balakrishna S.  
; APPLICANT: Reed, Michael W.  
; APPLICANT: Zhou, James H.  
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klein & Szekeres  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92715  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/202,927  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Szekeres, Gabor L.  
; REGISTRATION NUMBER: 28,675  
; REFERENCE/DOCKET NUMBER: 491-07-PA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 854-5502  
; TELEFAX: (714) 854-4897  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 10  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a  
; OTHER INFORMATION: cholesterol moiety which has its A ring linked to  
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
; OTHER INFORMATION: formula 3)."  
US-08-202-927-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTG 5  
|||  
Db 5 GGTG 1

RESULT 34  
US-08-060-952C-54  
; Sequence 54, Application US/08060952C  
; Patent No. 5695932  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
; TITLE OF INVENTION: TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/060,952C  
; FILING DATE: May 13, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,438  
; FILING DATE: May 13, 1992  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/045  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-060-952C-54

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTG 5  
|||  
Db 2 GGTG 6

RESULT 35  
US-08-368-071-7/c  
; Sequence 7, Application US/08368071  
; Patent No. 5707853  
; GENERAL INFORMATION:  
; APPLICANT: MILLAN, JOSE L.  
; TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE  
; TITLE OF INVENTION: PHOSPHATASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES  
; ZIP: 92122  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/368,071  
;; FILING DATE: 03-JAN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAMPBELL, CATHRYN  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1275  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-535-9001  
;; TELEFAX: 619-535-8949  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-368-071-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 10 GGGTG 6

RESULT 36  
US-08-532-904-6/c  
; Sequence 6, Application US/08532904  
; Patent No. 5710367  
; GENERAL INFORMATION:  
; APPLICANT: Kindinger, Bryan K.  
; APPLICANT: Sokolov, Victor  
; TITLE OF INVENTION: Apomictic Maize  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis P. Ribando  
; STREET: 1815 No. 5710367th University Street  
; CITY: Peoria  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 61604  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,904  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ribando, Curtis P  
; REGISTRATION NUMBER: 27976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 309-681-6513  
; TELEFAX: 309-681-6688  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-532-904-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 5 GGGTG 1

RESULT 37  
US-08-463-660-13/c  
; Sequence 13, Application US/08463660  
; Patent No. 5759776  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, HELENE S.  
; APPLICANT: CHEN, LING-CHUN  
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/463,660  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIOTTI, THOMAS E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 28888-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-463-660-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
Db 8 GGGTG 4

RESULT 38  
US-08-458-181-7/c  
; Sequence 7, Application US/08458181  
; Patent No. 5773226  
; GENERAL INFORMATION:  
; APPLICANT: MILLAN, JOSE L.  
; TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE  
; TITLE OF INVENTION: PHOSPHATASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA

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; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,181
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-458-181-7

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 10 GGGTG 6

RESULT 39
US-08-482-115B-11/c
; Sequence 11, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-482-115B-11

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 7 GGGTG 3

RESULT 40
US-08-678-280-13/c
; Sequence 13, Application US/08678280
; Patent No. 5776683
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHUN, LING-CHEN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,280
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 28888-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-678-280-13

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 8 GGGTG 4

RESULT 41
```

```
US-08-590-804-13
; Sequence 13, Application US/08590804
; Patent No. 5780273
; GENERAL INFORMATION:
; APPLICANT: Burg, J. Lawrence
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 55 Shuman Blvd., Suite 600
; CITY: Naperville
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,804
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,779
; FILING DATE:
; APPLICATION NUMBER: US 08/045,587
; FILING DATE: 09-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5780273val B
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: 32,468
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-717-2447
; TELEFAX: 708-717-2430
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-590-804-13

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 2 GGGTG 6

RESULT 42
US-08-729-447-3/c
; Sequence 3, Application US/08729447
; Patent No. 5789174
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DETECTION OF PERIODONTAL PATHOGENS INCLUDING
; TITLE OF INVENTION: BACTEROIDES FORSYTHUS, PORPHYROMONAS GINGIVALIS,
; TITLE OF INVENTION: PREVOTELLA INTERMEDIA AND PREVOTELLA NIGRESCENS
; NUMBER OF SEQUENCES: 20
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,447
; FILING DATE:
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```
US-08-590-804-13
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "AP-PCR primer for P.
; DESCRIPTION: intermedia and P. nigrescens"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-729-447-3

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 8 GGGTG 4

RESULT 43
US-08-151-477A-55
; Sequence 55, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-151-477A-55

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 44
US-08-660-678A-11/c
; Sequence 11, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Vilpeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-11

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      7 GGGTG 3

RESULT 45
```

```
US-08-590-571-17
; Sequence 17, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-17

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 46
US-08-590-571-45
; Sequence 45, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```



```
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-45

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 3 GGGTG 7

RESULT 47
US-08-286-819A-52
; Sequence 52, Application US/08286819A
; Patent No. 5871910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-MALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.819A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,682
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917,146
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
```

```
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-286-819A-52

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 6 GGGTG 10

RESULT 48
US-08-485-778-42/c
; Sequence 42, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-485-778-42

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
      |||||  
Db 7 GGGTG 3

RESULT 49

US-08-668-123-27/c  
; Sequence 27, Application US/08668123  
; Patent No. 5891631  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Briggs, Michael R.  
; APPLICANT: Wang, Xiaodong  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/668,123  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/131,365  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"

US-08-668-123-27

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
      |||||  
Db 7 GGGTG 3

RESULT 50

US-08-668-123-43

; Sequence 43, Application US/08668123  
; Patent No. 5891631  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Briggs, Michael R.  
; APPLICANT: Wang, Xiaodong  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/668,123  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/131,365  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"

US-08-668-123-43

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
      |||||  
Db 6 GGGTG 10

Search completed: January 7, 2005, 11:05:44  
Job time : 61 secs

**This Page Blank (uspto)**

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
(without alignments)  
106.177 Million cell updates/sec

Title: GGGTG  
Perfect score: 5  
Sequence: 1 gggtg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	5	100.0	10	9	US-09-823-699-1
5	5	100.0	10	9	US-09-154-750A-9
6	5	100.0	10	9	US-09-154-750A-66
7	5	100.0	10	9	US-09-785-632A-4
8	5	100.0	10	9	US-09-989-789-97
9	5	100.0	10	9	US-09-989-789-584
10	5	100.0	10	9	US-09-989-789-626
11	5	100.0	10	9	US-09-989-789-1287
12	5	100.0	10	9	US-09-989-789-1329
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					Sequence 3, Appl
					Sequence 11, Appl
					Sequence 1, Appl
					Sequence 9, Appl
					Sequence 66, Appl
					Sequence 4, Appl
					Sequence 97, Appl
					Sequence 584, App
					Sequence 626, App
					Sequence 1287, Ap

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15	5	100.0	10	9	US-09-989-789-1646	Sequence 1646, Ap
16	5	100.0	10	9	US-09-989-789-1660	Sequence 1660, Ap
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c 247	5	100.0	10	18	US-10-401-691-7	Sequence 7, Appli	Sequence 7, Appli
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c 264	5	100.0	11	9	US-09-879-813-20	Sequence 20, Appl	Sequence 20, Appl
c 265	5	100.0	11	9	US-09-879-813-42	Sequence 42, Appl	Sequence 42, Appl
c 266	5	100.0	11	9	US-09-945-901-9	Sequence 9, Appli	Sequence 9, Appli
267	5	100.0	11	9	US-09-745-317-79	Sequence 79, Appl	Sequence 79, Appl
268	5	100.0	11	10	US-09-918-715-86	Sequence 86, Appl	Sequence 86, Appl
269	5	100.0	11	10	US-09-918-715-93	Sequence 93, Appl	Sequence 93, Appl
270	5	100.0	11	10	US-09-918-715-122	Sequence 122, Appl	Sequence 122, Appl
c 271	5	100.0	11	10	US-09-943-115A-11	Sequence 11, Appl	Sequence 11, Appl
272	5	100.0	11	10	US-09-943-115A-13	Sequence 13, Appl	Sequence 13, Appl
273	5	100.0	11	10	US-09-249-155-7	Sequence 7, Appli	Sequence 7, Appli
c 274	5	100.0	11	10	US-09-249-155-74	Sequence 74, Appl	Sequence 74, Appl
275	5	100.0	11	10	US-09-249-155-100	Sequence 100, App	Sequence 100, App
c 276	5	100.0	11	10	US-09-249-155-109	Sequence 109, App	Sequence 109, App
277	5	100.0	11	10	US-09-249-155-165	Sequence 165, App	Sequence 165, App
c 278	5	100.0	11	10	US-09-942-310-66	Sequence 66, Appl	Sequence 66, Appl
279	5	100.0	11	10	US-09-942-310-73	Sequence 73, Appl	Sequence 73, Appl
c 280	5	100.0	11	10	US-09-916-466-100	Sequence 100, App	Sequence 100, App
281	5	100.0	11	13	US-10-007-747-9	Sequence 9, Appli	Sequence 9, Appli
c 282	5	100.0	11	14	US-10-038-937-9	Sequence 9, Appli	Sequence 9, Appli
c 283	5	100.0	11	14	US-10-146-354A-13	Sequence 13, Appl	Sequence 13, Appl
c 284	5	100.0	11	14	US-10-146-354A-14	Sequence 14, Appl	Sequence 14, Appl
c 285	5	100.0	11	15	US-10-146-505-20	Sequence 20, Appl	Sequence 20, Appl
c 286	5	100.0	11	15	US-10-146-505-42	Sequence 42, Appl	Sequence 42, Appl
287	5	100.0	11	15	US-10-266-138B-19	Sequence 19, Appl	Sequence 19, Appl
288	5	100.0	11	15	US-10-214-417A-33	Sequence 33, Appl	Sequence 33, Appl
289	5	100.0	11	15	US-10-055-728-8	Sequence 8, Appli	Sequence 8, Appli
290	5	100.0	11	15	US-10-265-509B-19	Sequence 19, Appl	Sequence 19, Appl
c 291	5	100.0	11	15	US-10-084-839-3364	Sequence 3364, Ap	Sequence 3364, Ap
c 292	5	100.0	11	15	US-10-277-494-100	Sequence 100, App	Sequence 100, App
c 293	5	100.0	11	15	US-10-091-281-77	Sequence 77, Appl	Sequence 77, Appl
c 294	5	100.0	11	15	US-10-091-281-170	Sequence 170, App	Sequence 170, App
c 295	5	100.0	11	15	US-10-091-281-183	Sequence 183, App	Sequence 183, App
c 296	5	100.0	11	15	US-10-091-281-245	Sequence 245, App	Sequence 245, App
297	5	100.0	11	15	US-10-310-677-8	Sequence 8, Appli	Sequence 8, Appli
298	5	100.0	11	15	US-10-314-322-7	Sequence 7, Appli	Sequence 7, Appli
c 299	5	100.0	11	15	US-10-314-322-74	Sequence 74, Appl	Sequence 74, Appl
300	5	100.0	11	15	US-10-314-322-100	Sequence 100, App	Sequence 100, App
c 301	5	100.0	11	15	US-10-314-322-109	Sequence 109, App	Sequence 109, App
302	5	100.0	11	15	US-10-314-322-165	Sequence 165, App	Sequence 165, App
303	5	100.0	11	15	US-10-314-322-318	Sequence 318, App	Sequence 318, App
c 304	5	100.0	11	15	US-10-314-322-325	Sequence 325, App	Sequence 325, App
305	5	100.0	11	15	US-10-170-332-79	Sequence 79, Appl	Sequence 79, Appl
306	5	100.0	11	16	US-10-415-620-18	Sequence 18, Appl	Sequence 18, Appl
c 307	5	100.0	11	16	US-10-297-058-22	Sequence 22, Appl	Sequence 22, Appl
c 308	5	100.0	11	17	US-10-203-969A-5	Sequence 5, Appli	Sequence 5, Appli
c 309	5	100.0	11	17	US-10-612-224-92	Sequence 92, Appl	Sequence 92, Appl
310	5	100.0	11	17	US-10-450-797-4	Sequence 4, Appli	Sequence 4, Appli
c 311	5	100.0	11	17	US-10-450-797-17	Sequence 17, Appl	Sequence 17, Appl
c 312	5	100.0	11	17	US-10-450-797-53	Sequence 53, Appl	Sequence 53, Appl
c 313	5	100.0	11	17	US-10-450-797-246	Sequence 246, App	Sequence 246, App
c 314	5	100.0	11	17	US-10-450-797-277	Sequence 277, App	Sequence 277, App
315	5	100.0	11	17	US-10-450-797-326	Sequence 326, App	Sequence 326, App
316	5	100.0	11	17	US-10-450-797-364	Sequence 364, App	Sequence 364, App
c 317	5	100.0	11	17	US-10-450-797-386	Sequence 386, App	Sequence 386, App
c 318	5	100.0	11	17	US-10-450-797-429	Sequence 429, App	Sequence 429, App
c 319	5	100.0	11	17	US-10-450-797-431	Sequence 431, App	Sequence 431, App
320	5	100.0	11	17	US-10-450-797-481	Sequence 481, App	Sequence 481, App
c 321	5	100.0	11	17	US-10-450-797-516	Sequence 516, App	Sequence 516, App
322	5	100.0	11	17	US-10-450-797-560	Sequence 560, App	Sequence 560, App
323	5	100.0	11	17	US-10-450-797-597	Sequence 597, App	Sequence 597, App
c 324	5	100.0	11	17	US-10-450-797-929	Sequence 929, App	Sequence 929, App
c 325	5	100.0	11	17	US-10-450-797-993	Sequence 993, App	Sequence 993, App
326	5	100.0	11	17	US-10-450-797-1039	Sequence 1039, Ap	Sequence 1039, Ap
327	5	100.0	11	17	US-10-450-797-1124	Sequence 1124, Ap	Sequence 1124, Ap
c 328	5	100.0	11	17	US-10-450-797-1153	Sequence 1153, Ap	Sequence 1153, Ap
329	5	100.0	11	17	US-10-450-797-1399	Sequence 1399, Ap	Sequence 1399, Ap
c 330	5	100.0	11	17	US-10-450-797-1406	Sequence 1406, Ap	Sequence 1406, Ap
331	5	100.0	11	17	US-10-803-622-213	Sequence 213, App	Sequence 213, App
332	5	100.0	11	17	US-10-803-653-213	Sequence 213, App	Sequence 213, App
333	5	100.0	11	18	US-10-474-794-86	Sequence 86, Appl	Sequence 86, Appl
334	5	100.0	11	18	US-10-474-794-93	Sequence 93, Appl	Sequence 93, Appl
335	5	100.0	11	18	US-10-474-794-122	Sequence 122, App	Sequence 122, App
336	5	100.0	11	18	US-10-149-109A-159	Sequence 159, App	Sequence 159, App
c 337	5	100.0	11	18	US-10-149-109A-160	Sequence 160, App	Sequence 160, App
338	5	100.0	11	18	US-10-149-109A-163	Sequence 163, App	Sequence 163, App
c 339	5	100.0	11	18	US-10-149-109A-165	Sequence 165, App	Sequence 165, App
c 340	5	100.0	11	18	US-10-715-844-35	Sequence 35, Appl	Sequence 35, Appl
341	5	100.0	12	8	US-08-463-404-55	Sequence 55, Appl	Sequence 55, Appl
c 342	5	100.0	12	9	US-09-365-029-23	Sequence 23, Appl	Sequence 23, Appl
c 343	5	100.0	12	9	US-09-365-029-24	Sequence 24, Appl	Sequence 24, Appl
344	5	100.0	12	9	US-09-365-029-38	Sequence 38, Appl	Sequence 38, Appl
345	5	100.0	12	9	US-09-365-029-89	Sequence 89, Appl	Sequence 89, Appl
346	5	100.0	12	9	US-09-365-029-90	Sequence 90, Appl	Sequence 90, Appl
c 347	5	100.0	12	9	US-09-263-959-698	Sequence 698, App	Sequence 698, App
c 348	5	100.0	12	9	US-09-263-959-887	Sequence 887, App	Sequence 887, App
c 349	5	100.0	12	9	US-09-263-959-907	Sequence 907, App	Sequence 907, App
c 350	5	100.0	12	9	US-09-263-959-915	Sequence 915, App	Sequence 915, App
351	5	100.0	12	9	US-09-879-813-38	Sequence 38, Appl	Sequence 38, Appl
352	5	100.0	12	9	US-09-976-736-17	Sequence 17, Appl	Sequence 17, Appl
353	5	100.0	12	9	US-09-835-371-33	Sequence 33, Appl	Sequence 33, Appl
c 354	5	100.0	12	9	US-09-841-157A-33	Sequence 32, Appl	Sequence 32, Appl
c 355	5	100.0	12	9	US-09-841-157A-33	Sequence 33, Appl	Sequence 33, Appl
c 356	5	100.0	12	10	US-09-765-061B-24	Sequence 24, Appl	Sequence 24, Appl
357	5	100.0	12	10	US-09-835-370-33	Sequence 33, Appl	Sequence 33, Appl
c 358	5	100.0	12	10	US-09-923-005-22	Sequence 22, Appl	Sequence 22, Appl
c 359	5	100.0	12	10	US-09-923-005-31	Sequence 31, Appl	Sequence 31, Appl
360	5	100.0	12	10	US-09-405-032-3	Sequence 3, Appli	Sequence 3, Appli
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c 362	5	100.0	12	14	US-10-054-429A-14	Sequence 14, Appl	Sequence 14, Appl
c 363	5	100.0	12	14	US-10-054-429A-29	Sequence 29, Appl	Sequence 29, Appl
364	5	100.0	12	15	US-10-146-505-38	Sequence 38, Appl	Sequence 38, Appl
c 365	5	100.0	12	15	US-10-101-030B-56	Sequence 56, Appl	Sequence 56, Appl
c 366	5	100.0	12	15	US-10-101-030B-65	Sequence 65, Appl	Sequence 65, Appl
c 367	5	100.0	12	15	US-10-021-425-60	Sequence 60, Appl	Sequence 60, Appl
c 368	5	100.0	12	15	US-10-279-061-60	Sequence 3010, Ap	Sequence 3010, Ap
c 369	5	100.0	12	15	US-10-084-839-3010	Sequence 374, App	Sequence 374, App
c 370	5	100.0	12	15	US-10-091-281-374	Sequence 434, App	Sequence 434, App
371	5	100.0	12	15	US-10-091-281-434	Sequence 76, Appl	Sequence 76, Appl
c 372	5	100.0	12	15	US-10-232-927A-76	Sequence 4, Appli	Sequence 4, Appli
373	5	100.0	12	15	US-10-343-943-4	Sequence 45, Appl	Sequence 45, Appl
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378	5	100.0	12	16	US-10-182-329-63	Sequence 63, Appl	Sequence 63, Appl
379	5	100.0	12	16	US-10-182-329-64	Sequence 64, Appl	Sequence 64, Appl
380	5	100.0	12	16	US-10-182-329-77	Sequence 77, Appl	Sequence 77, Appl
c 381	5	100.0	12	16	US-10-602-837-14	Sequence 14, Appl	Sequence 14, Appl
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c 383	5	100.0	12	16	US-10-380-774-2	Sequence 2, Appli	Sequence 2, Appli
c 384	5	100.0	12	16	US-10-297-058-17	Sequence 17, Appl	Sequence 17, Appl
c 385	5	100.0	12	16	US-10-297-058-18	Sequence 18, Appl	Sequence 18, Appl
386	5	100.0	12	17	US-10-661-165-449	Sequence 449, App	Sequence 449, App
387	5	100.0	12	17	US-10-667-891-50	Sequence 50, Appl	Sequence 50, Appl
388	5	100.0	12	18	US-10-691-633-55	Sequence 55, Appl	Sequence 55, Appl
c 389	5	100.0	12	18	US-10-849-072-9	Sequence 9, Appli	Sequence 9, Appli
c 390	5	100.0	12	18	US-10-849-072-16	Sequence 16, Appl	Sequence 16, Appl
391	5	100.0	12	18	US-10-477-086-12	Sequence 12, Appl	Sequence 12, Appl
392	5	100.0	12	18	US-10-477-086-16	Sequence 16, Appl	Sequence 16, Appl
c 393	5	100.0	12	18	US-10-836-670-24	Sequence 24, Appl	Sequence 24, Appl
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398	5	100.0	12	18	US-10-257-017B-268254	Sequence 268254,	Sequence 268254,
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405	5	100.0	12	18	US-10-257-017B-269170	Sequence 269170,	Sequence 269170,
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c 409	5	100.0	12	18	US-10-257-017B-269658	Sequence 269658,	Sequence 269658,
c 410	5	100.0	12	18	US-10-257-017B-269659	Sequence 269659,	Sequence 269659,
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c 415	5	100.0	12	18	US-10-257-017B-269972	Sequence 269972,	Sequence 269972,
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c 424	5	100.0	12	18	US-10-257-017B-270652	Sequence 270652,	Sequence 270652,
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c 426	5	100.0	12	18	US-10-257-017B-270938	Sequence 270938,	Sequence 270938,
c 427	5	100.0	12	18	US-10-257-017B-270971	Sequence 270971,	Sequence 270971,
c 428	5	100.0	12	18	US-10-257-017B-271061	Sequence 271061,	Sequence 271061,
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442	5	100.0	12	18	US-10-257-017B-272203	Sequence 272203,	Sequence 272203,
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446	5	100.0	12	18	US-10-257-017B-272496	Sequence 272496,	Sequence 272496,
447	5	100.0	12	18	US-10-257-017B-272500	Sequence 272500,	Sequence 272500,
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c 453	5	100.0	12	18	US-10-257-017B-273255	Sequence 273255,	Sequence 273255,
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c 460	5	100.0	12	18	US-10-257-017B-273796	Sequence 273796,	Sequence 273796,
c 461	5	100.0	12	18	US-10-257-017B-273942	Sequence 273942,	Sequence 273942,
462	5	100.0	12	18	US-10-257-017B-274273	Sequence 274273,	Sequence 274273,
c 463	5	100.0	12	18	US-10-257-017B-274503	Sequence 274503,	Sequence 274503,
c 464	5	100.0	12	18	US-10-257-017B-274504	Sequence 274504,	Sequence 274504,
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466	5	100.0	12	18	US-10-257-017B-274735	Sequence 274735,	Sequence 274735,
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c 472	5	100.0	12	18	US-10-257-017B-275043	Sequence 275043,	Sequence 275043,
c 473	5	100.0	12	18	US-10-257-017B-275214	Sequence 275214,	Sequence 275214,
c 474	5	100.0	12	18	US-10-257-017B-275354	Sequence 275354,	Sequence 275354,
c 475	5	100.0	12	18	US-10-257-017B-275355	Sequence 275355,	Sequence 275355,
c 476	5	100.0	12	18	US-10-257-017B-275423	Sequence 275423,	Sequence 275423,
c 477	5	100.0	12	18	US-10-257-017B-275458	Sequence 275458,	Sequence 275458,
c 478	5	100.0	12	18	US-10-257-017B-275534	Sequence 275534,	Sequence 275534,
c 479	5	100.0	12	18	US-10-257-017B-275649	Sequence 275649,	Sequence 275649,
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c 481	5	100.0	12	18	US-10-257-017B-275692	Sequence 275692,	Sequence 275692,
c 482	5	100.0	12	18	US-10-257-017B-275748	Sequence 275748,	Sequence 275748,
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c 485	5	100.0	12	18	US-10-257-017B-275841	Sequence 275841,	Sequence 275841,
c 486	5	100.0	12	18	US-10-257-017B-275846	Sequence 275846,	Sequence 275846,
c 487	5	100.0	12	18	US-10-257-017B-275849	Sequence 275849,	Sequence 275849,
c 488	5	100.0	12	18	US-10-257-017B-275868	Sequence 275868,	Sequence 275868,
c 489	5	100.0	12	18	US-10-257-017B-275869	Sequence 275869,	Sequence 275869,
c 490	5	100.0	12	18	US-10-257-017B-275961	Sequence 275961,	Sequence 275961,
c 491	5	100.0	12	18	US-10-257-017B-275962	Sequence 275962,	Sequence 275962,
c 492	5	100.0	12	18	US-10-257-017B-275983	Sequence 275983,	Sequence 275983,
493	5	100.0	12	18	US-10-257-017B-276065	Sequence 276065,	Sequence 276065,
494	5	100.0	12	18	US-10-257-017B-276174	Sequence 276174,	Sequence 276174,
c 496	5	100.0	12	18	US-10-257-017B-276177	Sequence 276177,	Sequence 276177,
c 497	5	100.0	12	18	US-10-257-017B-276195	Sequence 276195,	Sequence 276195,
c 498	5	100.0	12	18	US-10-257-017B-276247	Sequence 276247,	Sequence 276247,
499	5	100.0	12	18	US-10-257-017B-276269	Sequence 276269,	Sequence 276269,
c 500	5	100.0	12	18	US-10-257-017B-306178	Sequence 306178,	Sequence 306178,

ALIGNMENTS

RESULT 1  
US-08-463-404-54  
; Sequence 54, Application US/08463404  
; Publication No. US20020127634A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
; TITLE OF INVENTION: TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles



STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,404  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-463-404-54

Query Match 100.0%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
DB 2 GGGTG 6

RESULT 2  
US-09-758-073-3  
Sequence 3, Application US/09758073  
Patent No. US20010024785A1  
GENERAL INFORMATION:  
APPLICANT: Keinath, et al.  
TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in  
TITLE OF INVENTION: Plants Using a Polymerase Chain Reaction Assay  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Judy C. Jarecki-Black, Ph.D.  
ADDRESSEE: Dority & Manning, P.A.  
STREET: 700 E. No. US20010024785A1th Street, Suite 15  
CITY: Greenville  
STATE: South Carolina  
COUNTRY: USA  
ZIP: 29601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS Dos; Windows 95  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,073  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/078,103

FILING DATE: 16-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy C. Jarecki-Black, Ph.D.  
REGISTRATION NUMBER: P44,170  
REFERENCE/DOCKET NUMBER: CXU-291  
TELEPHONE: (864) 271-1592  
TELEFAX: (864) 233-7342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 Pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Other Nucleic Acid  
DESCRIPTION: Oligonucleotide Primer  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE: Operon Technologies (Alameda, CA)  
IMMEDIATE SOURCE: Operon Technologies  
POSITION IN GENOME: No. US20010024785A1 Applicable  
UNITS:  
FEATURE:  
OTHER INFORMATION: Commercially Available Primer  
PUBLICATION INFORMATION: No. US20010024785A1 Applicable  
US-09-758-073-3

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
DB 1 GGGTG 5

RESULT 3  
US-09-057-351-11/c  
Sequence 11, Application US/09057351  
Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:

```
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-11

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 7 GGGTG 3

RESULT 4
US-09-823-699-1/c
; Sequence 1, Application US/09823699
; Patent No. US2002002143A1
; GENERAL INFORMATION:
; APPLICANT: Kano, Munehide
; APPLICANT: Matano, Tetsuro
; APPLICANT: Kato, Atsushi
; APPLICANT: Nagai, Yoshiyuki
; APPLICANT: Hasegawa, Mamoru
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus
; FILE REFERENCE: 50026/022002
; CURRENT APPLICATION NUMBER: US/09/823,699
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,127
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificially synthesized sequence
US-09-823-699-1

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 9 GGGTG 5

RESULT 5
US-09-154-750A-9/c
; Sequence 9, Application US/09154750A
; Publication No. US2002005097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-9

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 6 GGGTG 2

RESULT 6
US-09-154-750A-66/c
; Sequence 66, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-66

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 10 GGGTG 6

RESULT 7
US-09-785-632A-4
; Sequence 4, Application US/09785632A
; Patent No. US20020061512A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Kwon, Young Do
; APPLICANT: Kim, Hyun-Won
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
; FILE REFERENCE: 12279-002001
; CURRENT APPLICATION NUMBER: US/09/785,632A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
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```
; ORGANISM: Homo sapiens
US-09-785-632A-4

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 8
US-09-989-789-97
; Sequence 97, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-97

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      5 GGGTG 9

RESULT 9
US-09-989-789-584
; Sequence 584, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-584

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6
```

```
RESULT 10
US-09-989-789-626
; Sequence 626, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-626

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 11
US-09-989-789-1287
; Sequence 1287, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1287

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 12
US-09-989-789-1329
; Sequence 1329, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
```

```

; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1329

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 13
US-09-989-789-1339
; Sequence 1339, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1339

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      6 GGGTG 10

RESULT 14
US-09-989-789-1645
; Sequence 1645, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1645
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```

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 15
US-09-989-789-1646
; Sequence 1646, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1646

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 16
US-09-989-789-1660
; Sequence 1660, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1660

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      5 GGGTG 9

RESULT 17
```

```
US-09-989-789-1669
; Sequence 1669, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1669

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 18
US-09-989-789-1670
; Sequence 1670, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1670

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 19
US-09-942-325A-5/c
; Sequence 5, Application US/09942325A
; Patent No. US20020106794A1
; GENERAL INFORMATION:
; APPLICANT: Iacovitti, Lorraine
; APPLICANT: Kessler, Mark
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter
; TITLE OF INVENTION: Sequence and Related Methods and Compositions
; FILE REFERENCE: IAC01.NP001
; CURRENT APPLICATION NUMBER: US/09/942,325A
; CURRENT FILING DATE: 2001-08-29
```

```
; PRIOR APPLICATION NUMBER: 60/228931
; PRIOR FILING DATE: 2000-02-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-942-325A-5

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      10 GGGTG 6

RESULT 20
US-09-816-763-110/c
; Sequence 110, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: SREBP1
; NAME/KEY: misc_binding
; LOCATION: (0)...(0)
; OTHER INFORMATION: non E-Box consensus binding sequence
US-09-816-763-110

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      7 GGGTG 3

RESULT 21
US-09-772-719-19/c
; Sequence 19, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
```

```

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
; US-09-772-719-19

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 10 GGGTG 6

RESULT 22
US-09-772-719-20/c
; Sequence 20, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: initiator (Inr) element
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-772-719-20

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 2

RESULT 23
US-09-966-277-63/c
; Sequence 63, Application US/09966277
; Patent No. US20020169306A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kaio
; APPLICANT: SHU, Tsugumine
; APPLICANT: KUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: TOKITOU, Fumino
; APPLICANT: HIRATA, Takahiro
; APPLICANT: TOKUSUMI, Tsuyoshi
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: 50026/028001
; CURRENT APPLICATION NUMBER: US/09/966,277
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/JP00/03195
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: JP 2001/283451
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: JP 11/200739
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
; US-09-966-277-63

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 9 GGGTG 5

```

RESULT 24  
US-09-961-700A-48  
; Sequence 48, Application US/09961700A  
; Publication No. US20020187482A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Zicai  
; APPLICANT: Zhang, Hong-Yan  
; APPLICANT: Wahlestedt, Claes  
; TITLE OF INVENTION: Methods and Means of RNA Analysis  
; FILE REFERENCE: 13522-003001  
; CURRENT APPLICATION NUMBER: US/09/961,700A  
; PRIOR FILING DATE: 2002-07-23  
; PRIOR FILING DATE: 2002-07-23  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
US-09-961-700A-48

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 3 GGGTG 7

RESULT 25  
US-09-916-228-3/c  
; Sequence 3, Application US/09916228  
; Publication No. US20030008290A1  
; GENERAL INFORMATION:  
; APPLICANT: Velculescu, Victor  
; APPLICANT: Sparks, Andrew  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: Serial analysis of transcript expression  
; TITLE OF INVENTION: using long tags  
; FILE REFERENCE: 001107.00172  
; CURRENT APPLICATION NUMBER: US/09/916,228  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/221,556  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/233,431  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: tag or tag concatamer  
US-09-916-228-3

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 6 GGGTG 2

RESULT 26  
US-09-799-880-7/c

; Sequence 7, Application US/09799880  
; Publication No. US20030014799P1  
; GENERAL INFORMATION:  
; APPLICANT: Kumar, Sushil  
; APPLICANT: Gupta, Ritika  
; APPLICANT: Sastry, Kakaraparthi  
; APPLICANT: Banerjee, Suchitra  
; APPLICANT: Mallavarapu, Gopal  
; APPLICANT: Ramesh, Srinivas  
; APPLICANT: Shasany, Ajit  
; APPLICANT: Darokar, Mahendra  
; APPLICANT: Khanuja, Suman  
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFAL'  
; FILE REFERENCE: 2734-102  
; CURRENT APPLICATION NUMBER: US/09/799,880  
; CURRENT FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-799-880-7

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 5 GGGTG 1

RESULT 27  
US-09-966-930-63/c  
; Sequence 63, Application US/09966930  
; Publication No. US20030022376A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, Kaio  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: HIRATA, Takahiro  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
; FILE REFERENCE: 50026/029001  
; CURRENT APPLICATION NUMBER: US/09/966,930  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/03194  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: JP 2001/283451  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: JP 11/200740  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-930-63

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 GGGTG 5  
|  
|  
|  
|  
Db 9 GGGTG 5

RESULT 28  
US-09-846-033B-144  
; Sequence 144, Application US/09846033B  
; Publication No. US2003004404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; TITLE OF INVENTION: Finger Proteins  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 144  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-144

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|  
|  
|  
|  
Db 3 GGGTG 7

RESULT 29  
US-09-846-033B-145  
; Sequence 145, Application US/09846033B  
; Publication No. US2003004404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; TITLE OF INVENTION: Finger Proteins  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 145  
; LENGTH: 10  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-145

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|  
|  
|  
|  
Db 3 GGGTG 7

RESULT 30  
US-09-967-237-20/c  
; Sequence 20, Application US/09967237  
; Publication No. US20030049828A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.5B-2  
; CURRENT APPLICATION NUMBER: US/09/967,237  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/178,115  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-09-967-237-20

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|  
|  
|  
|  
Db 6 GGGTG 2

RESULT 31  
US-09-916-466-116/c  
; Sequence 116, Application US/09916466  
; Publication No. US20030064945A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Akhtar, Saghir  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors  
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors  
; FILE REFERENCE: MBHB00-958-J (400/032)  
; CURRENT APPLICATION NUMBER: US/09/916,466  
; CURRENT FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 116  
; LENGTH: 10  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-916-466-116

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|  
|  
|  
|  
Db 10 GGGTG 6

```
RESULT 32
US-09-916-466-125/c
; Sequence 125, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-916-466-125

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      9 GGGTG 5

RESULT 33
US-09-990-186-97
; Sequence 97, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-97

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      9 GGGTG 5

RESULT 34
US-09-990-186-584
; Sequence 584, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
```

```
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-584

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      2 GGGTG 6

RESULT 35
US-09-990-186-626
; Sequence 626, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-626

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 36
US-09-990-186-1287
; Sequence 1287, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1287
```

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
      |||||  
Db 3 GGGTG 7

RESULT 37

US-09-990-186-1329  
; Sequence 1329, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1329  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1329

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
      |||||  
Db 6 GGGTG 10

RESULT 38

US-09-990-186-1339  
; Sequence 1339, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1339  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1339

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
      |||||  
Db 6 GGGTG 10

RESULT 39

US-09-990-186-1645  
; Sequence 1645, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1645  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1645

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
      |||||  
Db 2 GGGTG 6

RESULT 40

US-09-990-186-1646  
; Sequence 1646, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1646  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1646

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
      |||||  
Db 2 GGGTG 6

RESULT 41

US-09-990-186-1660  
; Sequence 1660, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1660

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      5 GGGTG 9

RESULT 42
US-09-990-186-1669
; Sequence 1669, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1669

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 43
US-09-990-186-1670
; Sequence 1670, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1670

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 44
US-09-979-593-43
; Sequence 43, Application US/09979593
; Publication No. US2003008255A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MWH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-43

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
Db      3 GGGTG 7

RESULT 45
US-09-989-994-97
; Sequence 97, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-97

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
```

```
Db          5 GGGTG 9

RESULT 46
US-09-989-994-584
; Sequence 584, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-584

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGTG 5
          |||||
Db          2 GGGTG 6

RESULT 47
US-09-989-994-626
; Sequence 626, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-626

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGTG 5
          |||||
Db          3 GGGTG 7

RESULT 48
US-09-989-994-1287
; Sequence 1287, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
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; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1287

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGTG 5
          |||||
Db          3 GGGTG 7

RESULT 49
US-09-989-994-1329
; Sequence 1329, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1329

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GGGTG 5
          |||||
Db          6 GGGTG 10

RESULT 50
US-09-989-994-1339
; Sequence 1339, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
```

; OTHER INFORMATION: DNA  
US-09-989-994-1339

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
    |||||  
Db 6 GGGTG 10

Search completed: January 7, 2005, 11:31:28  
Job time : 272.2 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GTGGG  
Perfect score: 5  
Sequence: 1 gtggg 5  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sta:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	5	100.0	10	6	A57560
C 3	5	100.0	10	6	A57562
C 4	5	100.0	10	6	A76253
C 5	5	100.0	10	6	AR016245
C 6	5	100.0	10	6	AR017948
C 7	5	100.0	10	6	AR017953
C 8	5	100.0	10	6	AR020527
C 9	5	100.0	10	6	AR030206
C 10	5	100.0	10	6	AR030217
C 11	5	100.0	10	6	AR030218
C 12	5	100.0	10	6	AR030234
C 13	5	100.0	10	6	AR030237
C 14	5	100.0	10	6	AR030238
C 15	5	100.0	10	6	AR032136
C 16	5	100.0	10	6	AR049904
C 17	5	100.0	10	6	AR069288
C 18	5	100.0	10	6	AR069301
C 19	5	100.0	10	6	AR074300
C 20	5	100.0	10	6	A08938 H.sapeins f
C 21	5	100.0	10	6	A57560 Sequence 52
C 22	5	100.0	10	6	A57562 Sequence 54
C 23	5	100.0	10	6	A76253 Sequence 24
C 24	5	100.0	10	6	AR016245 Sequence
C 25	5	100.0	10	6	AR017948 Sequence
C 26	5	100.0	10	6	AR017953 Sequence
C 27	5	100.0	10	6	AR020527 Sequence
C 28	5	100.0	10	6	AR030206 Sequence
C 29	5	100.0	10	6	AR030217 Sequence
C 30	5	100.0	10	6	AR030218 Sequence
C 31	5	100.0	10	6	AR030234 Sequence
C 32	5	100.0	10	6	AR030237 Sequence
C 33	5	100.0	10	6	AR030238 Sequence
C 34	5	100.0	10	6	AR032136 Sequence
C 35	5	100.0	10	6	AR049904 Sequence
C 36	5	100.0	10	6	AR069288 Sequence
C 37	5	100.0	10	6	AR069301 Sequence
C 38	5	100.0	10	6	AR074300 Sequence
C 39	5	100.0	10	6	AR074300 Sequence
C 40	5	100.0	10	6	AR074300 Sequence
C 41	5	100.0	10	6	AR074300 Sequence
C 42	5	100.0	10	6	AR074300 Sequence
C 43	5	100.0	10	6	AR074300 Sequence
C 44	5	100.0	10	6	AR074300 Sequence
C 45	5	100.0	10	6	AR074300 Sequence
C 46	5	100.0	10	6	AR074300 Sequence
C 47	5	100.0	10	6	AR074300 Sequence
C 48	5	100.0	10	6	AR074300 Sequence
C 49	5	100.0	10	6	AR074300 Sequence
C 50	5	100.0	10	6	AR074300 Sequence
C 51	5	100.0	10	6	AR074300 Sequence
C 52	5	100.0	10	6	AR074300 Sequence
C 53	5	100.0	10	6	AR074300 Sequence
C 54	5	100.0	10	6	AR074300 Sequence
C 55	5	100.0	10	6	AR074300 Sequence
C 56	5	100.0	10	6	AR074300 Sequence
C 57	5	100.0	10	6	AR074300 Sequence
C 58	5	100.0	10	6	AR074300 Sequence
C 59	5	100.0	10	6	AR074300 Sequence
C 60	5	100.0	10	6	AR074300 Sequence
C 61	5	100.0	10	6	AR074300 Sequence
C 62	5	100.0	10	6	AR074300 Sequence
C 63	5	100.0	10	6	AR074300 Sequence
C 64	5	100.0	10	6	AR074300 Sequence
C 65	5	100.0	10	6	AR074300 Sequence
C 66	5	100.0	10	6	AR074300 Sequence
C 67	5	100.0	10	6	AR074300 Sequence
C 68	5	100.0	10	6	AR074300 Sequence
C 69	5	100.0	10	6	AR074300 Sequence
C 70	5	100.0	10	6	AR074300 Sequence
C 71	5	100.0	10	6	AR074300 Sequence
C 72	5	100.0	10	6	AR074300 Sequence
C 73	5	100.0	10	6	AR074300 Sequence
C 74	5	100.0	10	6	AR074300 Sequence
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C 82	5	100.0	10	6	AR074300 Sequence
C 83	5	100.0	10	6	AR074300 Sequence
C 84	5	100.0	10	6	AR074300 Sequence
C 85	5	100.0	10	6	AR074300 Sequence
C 86	5	100.0	10	6	AR074300 Sequence
C 87	5	100.0	10	6	AR074300 Sequence
C 88	5	100.0	10	6	AR074300 Sequence
C 89	5	100.0	10	6	AR074300 Sequence
C 90	5	100.0	10	6	AR074300 Sequence
C 91	5	100.0	10	6	AR074300 Sequence
C 92	5	100.0	10	6	AR074300 Sequence

C 93	5	100.0	10	6	E39700	E39700 Genes with	C 166	5	100.0	10	6	AX152856	AX152856 Sequence
C 94	5	100.0	10	6	E39746	E39746 Genes with	C 167	5	100.0	10	6	AX152857	AX152857 Sequence
C 95	5	100.0	10	6	E39752	E39752 Genes with	C 168	5	100.0	10	6	AX152910	AX152910 Sequence
C 96	5	100.0	10	6	E54658	E54658 Human norma	C 169	5	100.0	10	6	AX152927	AX152927 Sequence
97	5	100.0	10	6	E54662	E54662 Human norma	170	5	100.0	10	6	AX152930	AX152930 Sequence
98	5	100.0	10	6	E54714	E54714 Human norma	171	5	100.0	10	6	AX152931	AX152931 Sequence
C 99	5	100.0	10	6	E54795	E54795 Human norma	172	5	100.0	10	6	AX152932	AX152932 Sequence
C 100	5	100.0	10	6	I18846	I18846 Sequence 27	C 173	5	100.0	10	6	AX152981	AX152981 Sequence
101	5	100.0	10	6	I21132	I21132 Sequence 17	C 174	5	100.0	10	6	AX152987	AX152987 Sequence
102	5	100.0	10	6	I21133	I21133 Sequence 18	175	5	100.0	10	6	AX153035	AX153035 Sequence
C 103	5	100.0	10	6	I22300	I22300 Sequence 27	C 176	5	100.0	10	6	AX153067	AX153067 Sequence
104	5	100.0	10	6	I22313	I22313 Sequence 43	177	5	100.0	10	6	AX153078	AX153078 Sequence
105	5	100.0	10	6	I42363	I42363 Sequence 44	178	5	100.0	10	6	AX153090	AX153090 Sequence
C 106	5	100.0	10	6	I48951	I48951 Sequence 4	C 179	5	100.0	10	6	AX153092	AX153092 Sequence
C 107	5	100.0	10	6	I54930	I54930 Sequence 20	C 180	5	100.0	10	6	AX153095	AX153095 Sequence
108	5	100.0	10	6	I54948	I54948 Sequence 38	181	5	100.0	10	6	AX153100	AX153100 Sequence
C 109	5	100.0	10	6	I54948	I54948 Sequence 38	C 182	5	100.0	10	6	AX153143	AX153143 Sequence
110	5	100.0	10	6	I59753	I59753 Sequence 17	183	5	100.0	10	6	AX153153	AX153153 Sequence
111	5	100.0	10	6	I59754	I59754 Sequence 18	184	5	100.0	10	6	AX153186	AX153186 Sequence
C 112	5	100.0	10	6	I73189	I73189 Sequence 3	185	5	100.0	10	6	AX153221	AX153221 Sequence
C 113	5	100.0	10	6	I73190	I73190 Sequence 4	C 186	5	100.0	10	6	AX153237	AX153237 Sequence
C 114	5	100.0	10	6	I73192	I73192 Sequence 6	C 187	5	100.0	10	6	AX153238	AX153238 Sequence
C 115	5	100.0	10	6	I73195	I73195 Sequence 9	188	5	100.0	10	6	AX153265	AX153265 Sequence
C 116	5	100.0	10	6	I73201	I73201 Sequence 15	C 189	5	100.0	10	6	AX153288	AX153288 Sequence
117	5	100.0	10	6	I73590	I73590 Sequence 44	C 190	5	100.0	10	6	AX153377	AX153377 Sequence
C 118	5	100.0	10	6	I79734	I79734 Sequence 30	C 191	5	100.0	10	6	AX153392	AX153392 Sequence
119	5	100.0	10	6	AR200295	AR200295 Sequence	192	5	100.0	10	6	AX153404	AX153404 Sequence
120	5	100.0	10	6	AR214813	AR214813 Sequence	193	5	100.0	10	6	AX153408	AX153408 Sequence
121	5	100.0	10	6	AR215024	AR215024 Sequence	194	5	100.0	10	6	AX153433	AX153433 Sequence
C 122	5	100.0	10	6	AR215025	AR215025 Sequence	195	5	100.0	10	6	AX153553	AX153553 Sequence
C 123	5	100.0	10	6	AR219543	AR219543 Sequence	196	5	100.0	10	6	AX153629	AX153629 Sequence
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REFERENCE	1 (bases 1 to 10)				
AUTHORS	Taniguchi,T.				
TITLE	Improvements in and relating to the regulation of gene expression				
JOURNAL	Patent: EP 0374503-A 5 27-JUN-1990;				
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AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 52 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
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SOURCE
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AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 54 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
FEATURES Other publication AU 5284296 961030.
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ACCESSION A76253
VERSION A76253.1 GI:6088352
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Sandal,N. and Marcker,K.
TITLE BIOLOGICAL MATERIAL
JOURNAL Patent: WO 9319181-A 24 30-SEP-1993;
FEATURES SANDOZ AG (AT); SANDOZ AG (DE)
source Location/Qualifiers
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VERSION AR016245.1 GI:3972522
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SOURCE
ORGANISM
REFERENCE 1
AUTHORS Smith,H.S. and Chen,L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 13 07-JUL-1998;
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Db      |||||
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RESULT 6
AR017948
LOCUS AR017948
DEFINITION Sequence 13 from patent US 5780273.
ACCESSION AR017948
VERSION AR017948.1 GI:3973551
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Burg,J.Lawrence.
TITLE Insertion elements and amplifiable nucleic acids
JOURNAL Patent: US 5780273-A 13 14-JUL-1998;
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      4 GTGGG 8

RESULT 7
AR017953
LOCUS      AR017953      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 18 from patent US 5780273.
ACCESSION  AR017953
VERSION     AR017953.1 GI:3973556
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Burg,J.Lawrence.
TITLE      Insertion elements and amplifiable nucleic acids
JOURNAL    Patent: US 5780273-A 18 14-JUL-1998;
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      6 GTGGG 10

RESULT 8
AR020527/c
LOCUS      AR020527      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5789174.
ACCESSION  AR020527
VERSION     AR020527.1 GI:3975142
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Mouton,C., Guillot,E. and Menard,C.
TITLE      Detection of periodontal pathogens including bacteroides forsythus,
      porphyromonas gingivalis, prevotella intermedia and prevotella
      nigrescens
JOURNAL    Patent: US 5789174-A 3 04-AUG-1998;
FEATURES
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      10 GTGGG 6
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RESULT 9
AR030206
LOCUS      AR030206      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5861246.
ACCESSION  AR030206
VERSION     AR030206.1 GI:5943420
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
      proteins
JOURNAL    Patent: US 5861246-A 17 19-JAN-1999;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 10
AR030217
LOCUS      AR030217      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 28 from patent US 5861246.
ACCESSION  AR030217
VERSION     AR030217.1 GI:5943431
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
      proteins
JOURNAL    Patent: US 5861246-A 28 19-JAN-1999;
FEATURES
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 11
AR030218
LOCUS      AR030218      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5861246.
ACCESSION  AR030218
VERSION     AR030218.1 GI:5943432
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Weissman,S.M., Nallur,G.N. and Kulkarni,P.
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TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 29 19-JAN-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

RESULT 12  
AR030234  
LOCUS AR030234 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 45 from patent US 5861246.  
ACCESSION AR030234  
VERSION AR030234.1 GI:5943448  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 45 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 1 GTGGG 5

RESULT 13  
AR030237  
LOCUS AR030237 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 48 from patent US 5861246.  
ACCESSION AR030237  
VERSION AR030237.1 GI:5943451  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 48 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..10  
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/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 1 GTGGG 5

TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 29 19-JAN-1999;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

RESULT 14  
AR030238  
LOCUS AR030238 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 49 from patent US 5861246.  
ACCESSION AR030238  
VERSION AR030238.1 GI:5943452  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 49 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..10  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 1 GTGGG 5

RESULT 15  
AR032136/c  
LOCUS AR032136 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 6 from patent US 5866699.  
ACCESSION AR032136  
VERSION AR032136.1 GI:5946425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Smyth,A.P.  
TITLE Oligonucleotides with anti-MDR-1 gene activity  
JOURNAL Patent: US 5866699-A 6 02-FEB-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 1 GTGGG 5

RESULT 16  
AR049904  
LOCUS AR049904 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 9 from patent US 5824787.  
ACCESSION AR049904  
VERSION AR049904.1 GI:5971896  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.



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REFERENCE 1 (bases 1 to 10)
AUTHORS Singer,P.A.
TITLE Polynucleotide sizing reagent
JOURNAL Patent: US 5824787-A 9 20-OCT-1998;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      6 GTGGG 10

RESULT 17
AR069288/c
LOCUS AR069288      10 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 27 from patent US 5891631.
ACCESSION AR069288
VERSION AR069288.1 GI:7220176
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
TITLE Methods relating tosterol regulatory element binding proteins
JOURNAL Patent: US 5891631-A 27 06-APR-1999;
FEATURES
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
        |||||
Db      10 GTGGG 6

RESULT 18
AR069301
LOCUS AR069301      10 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 43 from patent US 5891631.
ACCESSION AR069301
VERSION AR069301.1 GI:7220189
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
TITLE Methods relating tosterol regulatory element binding proteins
JOURNAL Patent: US 5891631-A 43 06-APR-1999;
FEATURES
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GTGGG 5
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Db      3 GTGGG 7

RESULT 19
AR074300
LOCUS AR074300      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 108 from patent US 5952490.
ACCESSION AR074300
VERSION AR074300.1 GI:10001055
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 108 14-SEP-1999;
FEATURES
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      3 GTGGG 7

RESULT 20
AR074448/c
LOCUS AR074448      10 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 19 from patent US 5955075.
ACCESSION AR074448
VERSION AR074448.1 GI:10001203
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 19 21-SEP-1999;
FEATURES
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      8 GTGGG 4

RESULT 21
AR081128/c
LOCUS AR081128      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 19 from patent US 5972353.
ACCESSION AR081128
VERSION AR081128.1 GI:10007856
KEYWORDS
SOURCE
    Unknown.
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ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 19 26-OCT-1999;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 22  
AR085325/c  
LOCUS AR085325 10 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 19 from patent US 5981711.  
ACCESSION AR085325  
VERSION AR085325.1 GI:10012094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN-specific antibodies and hybridomas  
JOURNAL Patent: US 5981711-A 19 09-NOV-1999;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 23  
AR088073/c  
LOCUS AR088073 10 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 19 from patent US 5989838.  
ACCESSION AR088073  
VERSION AR088073.1 GI:10014836  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Immunological methods of detecting MN proteins and MN polypeptides  
JOURNAL Patent: US 5989838-A 19 23-NOV-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 8 GTGGG 4

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 24  
AR092703  
LOCUS AR092703 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 15 from patent US 5998193.  
ACCESSION AR092703  
VERSION AR092703.1 GI:10019455  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 15 07-DEC-1999;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
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Db 5 GTGGG 9

RESULT 25  
AR098894/c  
LOCUS AR098894 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 30 from patent US 6077685.  
ACCESSION AR098894  
VERSION AR098894.1 GI:12808660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.  
TITLE Tumor suppressor merlin and antibodies thereof  
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 26  
AR102396/c  
LOCUS AR102396 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 21 from patent US 6083923.  
ACCESSION AR102396  
VERSION AR102396.1 GI:12813194  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and Mehta,R.C.  
TITLE Liposomal oligonucleotide compositions for modulating RAS gene expression  
JOURNAL Patent: US 6083923-A 21 04-JUL-2000;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4  
RESULT 27  
AR102399/c  
LOCUS AR102399 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 24 from patent US 6083923.  
ACCESSION AR102399  
VERSION AR102399.1 GI:12813197  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and Mehta,R.C.  
TITLE Liposomal oligonucleotide compositions for modulating RAS gene expression  
JOURNAL Patent: US 6083923-A 24 04-JUL-2000;  
FEATURES Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4  
RESULT 28  
AR104232/c  
LOCUS AR104232 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 19 from patent US 6093548.  
ACCESSION AR104232  
VERSION AR104232.1 GI:12816940  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Detection and quantitation of MN-specific antibodies  
JOURNAL Patent: US 6093548-A 19 25-JUL-2000;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
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Db 8 GTGGG 4  
RESULT 29  
AR106687  
LOCUS AR106687 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 15 from patent US 6107078.  
ACCESSION AR106687  
VERSION AR106687.1 GI:12821217  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 6107078-A 15 22-AUG-2000;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
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Db 5 GTGGG 9  
RESULT 30  
AR107349  
LOCUS AR107349 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 38 from patent US 6109776.  
ACCESSION AR107349  
VERSION AR107349.1 GI:12822836  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Haas,J.  
TITLE Method and system for computationally identifying clusters within a set of sequences  
JOURNAL Patent: US 6109776-A 38 29-AUG-2000;  
FEATURES Location/Qualifiers  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
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Db 2 GTGGG 6  
RESULT 31  
AR119493  
LOCUS AR119493 10 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 16 from patent US 6153382.  
ACCESSION AR119493  
VERSION AR119493.1 GI:14102192  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.  
TITLE Viral growth inhibition  
JOURNAL Patent: US 6153382-A 16 28-NOV-2000;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db |||||  
2 GTGGG 6  
RESULT 32  
AR137926  
LOCUS AR137926 10 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 2 from patent US 6197580.  
ACCESSION AR137926  
VERSION AR137926.1 GI:14479435  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Susulic,V.S. and Duzic,E.  
TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene  
JOURNAL Patent: US 6197580-A 2 06-MAR-2001;  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 19 from patent US 6204370.  
ACCESSION AR143496  
VERSION AR143496.1 GI:15104782  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6204370-A 19 20-MAR-2001;  
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LOCUS AR168826 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 52 from patent US 6288042.  
ACCESSION AR168826  
VERSION AR168826.1 GI:17904948  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 52 11-SEP-2001;  
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LOCUS AR175405 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 128 from patent US 6309823.  
ACCESSION AR175405  
VERSION AR175405.1 GI:17916704  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.  
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes and methods of using the same  
JOURNAL Patent: US 6309823-A 128 30-OCT-2001;  
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GO1N37/00,  
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LOCUS BD238733 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238733  
VERSION BD238733.1 GI:33048503  
KEYWORDS JP 2002534056-A/151.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 151 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/151  
PD 15-OCT-2002  
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PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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LOCUS BD238817 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238817  
VERSION BD238817.1 GI:33048587  
KEYWORDS JP 2002534056-A/235.  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 235 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/235  
PD 15-OCT-2002  
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PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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BD238834

LOCUS BD238834 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238834  
VERSION BD238834.1 GI:33048604  
KEYWORDS JP 2002534056-A/252.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 252 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
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PD 15-OCT-2002  
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238855  
VERSION BD238855.1 GI:33048625  
KEYWORDS JP 2002534056-A/273.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines

JOURNAL Patent: JP 2002534056-A 273 15-OCT-2002;  
GENZYME CORP  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238880  
VERSION BD238880.1 GI:33048650  
KEYWORDS JP 2002534056-A/298.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 298 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
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PD 15-OCT-2002  
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LOCUS BD238901 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
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VERSION BD238901.1 GI:33048671
KEYWORDS JP 2002534056-A/319.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 319 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/319
PD 15-OCT-2002
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RESULT 45
BD238903
LOCUS BD238903 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238903
VERSION BD238903.1 GI:33048673
KEYWORDS JP 2002534056-A/321.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 321 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/321
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21	5	100.0	10	2	AAQ96600 HIV-1 NL4

22	5	100.0	10	2	AAQ96492	HIV-1 NL4
23	5	100.0	10	2	AAQ96491	HIV-1 NL4
24	5	100.0	10	2	AAQ97088	HIV-1 NL4
25	5	100.0	10	2	AAQ96601	HIV-1 NL4
26	5	100.0	10	2	AAQ97086	HIV-1 NL4
27	5	100.0	10	2	AAQ97089	HIV-1 NL4
28	5	100.0	10	2	AAQ97090	HIV-1 NL4
29	5	100.0	10	2	AAQ96597	HIV-1 NL4
30	5	100.0	10	2	AAQ96490	HIV-1 NL4
31	5	100.0	10	2	AAQ96489	HIV-1 NL4
32	5	100.0	10	2	AAQ96599	HIV-1 NL4
33	5	100.0	10	2	AAQ97091	HIV-1 NL4
34	5	100.0	10	2	AAQ96598	HIV-1 NL4
35	5	100.0	10	2	AAQ97087	HIV-1 NL4
36	5	100.0	10	2	AAQ79835	H-ras mod
37	5	100.0	10	2	AAQ79834	H-ras mod
38	5	100.0	10	2	AAT14316	IgE bindi
39	5	100.0	10	2	AAT98863	Core-bind
40	5	100.0	10	2	AAT98860	Core-bind
41	5	100.0	10	2	AAT98847	Binding s
42	5	100.0	10	2	AAT98837	Binding s
43	5	100.0	10	2	AAT98848	Binding s
44	5	100.0	10	2	AAT98864	Core-bind
45	5	100.0	10	2	AAT51668	Viral int
46	5	100.0	10	2	AAT59107	Activated
47	5	100.0	10	2	AAT59104	Activated
48	5	100.0	10	2	AAV10687	Human bre
49	5	100.0	10	2	AAT96115	Target si
50	5	100.0	10	2	AAT96109	Calibrati
51	5	100.0	10	2	AAT96112	Calibrati
52	5	100.0	10	2	AAT96121	Oligo hav
53	5	100.0	10	2	AAT96110	Calibrati
54	5	100.0	10	2	AAV41212	Prevotell
55	5	100.0	10	2	AAV34554	Homo sapi
56	5	100.0	10	2	AAV61922	Molecular
57	5	100.0	10	2	AAV56034	Acacia sp
58	5	100.0	10	2	AAV50168	Yeast tag
59	5	100.0	10	2	AAV79250	Oligonuc
60	5	100.0	10	2	AAV35972	Primer us
61	5	100.0	10	2	AAX18637	p53 seria
62	5	100.0	10	2	AAX06502	Possible
63	5	100.0	10	2	AAX56980	Ras gene
64	5	100.0	10	2	AAX56977	Ras gene
65	5	100.0	10	2	AAX54743	Human end
66	5	100.0	10	2	AAX54790	Human maj
67	5	100.0	10	2	AAX99925	Human par
68	5	100.0	10	2	AAX86206	SAGE tag
69	5	100.0	10	2	AAZ21919	Fragment
70	5	100.0	10	2	AAZ21069	LDL recep
71	5	100.0	10	3	AAZ99303	Probe use
72	5	100.0	10	3	AAA34190	Human ade
73	5	100.0	10	3	AAA34237	Human ade
74	5	100.0	10	3	AAA11719	Human MIF
75	5	100.0	10	3	AAA38533	Random an
76	5	100.0	10	3	AAZ79533	Human den
77	5	100.0	10	3	AAZ78452	Human den
78	5	100.0	10	3	AAZ78522	Human den
79	5	100.0	10	3	AAZ79295	Human den
80	5	100.0	10	3	AAZ79343	Human den
81	5	100.0	10	3	AAZ77995	Human den
82	5	100.0	10	3	AAZ78097	Human den
83	5	100.0	10	3	AAZ78896	Human den
84	5	100.0	10	3	AAZ79096	Human den
85	5	100.0	10	3	AAZ79282	Human den
86	5	100.0	10	3	AAZ77982	Human den
87	5	100.0	10	3	AAZ78651	Human den
88	5	100.0	10	3	AAZ78838	Human den
89	5	100.0	10	3	AAZ77824	Human den
90	5	100.0	10	3	AAZ79579	Human den
91	5	100.0	10	3	AAZ77582	Human den
92	5	100.0	10	3	AAZ77960	Human den
93	5	100.0	10	3	AAZ77717	Human den
94	5	100.0	10	3	AAZ79074	Human den

95	5	100.0	10	3	AAZ79082	Aaz79082	Human	den
96	5	100.0	10	3	AAZ79653	Aaz79653	Human	den
c 97	5	100.0	10	3	AAZ79665	Aaz79665	Human	den
c 98	5	100.0	10	3	AAZ79668	Aaz79668	Human	den
99	5	100.0	10	3	AAZ77723	Aaz77723	Human	den
c 100	5	100.0	10	3	AAZ78302	Aaz78302	Human	den
101	5	100.0	10	3	AAZ79210	Aaz79210	Human	den
102	5	100.0	10	3	AAZ79300	Aaz79300	Human	den
c 103	5	100.0	10	3	AAZ79691	Aaz79691	Human	den
104	5	100.0	10	3	AAZ77807	Aaz77807	Human	den
105	5	100.0	10	3	AAZ78332	Aaz78332	Human	den
106	5	100.0	10	3	AAZ77891	Aaz77891	Human	den
107	5	100.0	10	3	AAZ77893	Aaz77893	Human	den
108	5	100.0	10	3	AAZ77959	Aaz77959	Human	den
109	5	100.0	10	3	AAZ78258	Aaz78258	Human	den
110	5	100.0	10	3	AAZ78298	Aaz78298	Human	den
111	5	100.0	10	3	AAZ78853	Aaz78853	Human	den
112	5	100.0	10	3	AAZ79480	Aaz79480	Human	den
113	5	100.0	10	3	AAZ77845	Aaz77845	Human	den
c 114	5	100.0	10	3	AAZ77870	Aaz77870	Human	den
c 115	5	100.0	10	3	AAZ78892	Aaz78892	Human	den
c 116	5	100.0	10	3	AAZ79240	Aaz79240	Human	den
c 117	5	100.0	10	3	AAZ79626	Aaz79626	Human	den
c 118	5	100.0	10	3	AAZ78030	Aaz78030	Human	den
119	5	100.0	10	3	AAZ79491	Aaz79491	Human	den
120	5	100.0	10	3	AAZ82077	Aaz82077	Metastati	
c 121	5	100.0	10	3	AAZ82692	Aaz82692	Metastati	
c 122	5	100.0	10	3	AAZ83173	Aaz83173	Metastati	
c 123	5	100.0	10	3	AAZ83806	Aaz83806	Metastati	
124	5	100.0	10	3	AAZ85126	Aaz85126	Metastati	
125	5	100.0	10	3	AAZ85906	Aaz85906	Metastati	
126	5	100.0	10	3	AAZ85952	Aaz85952	Metastati	
127	5	100.0	10	3	AAZ81537	Aaz81537	Metastati	
128	5	100.0	10	3	AAZ81685	Aaz81685	Metastati	
c 129	5	100.0	10	3	AAZ81738	Aaz81738	Metastati	
130	5	100.0	10	3	AAZ82136	Aaz82136	Metastati	
131	5	100.0	10	3	AAZ82303	Aaz82303	Metastati	
c 132	5	100.0	10	3	AAZ82622	Aaz82622	Metastati	
133	5	100.0	10	3	AAZ83235	Aaz83235	Metastati	
c 134	5	100.0	10	3	AAZ83670	Aaz83670	Metastati	
c 135	5	100.0	10	3	AAZ84055	Aaz84055	Metastati	
136	5	100.0	10	3	AAZ84983	Aaz84983	Metastati	
137	5	100.0	10	3	AAZ85812	Aaz85812	Metastati	
c 138	5	100.0	10	3	AAZ86359	Aaz86359	Metastati	
c 139	5	100.0	10	3	AAZ81518	Aaz81518	Metastati	
c 140	5	100.0	10	3	AAZ83346	Aaz83346	Metastati	
141	5	100.0	10	3	AAZ84949	Aaz84949	Metastati	
142	5	100.0	10	3	AAZ85005	Aaz85005	Metastati	
143	5	100.0	10	3	AAZ85077	Aaz85077	Metastati	
c 144	5	100.0	10	3	AAZ85128	Aaz85128	Metastati	
c 145	5	100.0	10	3	AAZ85373	Aaz85373	Metastati	
c 146	5	100.0	10	3	AAZ85429	Aaz85429	Metastati	
147	5	100.0	10	3	AAZ85905	Aaz85905	Metastati	
148	5	100.0	10	3	AAZ86647	Aaz86647	Metastati	
c 149	5	100.0	10	3	AAZ81058	Aaz81058	Metastati	
150	5	100.0	10	3	AAZ81641	Aaz81641	Metastati	
151	5	100.0	10	3	AAZ82810	Aaz82810	Metastati	
c 152	5	100.0	10	3	AAZ83000	Aaz83000	Metastati	
153	5	100.0	10	3	AAZ85848	Aaz85848	Metastati	
c 154	5	100.0	10	3	AAZ81153	Aaz81153	Metastati	
c 155	5	100.0	10	3	AAZ81530	Aaz81530	Metastati	
c 156	5	100.0	10	3	AAZ81943	Aaz81943	Metastati	
c 157	5	100.0	10	3	AAZ82313	Aaz82313	Metastati	
c 158	5	100.0	10	3	AAZ82384	Aaz82384	Metastati	
159	5	100.0	10	3	AAZ83971	Aaz83971	Metastati	
160	5	100.0	10	3	AAZ84193	Aaz84193	Metastati	
161	5	100.0	10	3	AAZ84711	Aaz84711	Metastati	
c 162	5	100.0	10	3	AAZ80956	Aaz80956	Metastati	
c 163	5	100.0	10	3	AAZ81143	Aaz81143	Metastati	
164	5	100.0	10	3	AAZ82267	Aaz82267	Metastati	
c 165	5	100.0	10	3	AAZ84353	Aaz84353	Metastati	
166	5	100.0	10	3	AAZ85202	Aaz85202	Metastati	
c 167	5	100.0	10	3	AAZ81573	Aaz81573	Metastati	

168	5	100.0	10	3	AAZ83148	Aaz83148	Metastati	
c 169	5	100.0	10	3	AAZ86340	Aaz86340	Metastati	
c 170	5	100.0	10	3	AAZ81470	Aaz81470	Metastati	
171	5	100.0	10	3	AAZ81487	Aaz81487	Metastati	
c 172	5	100.0	10	3	AAZ81619	Aaz81619	Metastati	
173	5	100.0	10	3	AAZ82078	Aaz82078	Metastati	
174	5	100.0	10	3	AAZ82082	Aaz82082	Metastati	
175	5	100.0	10	3	AAZ82588	Aaz82588	Metastati	
c 176	5	100.0	10	3	AAZ83819	Aaz83819	Metastati	
177	5	100.0	10	3	AAZ84672	Aaz84672	Metastati	
178	5	100.0	10	3	AAZ84852	Aaz84852	Metastati	
179	5	100.0	10	3	AAZ84889	Aaz84889	Metastati	
c 180	5	100.0	10	3	AAZ85630	Aaz85630	Metastati	
181	5	100.0	10	3	AAZ85849	Aaz85849	Metastati	
182	5	100.0	10	3	AAZ81353	Aaz81353	Metastati	
c 183	5	100.0	10	3	AAZ81627	Aaz81627	Metastati	
184	5	100.0	10	3	AAZ82441	Aaz82441	Metastati	
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186	5	100.0	10	3	AAZ82526	Aaz82526	Metastati	
c 187	5	100.0	10	3	AAZ82917	Aaz82917	Metastati	
188	5	100.0	10	3	AAZ82931	Aaz82931	Metastati	
189	5	100.0	10	3	AAZ83237	Aaz83237	Metastati	
190	5	100.0	10	3	AAZ83274	Aaz83274	Metastati	
191	5	100.0	10	3	AAZ83930	Aaz83930	Metastati	
c 192	5	100.0	10	3	AAZ84387	Aaz84387	Metastati	
193	5	100.0	10	3	AAZ85206	Aaz85206	Metastati	
c 194	5	100.0	10	3	AAZ85896	Aaz85896	Metastati	
c 195	5	100.0	10	3	AAZ86467	Aaz86467	Metastati	
c 196	5	100.0	10	3	AAZ81044	Aaz81044	Metastati	
197	5	100.0	10	3	AAZ81631	Aaz81631	Metastati	
c 198	5	100.0	10	3	AAZ81646	Aaz81646	Metastati	
199	5	100.0	10	3	AAZ81665	Aaz81665	Metastati	
c 200	5	100.0	10	3	AAZ81836	Aaz81836	Metastati	
c 201	5	100.0	10	3	AAZ82268	Aaz82268	Metastati	
c 202	5	100.0	10	3	AAZ82340	Aaz82340	Metastati	
203	5	100.0	10	3	AAZ82576	Aaz82576	Metastati	
c 204	5	100.0	10	3	AAZ83818	Aaz83818	Metastati	
c 205	5	100.0	10	3	AAZ84403	Aaz84403	Metastati	
c 206	5	100.0	10	3	AAZ84599	Aaz84599	Metastati	
c 207	5	100.0	10	3	AAZ85178	Aaz85178	Metastati	
208	5	100.0	10	3	AAZ85300	Aaz85300	Metastati	
c 209	5	100.0	10	3	AAZ85820	Aaz85820	Metastati	
210	5	100.0	10	3	AAZ81932	Aaz81932	Metastati	
c 211	5	100.0	10	3	AAZ82058	Aaz82058	Metastati	
c 212	5	100.0	10	3	AAZ82648	Aaz82648	Metastati	
c 213	5	100.0	10	3	AAZ85400	Aaz85400	Metastati	
c 214	5	100.0	10	3	AAZ86378	Aaz86378	Metastati	
215	5	100.0	10	3	AAZ80904	Aaz80904	Metastati	
216	5	100.0	10	3	AAZ82438	Aaz82438	Metastati	
217	5	100.0	10	3	AAZ82583	Aaz82583	Metastati	
c 218	5	100.0	10	3	AAZ82805	Aaz82805	Metastati	
c 219	5	100.0	10	3	AAZ83865	Aaz83865	Metastati	
c 220	5	100.0	10	3	AAZ83973	Aaz83973	Metastati	
221	5	100.0	10	3	AAZ85301	Aaz85301	Metastati	
c 222	5	100.0	10	3	AAZ85816	Aaz85816	Metastati	
c 223	5	100.0	10	3	AAZ85862	Aaz85862	Metastati	
c 224	5	100.0	10	3	AAZ81218	Aaz81218	Metastati	
225	5	100.0	10	3	AAZ81663	Aaz81663	Metastati	
226	5	100.0	10	3	AAZ82763	Aaz82763	Metastati	
227	5	100.0	10	3	AAZ83051	Aaz83051	Metastati	
c 228	5	100.0	10	3	AAZ83443	Aaz83443	Metastati	
229	5	100.0	10	3	AAZ86586	Aaz86586	Metastati	
c 230	5	100.0	10	3	AAZ81257	Aaz81257	Metastati	
c 231	5	100.0	10	3	AAZ81415	Aaz81415	Metastati	
232	5	100.0	10	3	AAZ82112	Aaz82112	Metastati	
233	5	100.0	10	3	AAZ83458	Aaz83458	Metastati	
234	5	100.0	10	3	AAZ84162	Aaz84162	Metastati	
c 235	5	100.0	10	3	AAZ85890	Aaz85890	Metastati	
236	5	100.0	10	3	AAZ85907	Aaz85907	Metastati	
237	5	100.0	10	3	AAZ86190	Aaz86190	Metastati	
238	5	100.0	10	3	AAZ86273	Aaz86273	Metastati	
c 239	5	100.0	10	3	AAZ82085	Aaz82085	Metastati	
c 240	5	100.0	10	3	AAZ82825	Aaz82825	Metastati	

C 241	5	100.0	10	3	AAZ82897	Aaz82897 Metastati
C 242	5	100.0	10	3	AAZ83469	Aaz83469 Metastati
C 243	5	100.0	10	3	AAZ84558	Aaz84558 Metastati
C 244	5	100.0	10	3	AAZ85227	Aaz85227 Metastati
C 245	5	100.0	10	3	AAZ85908	Aaz85908 Metastati
C 246	5	100.0	10	3	AAZ81426	Aaz81426 Metastati
C 247	5	100.0	10	3	AAZ83236	Aaz83236 Metastati
C 248	5	100.0	10	3	AAZ84106	Aaz84106 Metastati
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C 252	5	100.0	10	3	AAZ85909	Aaz85909 Metastati
C 253	5	100.0	10	3	AAZ86349	Aaz86349 Metastati
C 254	5	100.0	10	3	AAA93870	Aaa93870 Oligonuc
C 255	5	100.0	10	3	AAZ74192	Aac74192 Human mon
C 256	5	100.0	10	3	AAZ74198	Aac74198 Human mon
C 257	5	100.0	10	3	AAZ74131	Aac74131 Human mon
C 258	5	100.0	10	3	AAZ74116	Aac74116 Human mon
C 259	5	100.0	10	3	AAZ74140	Aac74140 Human mon
C 260	5	100.0	10	3	AAZ74146	Aac74146 Human mon
C 261	5	100.0	10	3	AAZ73943	Aac73943 Human den
C 262	5	100.0	10	3	AAA56447	Aaa56447 Human mac
C 263	5	100.0	10	3	AAA56470	Aaa56470 Human mac
C 264	5	100.0	10	3	AAA56510	Aaa56510 Human mac
C 265	5	100.0	10	3	AAA56127	Aaa56127 Human mon
C 266	5	100.0	10	3	AAA56427	Aaa56427 Human mac
C 267	5	100.0	10	3	AAA56255	Aaa56255 Human mac
C 268	5	100.0	10	3	AAA56439	Aaa56439 Human mac
C 269	5	100.0	10	3	AAA56516	Aaa56516 Human mac
C 270	5	100.0	10	3	AAA56350	Aaa56350 Human mac
C 271	5	100.0	10	3	AAA56458	Aaa56458 Human mac
C 272	5	100.0	10	3	AAA56210	Aaa56210 Human mac
C 273	5	100.0	10	3	AAA56190	Aaa56190 Human mon
C 274	5	100.0	10	3	AAA56366	Aaa56366 Human mac
C 275	5	100.0	10	3	AAA56506	Aaa56506 Human mac
C 276	5	100.0	10	3	AAA56310	Aaa56310 Human mac
C 277	5	100.0	10	3	AAA56409	Aaa56409 Human mac
C 278	5	100.0	10	3	AAA56493	Aaa56493 Human mac
C 279	5	100.0	10	3	AAA56249	Aaa56249 Human mac
C 280	5	100.0	10	3	AAA56303	Aaa56303 Human mac
C 281	5	100.0	10	3	AAA53295	AAA53295 Putative
C 282	5	100.0	10	3	AAZ79727	Aaz79727 Human col
C 283	5	100.0	10	3	AAZ79795	Aaz79795 Human cys
C 284	5	100.0	10	3	AAZ79914	Aaz79914 Human den
C 285	5	100.0	10	3	AAZ88680	Aaz88680 Ras RNA b
C 286	5	100.0	10	3	AAZ88681	Aaz88681 Ras RNA b
C 287	5	100.0	10	3	AAZ88692	Aaz88692 Ras RNA b
C 288	5	100.0	10	3	AAZ88686	Aaz88686 Ras RNA R
C 289	5	100.0	10	3	AAZ88683	Aaz88683 Ras RNA b
C 290	5	100.0	10	3	AAF20359	Aaf20359 Human eos
C 291	5	100.0	10	3	AAF20312	Aaf20312 Human end
C 292	5	100.0	10	3	AAAG1026	Aaa61026 Protein b
C 293	5	100.0	10	3	AAA61030	Aaa61030 Protein b
C 294	5	100.0	10	3	AAA61002	Aaa61002 Protein b
C 295	5	100.0	10	3	AAA61012	Aaa61012 Protein b
C 296	5	100.0	10	3	AAA61029	Aaa61029 Protein b
C 297	5	100.0	10	3	AAA61013	Aaa61013 Protein b
C 298	5	100.0	10	3	AAA87903	Aaa87903 Human bet
C 299	5	100.0	10	3	AAZ74367	Aaa74367 Mouse tra
C 300	5	100.0	10	4	AAH18983	Aah18983 UCP3 poly
C 301	5	100.0	10	4	AAH18997	Aah18997 UCP3 poly
C 302	5	100.0	10	4	AAF92227	Aaf92227 Human IGE
C 303	5	100.0	10	4	AAH44165	Aah44165 Mycoplasm
C 304	5	100.0	10	4	AAH19959	Aah19959 Mouse Tre
C 305	5	100.0	10	4	AAI67368	Aai67368 Human FXB
C 306	5	100.0	10	4	AAI67366	Aai67366 Human FXB
C 307	5	100.0	10	4	AAI67376	Aai67376 Human FXB
C 308	5	100.0	10	4	AAI67386	Aai67386 Human FXB
C 309	5	100.0	10	4	AAD20861	Aad20861 Human CHR
C 310	5	100.0	10	4	AAF92848	Aaf92848 Transcrip
C 311	5	100.0	10	4	AAO44442	Aas04442 Human DAX
C 312	5	100.0	10	4	AAO44445	Aas04445 Human DAX
C 313	5	100.0	10	4	AAH63392	Aah63392 Human can

C 314	5	100.0	10	4	AAH63932	Aah63932 Human ubi
C 315	5	100.0	10	4	AAH63985	Aah63985 Human ubi
C 316	5	100.0	10	4	AAH64002	Aah64002 Human ubi
C 317	5	100.0	10	4	AAH64452	Aah64452 Human ubi
C 318	5	100.0	10	4	AAH64467	Aah64467 Human ubi
C 319	5	100.0	10	4	AAH63172	Aah63172 Human col
C 320	5	100.0	10	4	AAH63774	Aah63774 Human ubi
C 321	5	100.0	10	4	AAH63829	Aah63829 Human ubi
C 322	5	100.0	10	4	AAH64056	Aah64056 Human ubi
C 323	5	100.0	10	4	AAH64167	Aah64167 Human ubi
C 324	5	100.0	10	4	AAH64218	Aah64218 Human ubi
C 325	5	100.0	10	4	AAH64363	Aah64363 Human ubi
C 326	5	100.0	10	4	AAH64508	Aah64508 Human ubi
C 327	5	100.0	10	4	AAH64261	Aah64261 Human ubi
C 328	5	100.0	10	4	AAH64312	Aah64312 Human ubi
C 329	5	100.0	10	4	AAH64704	Aah64704 Human hig
C 330	5	100.0	10	4	AAH63380	Aah63380 Human kid
C 331	5	100.0	10	4	AAH64062	Aah64062 Human ubi
C 332	5	100.0	10	4	AAH64228	Aah64228 Human ubi
C 333	5	100.0	10	4	AAH64005	Aah64005 Human ubi
C 334	5	100.0	10	4	AAH64110	Aah64110 Human ubi
C 335	5	100.0	10	4	AAH64153	Aah64153 Human ubi
C 336	5	100.0	10	4	AAH64175	Aah64175 Human ubi
C 337	5	100.0	10	4	AAH64296	Aah64296 Human ubi
C 338	5	100.0	10	4	AAH64628	Aah64628 Human col
C 339	5	100.0	10	4	AAH63625	Aah63625 Human ubi
C 340	5	100.0	10	4	AAH64142	Aah64142 Human ubi
C 341	5	100.0	10	4	AAH64165	Aah64165 Human ubi
C 342	5	100.0	10	4	AAH63434	Aah63434 Human ubi
C 343	5	100.0	10	4	AAH64006	Aah64006 Human ubi
C 344	5	100.0	10	4	AAH64170	Aah64170 Human ubi
C 345	5	100.0	10	4	AAH63931	Aah63931 Human ubi
C 346	5	100.0	10	4	AAH63437	Aah63437 Human ubi
C 347	5	100.0	10	4	AAH64007	Aah64007 Human ubi
C 348	5	100.0	10	4	AAH64313	Aah64313 Human ubi
C 349	5	100.0	10	4	AAH64340	Aah64340 Human ubi
C 350	5	100.0	10	4	AAH64479	Aah64479 Human ubi
C 351	5	100.0	10	4	AAH64483	Aah64483 Human ubi
C 352	5	100.0	10	4	AAH63542	Aah63542 Human ubi
C 353	5	100.0	10	4	AAH63272	Aah63272 Human col
C 354	5	100.0	10	4	AAO57300	Aas57300 Human CHR
C 355	5	100.0	10	4	AAO57302	Aas57302 Human CHR
C 356	5	100.0	10	4	AAO57322	Aas57322 Human CHR
C 357	5	100.0	10	4	AAO57297	Aas57297 Human CHR
C 358	5	100.0	10	4	AAH20534	Aah20534 Human MTR
C 359	5	100.0	10	4	AAD20724	Aad20724 Primer #1
C 360	5	100.0	10	4	AAH32836	Aah32836 LPS activ
C 361	5	100.0	10	4	AAH32744	Aah32744 LPS activ
C 362	5	100.0	10	4	AAH32791	Aah32791 LPS activ
C 363	5	100.0	10	4	AAH32695	Aah32695 LPS activ
C 364	5	100.0	10	4	AAH32683	Aah32683 LPS activ
C 365	5	100.0	10	4	AAH32902	Aah32902 LPS activ
C 366	5	100.0	10	4	AAH32823	Aah32823 LPS activ
C 367	5	100.0	10	4	AAH32820	Aah32820 LPS activ
C 368	5	100.0	10	4	AAH32646	Aah32646 LPS activ
C 369	5	100.0	10	4	AAH32853	Aah32853 LPS activ
C 370	5	100.0	10	4	ABA81639	Aba81639 Human pho
C 371	5	100.0	10	4	ABA81642	Aba81642 Human pho
C 372	5	100.0	10	4	ABA81658	Aba81658 Human pho
C 373	5	100.0	10	4	ABA81679	Aba81679 Human pho
C 374	5	100.0	10	5	ABA06033	Aba06033 Human nor
C 375	5	100.0	10	5	ABA06089	Aba06089 Human nor
C 376	5	100.0	10	5	ABA06170	Aba06170 Human nor
C 377	5	100.0	10	5	ABA06037	Aba06037 Human nor
C 378	5	100.0	10	5	AAH18799	Aah18799 Human IL4
C 379	5	100.0	10	5	AAH42689	Aah42689 Nucleotid
C 380	5	100.0	10	5	AAF70437	Aaf70437 Human DRD
C 381	5	100.0	10	5	AAF70447	Aaf70447 Human DRD
C 382	5	100.0	10	5	AAF70449	Aaf70449 Human DRD
C 383	5	100.0	10	5	AAF27930	Aaf27930 Interleuk
C 384	5	100.0	10	5	AAF69606	Aaf69606 Human IL4
C 385	5	100.0	10	5	AAF69607	Aaf69607 Human IL4
C 386	5	100.0	10	5	AAF69657	Aaf69657 Human IL4



C 387	5	100.0	10	5	AAF69621	Aaf69621	Human IL4
C 388	5	100.0	10	5	AAF74057	Aaf74057	Human SLC
C 389	5	100.0	10	5	AAF74045	Aaf74045	Human SLC
C 390	5	100.0	10	5	AAF74009	Aaf74009	Human SLC
C 391	5	100.0	10	5	ABA83159	Aba83159	Apolipopr
C 392	5	100.0	10	5	ABA83152	Aba83152	Leukocyte
C 393	5	100.0	10	5	ABA83181	Aba83181	Human ova
C 394	5	100.0	10	5	AAF37432	Aaf37432	Yeast NOR
C 395	5	100.0	10	5	AAF37976	Aaf37976	Yeast NOR
C 396	5	100.0	10	5	AAF39447	Aaf39447	Yeast NOR
C 397	5	100.0	10	5	AAF39820	Aaf39820	Yeast NOR
C 398	5	100.0	10	5	AAF40013	Aaf40013	Yeast NOR
C 399	5	100.0	10	5	AAF35350	Aaf35350	Yeast NOR
C 400	5	100.0	10	5	AAF37938	Aaf37938	Yeast NOR
C 401	5	100.0	10	5	AAF40211	Aaf40211	Yeast NOR
C 402	5	100.0	10	5	AAF42869	Aaf42869	Yeast NOR
C 403	5	100.0	10	5	AAF42871	Aaf42871	Yeast NOR
C 404	5	100.0	10	5	AAF33385	Aaf33385	Yeast NOR
C 405	5	100.0	10	5	AAF333917	Aaf333917	Yeast NOR
C 406	5	100.0	10	5	AAF34850	Aaf34850	Yeast NOR
C 407	5	100.0	10	5	AAF40921	Aaf40921	Yeast NOR
C 408	5	100.0	10	5	AAF43725	Aaf43725	Yeast NOR
C 409	5	100.0	10	5	AAF36503	Aaf36503	Yeast NOR
C 410	5	100.0	10	5	AAF37657	Aaf37657	Yeast NOR
C 411	5	100.0	10	5	AAF38182	Aaf38182	Yeast NOR
C 412	5	100.0	10	5	AAF41877	Aaf41877	Yeast NOR
C 413	5	100.0	10	5	AAF33958	Aaf33958	Yeast NOR
C 414	5	100.0	10	5	AAF35176	Aaf35176	Yeast NOR
C 415	5	100.0	10	5	AAF43379	Aaf43379	Yeast NOR
C 416	5	100.0	10	5	AAF34255	Aaf34255	Yeast NOR
C 417	5	100.0	10	5	AAF38950	Aaf38950	Yeast NOR
C 418	5	100.0	10	5	AAF40918	Aaf40918	Yeast NOR
C 419	5	100.0	10	5	AAF40920	Aaf40920	Yeast NOR
C 420	5	100.0	10	5	AAF41626	Aaf41626	Yeast NOR
C 421	5	100.0	10	5	AAF43293	Aaf43293	Yeast NOR
C 422	5	100.0	10	5	AAF43762	Aaf43762	Yeast NOR
C 423	5	100.0	10	5	AAF33918	Aaf33918	Yeast NOR
C 424	5	100.0	10	5	AAF34643	Aaf34643	Yeast NOR
C 425	5	100.0	10	5	AAF39821	Aaf39821	Yeast NOR
C 426	5	100.0	10	5	AAF40922	Aaf40922	Yeast NOR
C 427	5	100.0	10	5	AAF42078	Aaf42078	Yeast NOR
C 428	5	100.0	10	5	AAF43603	Aaf43603	Yeast NOR
C 429	5	100.0	10	5	AAF35838	Aaf35838	Yeast NOR
C 430	5	100.0	10	5	AAF36522	Aaf36522	Yeast NOR
C 431	5	100.0	10	5	AAF37164	Aaf37164	Yeast NOR
C 432	5	100.0	10	5	AAF39252	Aaf39252	Yeast NOR
C 433	5	100.0	10	5	AAF40919	Aaf40919	Yeast NOR
C 434	5	100.0	10	5	AAF42060	Aaf42060	Yeast NOR
C 435	5	100.0	10	5	AAF42118	Aaf42118	Yeast NOR
C 436	5	100.0	10	5	AAF37459	Aaf37459	Yeast NOR
C 437	5	100.0	10	5	AAF37691	Aaf37691	Yeast NOR
C 438	5	100.0	10	5	AAF42861	Aaf42861	Yeast NOR
C 439	5	100.0	10	5	AAF38128	Aaf38128	Yeast NOR
C 440	5	100.0	10	5	AAF43380	Aaf43380	Yeast NOR
C 441	5	100.0	10	5	AAF35354	Aaf35354	Yeast NOR
C 442	5	100.0	10	5	AAF36493	Aaf36493	Yeast NOR
C 443	5	100.0	10	5	AAF33916	Aaf33916	Yeast NOR
C 444	5	100.0	10	5	AAF39535	Aaf39535	Yeast NOR
C 445	5	100.0	10	5	AAF40917	Aaf40917	Yeast NOR
C 446	5	100.0	10	5	AAF37936	Aaf37936	Yeast NOR
C 447	5	100.0	10	5	AAF34394	Aaf34394	Yeast NOR
C 448	5	100.0	10	5	AAF37937	Aaf37937	Yeast NOR
C 449	5	100.0	10	5	AAF41499	Aaf41499	Yeast NOR
C 450	5	100.0	10	5	AAF42059	Aaf42059	Yeast NOR
C 451	5	100.0	10	5	AAF42804	Aaf42804	Yeast NOR
C 452	5	100.0	10	5	AAF37786	Aaf37786	Yeast NOR
C 453	5	100.0	10	5	AAF38496	Aaf38496	Yeast NOR
C 454	5	100.0	10	5	AAF40576	Aaf40576	Yeast NOR
C 455	5	100.0	10	5	AAF43044	Aaf43044	Yeast NOR
C 456	5	100.0	10	5	AAF43607	Aaf43607	Yeast NOR
C 457	5	100.0	10	5	AAF43738	Aaf43738	Yeast NOR
C 458	5	100.0	10	5	AAA89321	Aaa89321	Zif268 zi
C 459	5	100.0	10	5	AAH42236	Aah42236	Nucleotid

460	5	100.0	10	6	ABN86238	Abn86238	Nucleotid
C 461	5	100.0	10	6	AAS18734	Aas18734	Primer-ex
C 462	5	100.0	10	6	AAS18736	Aas18736	Primer-ex
C 463	5	100.0	10	6	AAS18717	Aas18717	Primer-ex
C 464	5	100.0	10	6	AAD25082	Aad25082	Primer #9
C 465	5	100.0	10	6	AAS98399	Aas98399	Galanin r
C 466	5	100.0	10	6	AAS98402	Aas98402	Galanin r
C 467	5	100.0	10	6	AAD26712	Aad26712	Human GPR
C 468	5	100.0	10	6	ABK51085	Abk51085	Human CCR
C 469	5	100.0	10	6	ABK97527	Abk97527	Human LCA
C 470	5	100.0	10	6	ABL59314	AbL59314	Primer fo
C 471	5	100.0	10	6	AAS18299	Aas18299	Primer-ex
C 472	5	100.0	10	6	AAD26032	Aad26032	Primer #3
C 473	5	100.0	10	6	AAD26006	Aad26006	Primer #8
C 474	5	100.0	10	6	AAD26022	Aad26022	Primer #2
C 475	5	100.0	10	6	ABL88354	AbL88354	Human CHR
C 476	5	100.0	10	6	ABL88334	AbL88334	Human CHR
C 477	5	100.0	10	6	ABL88338	AbL88338	Human CHR
C 478	5	100.0	10	6	ABL52190	AbL52190	Human PER
C 479	5	100.0	10	6	ABL52194	AbL52194	Human PER
C 480	5	100.0	10	6	AAL39611	Aal39611	SSTR4 gen
C 481	5	100.0	10	6	AAL39596	Aal39596	SSTR4 gen
C 482	5	100.0	10	6	ABK81951	Abk81951	Human CYP
C 483	5	100.0	10	6	ABK81956	Abk81956	Human CYP
C 484	5	100.0	10	6	ABK95844	Abk95844	Solute Ca
C 485	5	100.0	10	6	ABL01210	AbL01210	Human AKR
C 486	5	100.0	10	6	AAS98880	Aas98880	Colony st
C 487	5	100.0	10	6	AAS98913	Aas98913	Colony st
C 488	5	100.0	10	6	AAS98907	Aas98907	Colony st
C 489	5	100.0	10	6	AAS98911	Aas98911	Colony st
C 490	5	100.0	10	6	ABL42719	AbL42719	Human mat
C 491	5	100.0	10	6	ABL42816	AbL42816	Human mat
C 492	5	100.0	10	6	ABL42705	AbL42705	Human mat
C 493	5	100.0	10	6	ABL99044	AbL99044	Mouse neu
C 494	5	100.0	10	6	ABL60214	AbL60214	Human MUC
C 495	5	100.0	10	6	ABK93934	Abk93934	Human pro
C 496	5	100.0	10	6	ABK93939	Abk93939	Human pro
C 497	5	100.0	10	6	ABK93918	Abk93918	Human pro
C 498	5	100.0	10	6	ABK93925	Abk93925	Human pro
C 499	5	100.0	10	6	ABK93941	Abk93941	Human pro
C 500	5	100.0	10	12	ADI13733	Adi13733	Cytoplasm

ALIGNMENTS

RESULT 1	
AAQ49540	
ID	AAQ49540 standard; DNA; 10 BP.
XX	
AC	AAQ49540;
XX	
DT	25-MAR-2003 (revised)
DT	20-APR-1994 (first entry)
XX	
DE	Primer to amplify BCNR locus marker Y10.
XX	
KW	Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;
KW	sugar beet; ss.
XX	
OS	Synthetic.
XX	
PN	WO9319181-A1.
XX	
PD	30-SEP-1993.
XX	
PF	23-MAR-1993; 93WO-EP000702.
XX	
PR	25-MAR-1992; 92DK-00000396.
XX	
PA	(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
PA	(SANO ) SANDOZ PATENT GMBH.
PA	(SANO ) SANDOZ LTD.

XX Sandal N, Marcker K, Stiekema W, Lange W, Klein-Lankhorst R;  
 PI Steen P;  
 XX WPI; 1993-320747/40.  
 XX Recombinant DNA comprising Beet Cyst Nematode Resistance Locus - confers  
 PT nematode resistance to beet species.  
 PT Claim 2; Page 61; 82pp; English.  
 XX This primer is used to amplify a BCNR locus marker of ca. 391bp from wild  
 CC beet species belonging to section Procumbentes. (Updated on 25-MAR-2003  
 CC to correct PN field.)  
 XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGG 5  
 Db |||||  
 6 GTGGG 10

RESULT 2  
 AAQ38702/c  
 ID AAQ38702 standard; RNA; 10 BP.  
 XX  
 AC AAQ38702;  
 XX 25-MAR-2003 (revised)  
 DT 15-JUL-1993 (first entry)  
 XX 2'-O-methyl oligonucleotide for calibration of ras binding.  
 DE oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;  
 XX treatment; diagnosis; testing; assay; Candida; papillomavirus;  
 KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;  
 KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;  
 KW human immunodeficiency virus; HIV; AIDS; influenza virus;  
 KW genetic disease; genetic abnormalities.  
 XX Synthetic.  
 OS WO9305182-A1.  
 XX 18-MAR-1993.  
 PN 04-SEP-1992; 92WO-US007489.  
 XX 05-SEP-1991; 91US-00755485.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Bruice TW;  
 PI WPI; 1993-101001/12.  
 XX Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule  
 PT - for use in therapeutics, diagnostics and research reagents.  
 PT Example 12; Page 36; 61pp; English.  
 XX This sequence was used as a calibration oligonucleotide to investigate  
 CC random 2'-O-methyl oligonucleotide binding to ras RNA using continuous  
 CC flow mass transport methodology to effect stringent binding selection.  
 CC The oligonucleotides are added to a FPLC column together with a mixture  
 CC of calibration oligonucleotides that have been incubated with ras RNA to  
 CC form any possible hybridisation complexes. This is to enable an elution  
 CC profile to be obtained. Following calibration, either the random  
 CC oligonucleotide pool is loaded onto the column followed by the ras RNA or  
 CC bound oligonucleotide/ras RNA complexes are dissociated using stepwise or  
 CC gradient low salt and/or increased temperature and the oligonucleotides  
 CC are recovered by RNase treatment to selectively degrade the ras RNA. The

CC the pool and ras RNA are pre-incubated prior to loading on the column.  
 CC Bound oligonucleotide/ras RNA complexes are dissociated using stepwise or  
 CC gradient low salt and/or increased temperature and the oligonucleotides  
 CC are recovered by RNase treatment to selectively degrade the ras RNA. The  
 CC selected 2'-O-methyl oligonucleotides are characterised by microbore  
 CC HPLC. Complete and limited fragmentation of the recovered 2'-O-methyl  
 CC oligonucleotides can be accomplished by appropriate base and nuclease  
 CC treatment to facilitate sequence reconstruction in comparison to pre-  
 CC calibrated retention times of standard mono, di, and tri 2'-O-methyl  
 CC standards. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 10 BP; 2 A; 4 C; 1 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGG 5  
 Db |||||  
 8 GTGGG 4

RESULT 3  
 AAQ38701/c  
 ID AAQ38701 standard; RNA; 10 BP.  
 XX  
 AC AAQ38701;  
 XX 25-MAR-2003 (revised)  
 DT 15-JUL-1993 (first entry)  
 XX 2'-O-methyl oligonucleotide for calibration of ras binding.  
 DE oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;  
 XX treatment; diagnosis; testing; assay; Candida; papillomavirus;  
 KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;  
 KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;  
 KW human immunodeficiency virus; HIV; AIDS; influenza virus;  
 KW genetic disease; genetic abnormalities.  
 XX Synthetic.  
 OS WO9305182-A1.  
 XX 18-MAR-1993.  
 PN 04-SEP-1992; 92WO-US007489.  
 XX 05-SEP-1991; 91US-00755485.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Bruice TW;  
 PI WPI; 1993-101001/12.  
 XX Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule  
 PT - for use in therapeutics, diagnostics and research reagents.  
 PT Example 12; Page 36; 61pp; English.  
 XX This sequence was used as a calibration oligonucleotide to investigate  
 CC random 2'-O-methyl oligonucleotide binding to ras RNA using continuous  
 CC flow mass transport methodology to effect stringent binding selection.  
 CC The oligonucleotides are added to a FPLC column together with a mixture  
 CC of calibration oligonucleotides that have been incubated with ras RNA to  
 CC form any possible hybridisation complexes. This is to enable an elution  
 CC profile to be obtained. Following calibration, either the random  
 CC oligonucleotide pool is loaded onto the column followed by the ras RNA or  
 CC the pool and ras RNA are pre-incubated prior to loading on the column.  
 CC Bound oligonucleotide/ras RNA complexes are dissociated using stepwise or  
 CC gradient low salt and/or increased temperature and the oligonucleotides  
 CC are recovered by RNase treatment to selectively degrade the ras RNA. The

CC selected 2'-O-methyl oligonucleotides are characterised by microbore  
CC HPLC. Complete and limited fragmentation of the recovered 2'-O-methyl  
CC oligonucleotides can be accomplished by appropriate base and nuclease  
CC treatment to facilitate sequence reconstruction in comparison to pre-  
CC calibrated retention times of standard mono, di, and tri 2'-O-methyl  
CC standards. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other; 0; Gaps 0;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 8 GTGGG 4  
RESULT 4  
AAQ38704/c  
ID AAQ38704 standard; RNA; 10 BP.  
XX  
AC AAQ38704;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-JUL-1993 (first entry)  
XX  
DE 2'-O-methyl oligonucleotide for calibration of ras binding.  
XX  
KW oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;  
KW treatment; diagnosis; testing; assay; Candida; papillomavirus;  
KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;  
KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;  
KW human immunodeficiency virus; HIV; AIDS; influenza virus;  
KW genetic disease; genetic abnormalities.  
XX  
OS Synthetic.  
XX  
PN WO9305182-A1.  
XX  
PD 18-MAR-1993.  
XX  
PF 04-SEP-1992; 92WO-US007489.  
XX  
PR 05-SEP-1991; 91US-00755485.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bruice TW;  
XX  
DR WPI; 1993-101001/12.  
XX  
PT Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule  
PT - for use in therapeutics, diagnostics and research reagents.  
XX  
PS Example 12; Page 37; 61pp; English.  
XX  
CC This sequence was used as a calibration oligonucleotide to investigate  
CC random 2'-O-methyl oligonucleotide binding to ras RNA using continuous  
CC flow mass transport methodology to effect stringent binding selection.  
CC The oligonucleotides are added to a FPLC column together with a mixture  
CC of calibration oligonucleotides that have been incubated with ras RNA to  
CC form any possible hybridisation complexes. This is to enable an elution  
CC profile to be obtained. Following calibration, either the random  
CC oligonucleotide pool is loaded onto the column followed by the ras RNA or  
CC the pool and ras RNA are pre-incubated prior to loading on the column.  
CC Bound oligonucleotide/ras RNA complexes are dissociated using stepwise or  
CC gradient low salt and/or increased temperature and the oligonucleotides  
CC are recovered by RNase treatment to selectively degrade the ras RNA. The  
CC selected 2'-O-methyl oligonucleotides are characterised by microbore  
CC HPLC. Complete and limited fragmentation of the recovered 2'-O-methyl  
CC oligonucleotides can be accomplished by appropriate base and nuclease  
CC treatment to facilitate sequence reconstruction in comparison to pre-

CC calibrated retention times of standard mono, di, and tri 2'-O-methyl  
CC standards. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other; 0; Gaps 0;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 8 GTGGG 4  
RESULT 5  
AAQ79368  
ID AAQ79368 standard; DNA; 10 BP.  
XX  
AC AAQ79368;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Regulatory element AP2/Rev located at posn. 708 of the extended 3'  
DE flanking region of human erythropoietin.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
XX  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UYNY ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table II, page 14; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
CC 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region  
CC of AAQ79753 and includes all the regulatory elements contained therein.  
CC It extends from the 5'-most PstI site 3' of the end of the coding  
CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
CC structures. It also contains TATA boxes in forward and reverse  
CC orientation, and at least about 184 potential transcriptional regulatory  
CC elements. AAQ79365-Q79369 list several of these elements and their  
CC positions. The nucleotide posns. are measured from first nucleotide at  
CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 8 GTGGG 4

Db 3 GTGGG 7

RESULT 6  
AAQ79367  
ID AAQ79367 standard; DNA; 10 BP.  
XX  
AC AAQ79367;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX  
DE Regulatory element AP2/Rev located at posn. 707 of the extended 3'  
DE flanking region of human erythropoietin.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
DT 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UYNV ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PF 15-APR-1994; 94WO-US004141.  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UYNV ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table II, page 14; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
CC 1777 bases of AAQ79753. It corresp. to the non- coding 3' flanking region  
CC of AAQ79753 and includes all the regulatory elements contained therein.  
CC It extends from the 5'-most PstI site 3' of the end of the coding  
CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
CC structures. It also contains TATA boxes in forward and reverse  
CC orientation, and at least about 184 potential transcriptional regulatory  
CC elements. AAQ79365-Q79369 list several of these elements and their  
CC positions. The nucleotide posns. are measured from first nucleotide at  
CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 4 GTGGG 8  
RESULT 7  
AAQ79359/c  
ID AAQ79359 standard; DNA; 10 BP.  
XX  
AC AAQ79359;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-JUN-1995 (first entry)  
XX

XX  
DE Sequence of AP2 regulatory sequence located at posn. 2621 in hEpsLH.  
XX  
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
XX  
OS Synthetic.  
XX  
PN WO9423570-A1.  
XX  
DT 27-OCT-1994.  
XX  
PF 15-APR-1994; 94WO-US004141.  
PR 15-APR-1993; 93US-00046295.  
PR 23-JUN-1993; 93US-00082850.  
XX  
PA (UYNV ) UNIV NEW YORK STATE.  
XX  
PI Lee-Huang S;  
XX  
DR WPI; 1994-341353/42.  
XX  
PT New regulatory regions of human erythropoietin gene - used for studying  
PT and treating diseases and for prodn. of transgenic animal models (Eng).  
XX  
PS Disclosure; Table I, p. 12; 81pp; English.  
XX  
CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
CC flanking region contg. multiple regulatory elements and a 3' flanking  
CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
CC 5' flanking region and includes all the 5' regulatory elements. This  
CC region, consisting of the first 3892 of AAQ79353, was not found in the  
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
CC show several of these elements and their positions. The nucleotide  
CC position of these elements is measured from the BamHI site at the 5' end  
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 8 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 8 GTGGG 4  
RESULT 8  
AAQ71089/c  
ID AAQ71089 standard; cDNA; 10 BP.  
XX  
AC AAQ71089;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 7 splice acceptor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D2S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX

PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GEOH ) GEN HOSPITAL CORP.  
XX  
PI Trofatter JA, Maccollin MM, Gusella JF;  
XX  
DR WPI; 1994-272992/34.  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
PT tumours and neurofibromatosis (NF2).  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance  
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
Db |||||  
8 GTGGG 4  
  
RESULT 9  
AAQ61967  
ID AAQ61967 standard; DNA; 10 BP.  
XX  
AC AAQ61967;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-NOV-1994 (first entry)  
XX  
DE Phospholipase A2 inhibiting oligomer, ISIS no 4962.  
XX  
KW Inhibition; replication; herpes simplex virus; HSV; HIV; aging;  
KW human cytomegalovirus; influenza virus; inflammation; telomere length;  
KW neurological disorders; phospholipase A2 activity; hyperproliferation;  
KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..10  
FT /\*tag= a  
FT /note= "Phosphorothioate intersugar linkages"  
XX  
PN WO9408053-A1.

XX 14-APR-1994.  
PD  
XX 29-SEP-1993; 93WO-US009297.  
PF  
XX 29-SEP-1992; 92US-00954185.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;  
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;  
XX  
DR WPI; 1994-135613/16.  
XX  
PT New modified oligo-nucleotide contg guanine quartet - inhibits activity  
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length  
PT of chromosomes.  
XX  
PS Disclosure; Page 29; 144pp; English.  
XX  
CC The sequences given in AAQ61956-67 are oligonucleotides which represent  
CC the core sequences of G4 containing oligos which may be used for  
CC inhibiting phospholipase A2 enzyme activity. Oligonucleotides such as  
CC these may also be used for inhibiting activity of HSV, HIV, human  
CC cytomegalovirus or influenza virus, or for treating inflammatory and  
CC neurological disorders caused by phospholipase A2 activity in cases of  
CC hyperproliferation, malignancy, cardiovascular disease and snake bite.  
CC They may also be used for inhibiting division of malignant cells by  
CC modulating telomere length, which may also retard aging. (Updated on 25-  
CC MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
Db |||||  
3 GTGGG 7  
  
RESULT 10  
AAQ63558  
ID AAQ63558 standard; DNA; 10 BP.  
XX  
AC AAQ63558;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-DEC-1994 (first entry)  
XX  
DE C11 3' spacer element.  
XX  
KW Insertion element; junk DNA; spacer element; functional DNA sequence;  
KW primer binding site; reaction product; binding specificity; primer;  
KW recombinant molecule; structural stress; hybridisation assay; ss.  
XX  
OS Synthetic.  
XX  
PN WO9409159-A2.  
XX  
PD 28-APR-1994.  
XX  
PF 08-OCT-1993; 93WO-US009702.  
XX  
PR 09-OCT-1992; 92US-00959939.  
PR 09-APR-1993; 93US-00045587.  
XX  
PA (STAD ) AMOCO CORP.  
XX  
PI Burg J;  
XX  
DR WPI; 1994-151343/18.

XX Insertion elements an amplifiable nucleic acids - for use as probes in  
PT hybridisation assays and for the prepn. of libraries used to identify  
PT preferred insertion elements.  
XX  
PS Disclosure; Page 23; 39pp; English.  
XX  
CC The sequences given in AAQ63549-60 are spacer elements used within the  
CC insertion elements of the invention. These insertion elements contain  
CC junk DNA, two spacer elements, a functional DNA sequence and a primer  
CC binding site. They also contain an MluI site, an MluI/NheI site and a  
CC NheI site. The junk DNA serves to keep the MluI site from being at the  
CC extreme end of the molecule and also allows determination that the MluI  
CC cleavage has occurred because the extended DNA will be reduced in size by  
CC the length of the junk sequence and the junk sequence will appear as a  
CC reaction product. The nucleotides making up the spacer elements are  
CC chosen randomly and the functional nucleotide sequence is chosen to  
CC achieve the binding specificity required of the amplifiable nucleic acid.  
CC The primer binding site can be any nucleotide sequence for which a  
CC complementary primer is available or can be synthesised. However, the  
CC primer and primer binding site are chosen such that the primer itself  
CC does not bind to any other portion of the insertion element under  
CC construction. Insertion sequences such as these can be used to insert a  
CC functional molecule into a host molecule to form a recombinant molecule.  
CC The spacer elements are thought to relieve structural stresses imposed on  
CC the host by addition of the functional nucleotide sequence. The insertion  
CC elements can be used with nucleic acid hybridisation assays. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GTGGG 5  
Db |||||  
6 GTGGG 10  
  
RESULT 11  
AAQ63553  
ID AAQ63553 standard; DNA; 10 BP.  
XX  
AC AAQ63553;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-DEC-1994 (first entry)  
XX  
DE C22 5' spacer element.  
XX  
KW Insertion element; junk DNA; spacer element; functional DNA sequence;  
KW primer binding site; reaction product; binding specificity; primer;  
KW recombinant molecule; structural stress; hybridisation assay; ss.  
XX  
OS Synthetic.  
XX  
XX WO9409159-A2.  
PN  
XX 28-APR-1994.  
PD  
XX 08-OCT-1993; 93WO-US009702.  
PF  
XX 09-OCT-1992; 92US-00959939.  
PR  
PR 09-APR-1993; 93US-00045587.  
XX  
XX (STAD ) AMOCO CORP.  
PA  
XX Burg J;  
PI  
XX WPI; 1994-151343/18.  
DR  
XX Insertion elements an amplifiable nucleic acids - for use as probes in  
PT

PT hybridisation assays and for the prepn. of libraries used to identify  
PT preferred insertion elements.  
XX  
PS Disclosure; Page 23; 39pp; English.  
XX  
CC The sequences given in AAQ63549-60 are spacer elements used within the  
CC insertion elements of the invention. These insertion elements contain  
CC junk DNA, two spacer elements, a functional DNA sequence and a primer  
CC binding site. They also contain an MluI site, an MluI/NheI site and a  
CC NheI site. The junk DNA serves to keep the MluI site from being at the  
CC extreme end of the molecule and also allows determination that the MluI  
CC cleavage has occurred because the extended DNA will be reduced in size by  
CC the length of the junk sequence and the junk sequence will appear as a  
CC reaction product. The nucleotides making up the spacer elements are  
CC chosen randomly and the functional nucleotide sequence is chosen to  
CC achieve the binding specificity required of the amplifiable nucleic acid.  
CC The primer binding site can be any nucleotide sequence for which a  
CC complementary primer is available or can be synthesised. However, the  
CC primer and primer binding site are chosen such that the primer itself  
CC does not bind to any other portion of the insertion element under  
CC construction. Insertion sequences such as these can be used to insert a  
CC functional molecule into a host molecule to form a recombinant molecule.  
CC The spacer elements are thought to relieve structural stresses imposed on  
CC the host by addition of the functional nucleotide sequence. The insertion  
CC elements can be used with nucleic acid hybridisation assays. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GTGGG 5  
Db |||||  
4 GTGGG 8  
  
RESULT 12  
AAQ79252  
ID AAQ79252 standard; DNA; 10 BP.  
XX  
AC AAQ79252;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-JUL-1995 (first entry)  
XX  
DE Guanosine rich oligonucleotide used to treat viral infection.  
XX  
KW Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;  
KW infection; herpes simplex virus; human papilloma virus;  
KW Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;  
KW hepatitis B virus; human cytomegalovirus; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 10  
FT /\*tag= a  
FT /mod\_base  
FT /note= "Propanolamine group attached to this base."  
XX  
PN WO9425037-A1.  
XX  
XX 10-NOV-1994.  
PD  
XX 25-APR-1994; 94WO-US004529.  
PF  
XX 23-APR-1993; 93US-00053027.  
PR  
PR 28-OCT-1993; 93US-00145704.  
XX  
XX (TRIP-) TRIPLEX PHARM CORP.  
PA  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.



XX Rando RF, Fennewald S, ZendeGUI JG, Ojwang JO, Hogan ME;  
PI WPI; 1994-357890/44.  
XX  
XX Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used  
PT to treat viral infections, e.g. herpes-virus and HIV.  
XX  
XX Claim 41; Page 71; 101pp; English.  
XX  
XX The oligonucleotides (See AAQ79201-52) can be used to treat viral  
CC infections. The oligonucleotides inhibit viral replication by forming  
CC guanosine tetrads which form a stabilised 3D structure. Preferred  
CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases  
CC and may be capped at the 3' terminus with a modifier selected from  
CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also  
CC have a modified phosphodiester linkage or be modified to contain a  
CC phosphorothioate linkage. They are used to treat infections with viruses  
CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,  
CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human  
CC cytomegalovirus. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
Db |||||  
1 GTGGG 5  
  
RESULT 13  
AAQ73141  
ID AAQ73141 standard; cDNA; 10 BP.  
XX  
AC AAQ73141;  
XX  
DT 26-MAY-1995 (first entry)  
XX  
DE Mutant rab16 motif I probe M5.  
XX  
KW Transactivating factor; TAF-1; transcription activator; transgenic plant;  
KW gene expression; G-box motif; rab16 motif I; tobacco; probe; ds.  
XX  
OS Synthetic.  
XX  
PN US5362864-A.  
XX  
PD 08-NOV-1994.  
XX  
PF 06-FEB-1991; 91US-00651710.  
XX  
PR 06-FEB-1991; 91US-00651710.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Chua N;  
XX  
DR WPI; 1994-357424/44.  
XX  
PT Isolated trans:activating factor, TAF-1 and encoding DNA - useful to  
PT increase gene expression in plants.  
XX  
PS Disclosure; Col 29; 39pp; English.  
XX  
CC Partial cDNA clone p5a, encoding a C-terminal portion of transactivating  
CC factor TAF-1 was isolated from a tobacco cDNA expression library. The  
CC truncated TAF-1 protein (AAR62822) binds to rab16 motif I and the B-box  
CC motif, and can be used to modulate gene expression in transgenic plants  
CC or cell cultures. Tetramers of wild-type motif I (given in AAQ73135) and  
CC of mutants M1-M5 (AAQ73137-41) were assayed for their ability to interact

CC with recombinant TAF-1 protein produced in Escherichia coli by gel  
CC mobility shift  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
Db |||||  
5 GTGGG 9  
  
RESULT 14  
AAQ73134  
ID AAQ73134 standard; cDNA; 10 BP.  
XX  
AC AAQ73134;  
XX  
DT 16-OCT-2003 (revised)  
DT 26-MAY-1995 (first entry)  
XX  
DE TAF-1 binding motif.  
XX  
KW Transactivating factor; TAF-1; transcription activator; transgenic plant;  
KW gene expression; binding motif; tobacco; ds.  
XX  
OS Nicotiana tabacum; cv. SR1.  
XX  
PN US5362864-A.  
XX  
PD 08-NOV-1994.  
XX  
PF 06-FEB-1991; 91US-00651710.  
XX  
PR 06-FEB-1991; 91US-00651710.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Chua N;  
XX  
DR WPI; 1994-357424/44.  
XX  
PT Isolated trans:activating factor, TAF-1 and encoding DNA - useful to  
PT increase gene expression in plants.  
XX  
PS Claim 9; Col 45; 39pp; English.  
XX  
CC Partial cDNA clone p5a (given in AAQ73130), encoding a C-terminal portion  
CC of transactivating factor TAF-1 (AAR62822), was isolated from a tobacco  
CC cDNA expression library. In host cells or transgenic plants, the TAF-1  
CC sequence is controlled by a regulatory sequence containing 1 or more  
CC copies of a binding site (e.g. AAQ73131-34) for TAF-1, so that expression  
CC of a gene of interest is increased when TAF-1 is expressed. (Updated on  
CC 16-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
Db |||||  
6 GTGGG 10  
  
RESULT 15  
AAX32620/c  
ID AAX32620 standard; DNA; 10 BP.  
XX  
AC AAX32620;



```
XX 23-JUN-1999 (first entry)
DT Anticancer duplex forming oligonucleotide SEQ ID #20.
XX
DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
KW Synthetic.
XX
OS WO9523162-A1.
XX
PN 31-AUG-1995.
XX
PD 27-FEB-1995; 95WO-US002419.
XX
PF 28-FEB-1994; 94US-00202927.
XX
PR (MICR-) MICROPROBE CORP.
XX (UYA ) UNIV YALE.
PA
PA Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
PI WPI; 1995-311501/40.
XX
DR New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 52; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTGGG 5
Db 5 GTGGG 1
RESULT 16
AAX32638
ID AAX32638 standard; DNA; 10 BP.
XX
AC AAX32638;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
```

```
PR 28-FEB-1994; 94US-00202927.
XX (MICR-) MICROPROBE CORP.
PA (UYA ) UNIV YALE.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX WPI; 1995-311501/40.
DR
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 59; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTGGG 5
Db 1 GTGGG 5
RESULT 17
AAX32638/c
ID AAX32638 standard; DNA; 10 BP.
XX
AC AAX32638;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
DE (MICR-) MICROPROBE CORP.
PA (UYA ) UNIV YALE.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX WPI; 1995-311501/40.
DR
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 59; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTGGG 5
Db 1 GTGGG 5
RESULT 17
AAX32638/c
ID AAX32638 standard; DNA; 10 BP.
XX
AC AAX32638;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
DE (MICR-) MICROPROBE CORP.
PA (UYA ) UNIV YALE.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX WPI; 1995-311501/40.
DR
XX New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 59; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
```

CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance

XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
Db |||||  
10 GTGGG 6

RESULT 18  
AAQ96493  
ID AAQ96493 standard; DNA; 10 BP.  
XX  
AC AAQ96493;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
XX HIV-1 NL4-3 nef gene nucleotide deletion 88.  
DE  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 30lpp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
Db |||||  
1 GTGGG 5

RESULT 19  
AAQ96488  
ID AAQ96488 standard; DNA; 10 BP.  
XX  
AC AAQ96488;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 83.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.  
DR  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 189; 30lpp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX  
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
Db |||||  
6 GTGGG 10

RESULT 20  
AAQ96596  
ID AAQ96596 standard; DNA; 10 BP.  
XX  
AC AAQ96596;  
XX  
DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 191.

```
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 190; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
6 GTGGG 10

RESULT 21
AAQ96600
ID AAQ96600 standard; DNA; 10 BP.
XX
AC AAQ96600;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 195.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
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PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 190; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX Sequence 10 BP; 0 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
2 GTGGG 6

RESULT 22
AAQ96492
ID AAQ96492 standard; DNA; 10 BP.
XX
AC AAQ96492;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 87.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 189; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
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```
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
2 GTGGG 6

RESULT 23
AAQ96491
ID AAQ96491 standard; DNA; 10 BP.
XX
AC AAQ96491;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 86.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 13; Page 189; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
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```
Db 3 GTGGG 7

RESULT 24
AAQ97088/c
ID AAQ97088 standard; DNA; 10 BP.
XX
AC AAQ97088;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 LTR nucleotide deletion 70.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX Claim 14; Page 197; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
8 GTGGG 4

RESULT 25
AAQ96601
ID AAQ96601 standard; DNA; 10 BP.
XX
AC AAQ96601;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 196.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
```

XX OS Human immunodeficiency virus 1.  
XX PN WO9521912-A1.  
XX PD 17-AUG-1995.  
XX PF 14-FEB-1995; 95WO-AU0000063.  
XX PR 14-FEB-1994; 94AU-00003864.  
XX PR 21-FEB-1994; 94AU-00004002.  
XX PR 23-DEC-1994; 94AU-00000284.  
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX XX WPI; 1995-293115/38.  
XX DR  
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX PS Claim 13; Page 190; 301pp; English.  
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX XX  
XX SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db |||||  
1 GTGGG 5  
RESULT 26  
AAQ97086/c  
ID AAQ97086 standard; DNA; 10 BP.  
XX AC  
XX AC AAQ97086;  
XX DT 16-OCT-2003 (revised)  
XX DT 27-MAR-1996 (first entry)  
XX XX  
XX DE HIV-1 NL4-3 LTR nucleotide deletion 68.  
XX XX  
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX OS Human immunodeficiency virus 1.  
XX PN WO9521912-A1.  
XX PD 17-AUG-1995.  
XX XX  
XX PF 14-FEB-1995; 95WO-AU0000063.  
XX PR 14-FEB-1994; 94AU-00003864.  
XX PR 21-FEB-1994; 94AU-00004002.  
XX PR 23-DEC-1994; 94AU-00000284.  
XX XX  
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX XX WPI; 1995-293115/38.  
XX DR  
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX XX  
XX PS Claim 14; Page 197; 301pp; English.  
XX XX  
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX XX  
XX SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db |||||  
10 GTGGG 6  
RESULT 27  
AAQ97089/c  
ID AAQ97089 standard; DNA; 10 BP.  
XX AC  
XX AC AAQ97089;  
XX XX  
XX DT 16-OCT-2003 (revised)  
XX DT 27-MAR-1996 (first entry)  
XX XX  
XX DE HIV-1 NL4-3 LTR nucleotide deletion 71.  
XX XX  
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX XX  
XX OS Human immunodeficiency virus 1.  
XX XX  
XX PN WO9521912-A1.  
XX XX  
XX PD 17-AUG-1995.  
XX XX  
XX PF 14-FEB-1995; 95WO-AU0000063.  
XX XX  
XX PR 14-FEB-1994; 94AU-00003864.  
XX PR 21-FEB-1994; 94AU-00004002.  
XX PR 23-DEC-1994; 94AU-00000284.  
XX XX  
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX XX WPI; 1995-293115/38.  
XX DR  
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX XX  
XX PS Claim 14; Page 197; 301pp; English.  
XX XX  
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
Db 7 GTGGG 3

RESULT 28  
AAQ97090/c  
ID AAQ97090 standard; DNA; 10 BP.

XX AC AAQ97090;

XX DT 16-OCT-2003 (revised)  
DT 27-MAR-1996 (first entry)

XX DE HIV-1 NL4-3 LTR nucleotide deletion 72.

XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX OS Human immunodeficiency virus 1.

XX PN WO9521912-A1.

XX PD 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.

XX PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.

XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.

XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.

XX PS Claim 14; Page 197; 301pp; English.

XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
Db 6 GTGGG 2

RESULT 29  
AAQ96597  
ID AAQ96597 standard; DNA; 10 BP.

XX AC AAQ96597;

XX DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)

XX DE HIV-1 NL4-3 nef gene nucleotide deletion 192.

XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX OS Human immunodeficiency virus 1.

XX PN WO9521912-A1.

XX PD 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.

XX PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.

XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.

XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.

XX PS Claim 13; Page 190; 301pp; English.

XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
Db 5 GTGGG 9

RESULT 30  
AAQ96490  
ID AAQ96490 standard; DNA; 10 BP.

XX AC AAQ96490;

XX DT 16-OCT-2003 (revised)  
DT 20-MAR-1996 (first entry)

XX DE HIV-1 NL4-3 nef gene nucleotide deletion 85.

XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX OS Human immunodeficiency virus 1.

```
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX PS Claim 13; Page 189; 301pp; English.
XX
XX SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTGGG 5
XX Db |||||
XX 4 GTGGG 8
XX
XX RESULT 31
XX AAQ96489
XX ID AAQ96489 standard; DNA; 10 BP.
XX
XX AC AAQ96489;
XX
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 84.
XX
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX OS Human immunodeficiency virus 1.
XX
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
```

```
XX WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX PS Claim 13; Page 189; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTGGG 5
XX Db |||||
XX 5 GTGGG 9
XX
XX RESULT 32
XX AAQ96599
XX ID AAQ96599 standard; DNA; 10 BP.
XX
XX AC AAQ96599;
XX
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 194.
XX
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX OS Human immunodeficiency virus 1.
XX
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX PS Claim 13; Page 190; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
```



```
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
3 GTGGG 7

RESULT 33
AAQ97091/c
ID AAQ97091 standard; DNA; 10 BP.
XX
AC AAQ97091;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 LTR nucleotide deletion 73.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
PS Claim 14; Page 197; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
5 GTGGG 1

RESULT 34
```

```
AAQ96598
ID AAQ96598 standard; DNA; 10 BP.
XX
AC AAQ96598;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 193.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
PS Claim 13; Page 190; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
4 GTGGG 8

RESULT 35
AAQ97087/c
ID AAQ97087 standard; DNA; 10 BP.
XX
AC AAQ97087;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 LTR nucleotide deletion 69.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
```

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XX 17-AUG-1995.
XX
XX
XX 14-FEB-1995; 95WO-AU0000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX
XX 21-FEB-1994; 94AU-00004002.
XX
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACPARLANE BURNET CENT MEDICAL.
XX
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 9 GTGGG 5

RESULT 36
AAQ79835/c
ID AAQ79835 standard; RNA; 10 BP.
XX
XX AAQ79835;
XX
XX 25-MAR-2003 (revised)
XX 04-SEP-1995 (first entry)
XX
XX H-ras modulating sequence, targetted to hairpin loop.
XX
XX Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;
XX expression; ras gene; mutation; tumour; cancer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..10
XX /*tag= a
XX /note= "Each base is attached to a N-acetyl(2-amino-
XX ethyl)Gly residue through the N-acetyl group"
XX
XX WO9428720-A1.
XX
XX 22-DEC-1994.
XX
XX 10-JUN-1994; 94WO-US0006620.
XX
XX 11-JUN-1993; 93US-00076234.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Lima W, Monia B, Freier S, Ecker D;
XX
XX WPI; 1995-035955/05.
XX
XX New peptide nucleic acid oligomers for ras oncogene modulation -
XX including specific inhibition of the activated gene, for diagnosis and
XX treatment esp. of tumours.

```

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XX Lima W, Monia B, Freier S, Ecker D;
XX
XX WPI; 1995-035955/05.
XX
XX New peptide nucleic acid oligomers for ras oncogene modulation -
XX including specific inhibition of the activated gene, for diagnosis and
XX treatment esp. of tumours.
XX
XX Claim 1; Page 133; 148pp; English.
XX
XX The sequences given in AAQ79822-57 represent peptide nucleic acids (PNA)
XX that bind to complementary ssDNA and RNA strands through their
XX oligoribonucleotide ligands which are linked to a peptide backbone. These
XX sequences are directed to the human H-ras and K-ras genes and they
XX modulate the expression of the ras gene in cells or tissues and
XX specifically modulate the expression of the activated ras in cells or
XX tissues suspected of harbouring a mutated gene. These sequences are
XX designed to hybridise with the mRNA from the H-ras and K-ras genes which
XX interferes with the normal role of mRNA causing a loss of function in the
XX cell. These sequences are used in the treatment of tumours. (Updated on
XX 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 8 GTGGG 4

RESULT 37
AAQ79834/c
ID AAQ79834 standard; DNA; 10 BP.
XX
XX AAQ79834;
XX
XX 25-MAR-2003 (revised)
XX 04-SEP-1995 (first entry)
XX
XX H-ras modulating sequence, targetted to hairpin stem.
XX
XX Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;
XX expression; ras gene; mutation; tumour; cancer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..10
XX /*tag= a
XX /note= "Each base is attached to a N-acetyl(2-amino-
XX ethyl)Gly residue through the N-acetyl group"
XX
XX WO9428720-A1.
XX
XX 22-DEC-1994.
XX
XX 10-JUN-1994; 94WO-US0006620.
XX
XX 11-JUN-1993; 93US-00076234.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Lima W, Monia B, Freier S, Ecker D;
XX
XX WPI; 1995-035955/05.
XX
XX New peptide nucleic acid oligomers for ras oncogene modulation -
XX including specific inhibition of the activated gene, for diagnosis and
XX treatment esp. of tumours.

```

```
XX
PS Claim 1; Page 133; 148pp; English.
XX
CC The sequences given in AAQ79822-57 represent peptide nucleic acids (PNA)
CC that bind to complementary ssDNA and RNA strands through their
CC oligoribonucleotide ligands which are linked to a peptide backbone. These
CC sequences are directed to the human H-ras and K-ras genes and they
CC modulate the expression of the ras gene in cells or tissues and
CC specifically modulate the expression of the activated ras in cells or
CC tissues suspected of harbouring a mutated gene. These sequences are
CC designed to hybridise with the mRNA from the H-ras and K-ras genes which
CC interferes with the normal role of mRNA causing a loss of function in the
CC cell. These sequences are used in the treatment of tumours. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
Db      |||||
      8 GTGGG 4

RESULT 38
AAT14316
ID AAT14316 standard; RNA; 10 BP.
XX
AC AAT14316;
XX
DT 21-NOV-1996 (first entry)
XX
DE IgE binding ligand group B consensus sequence.
XX
KW Immunoglobulin E; RNA ligand; inhibitor; IgE receptor; therapy; asthma;
KW IgE dependent reaction; allergic disease; allergic rhinitis; hay fever;
KW atopic dermatitis; chronic skin irritation; anaphylactic shock; IgE; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /*tag= a
FT /note= "all C's are 2'NH2 cytosine, and all U's are 2'NH2
FT uracil"
XX
PN WO9610576-A1.
XX
PD 11-APR-1996.
XX
PF 27-SEP-1995; 95WO-US012401.
XX
PR 03-OCT-1994; 94US-00317403.
PR 06-JUN-1995; 95US-00471985.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Wiegand TW, Tasset D, Gold L;
XX
DR WPI; 1996-209316/21.
XX
PT Identification of high-affinity IgE oligo:nucleotide ligands - which
PT inhibit interaction of IgE with its receptor, which are therefore useful
PT in diagnostic and therapeutic applications.
XX
PS Claim 9; Page 39; 88pp; English.
XX
CC AAT14280-T14320 represent RNA ligands for immunoglobulin E (IgE). These
CC sequences are non-naturally occurring RNA ligands, and were isolated and
CC purified using the method of the invention. In this method, a candidate
CC mixture of nucleic acids is prepared, and contacted with IgE. The
```

```
CC sequences with an increased affinity to IgE relative to the mixture are
CC partitioned off from the rest of the mixture. The partitioned sequences
CC are then amplified, to yield a mixture of nucleic acids enriched for
CC those with relatively higher affinity and specificity for IgE binding.
CC The steps of this method can be repeated in order to obtain a mixture of
CC higher specificity for IgE binding. This method can be carried out with
CC RNA or DNA. AAT14240-T14243, and AAT14431-T14487 represent the DNA
CC ligands identified by this method. The IgE ligands inhibit the function
CC of IgE by preventing the IgE/receptor interaction. The ligands are
CC therefore useful in diagnostic and therapeutic applications for diseases
CC associated with IgE dependent reactions. The IgE dependent reactions
CC include allergic diseases such as allergic rhinitis (hay fever), asthma,
CC atopic dermatitis (chronic skin irritations), and anaphylactic shock
XX
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 0 T; 2 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
Db      |:|||
      3 GUGGG 7

RESULT 39
AAT98863
ID AAT98863 standard; DNA; 10 BP.
XX
AC AAT98863;
XX
DT 20-MAR-1998 (first entry)
XX
DE Core-binding site clone 6-11-2.
XX
KW protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYYA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 22; 52pp; English.
XX
CC This sequence represents a core-binding site identified using the method
CC of the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
```

CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors

SQ Sequence 10 BP; 0 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

## RESULT 40

AAT98860  
ID AAT98860 standard; DNA; 10 BP.

XX AC AAT98860;

XX DT 20-MAR-1998 (first entry)

XX DE Core-binding site clone 6-7-1.

XX KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.

XX OS Synthetic.

XX PN WO9727330-A1.

XX PD 31-JUL-1997.

XX PF 24-JAN-1997; 97WO-US001230.

XX PR 24-JAN-1996; 96US-00590571.

XX PA (UYA ) UNIV YALE.

XX PI Weissman SM, Kulkarni P, Nallur GN;

XX DR WPI; 1997-393714/36.

XX PT Identifying protein-binding sites for DNA-binding proteins - using  
PT duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.

XX PS Example 3; Page 22; 52pp; English.

XX CC This sequence represents a core-binding site identified using the method  
CC of the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors

XX SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

## RESULT 41

AAT98847  
ID AAT98847 standard; DNA; 10 BP.

XX AC AAT98847;

XX DT 20-MAR-1998 (first entry)

XX DE Binding site BSN1 identified using the method of the invention.

XX KW Protein-binding site isolation; transcription factor modification;  
KW DNA-binding protein; inhibitor identification; ss.

XX OS Synthetic.

XX PN WO9727330-A1.

XX PD 31-JUL-1997.

XX PF 24-JAN-1997; 97WO-US001230.

XX PR 24-JAN-1996; 96US-00590571.

XX PA (UYA ) UNIV YALE.

XX PI Weissman SM, Kulkarni P, Nallur GN;

XX DR WPI; 1997-393714/36.

XX PT Identifying protein-binding sites for DNA-binding proteins - using  
PT duplexes having 5' and 3' sequences for annealing to amplification  
PT primers with an internal potential protein-binding site sequence.

XX PS Example 3; Page 19; 52pp; English.

XX CC This sequence represents a binding site identified using the method of  
CC the invention. This sequence was identified using the 32P-labelled  
CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
CC AAT76582-T76583 in the method of the invention. The method is for  
CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
CC having 5' and 3' sequences capable of annealing to primers for  
CC amplification and an internal sequence having a potential protein-binding  
CC site, a non-specific inhibitor and a sample containing DNA-binding  
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
CC binding proteins. The methods can be used to identify protein-binding  
CC sites which can be used to identify corresponding DNA-binding proteins in  
CC an expression library. They can also be used to develop products to  
CC inhibit the function of a given DNA-binding protein or for the  
CC modification of transcription factors

XX SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

## RESULT 42

AAT98837

```
ID AAT98837 standard; DNA; 10 BP.
XX
AC AAT98837;
XX
DT 20-MAR-1998 (first entry)
DE
DE Binding site BSN7 identified using the method of the invention.
XX
KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
PD
PD 31-JUL-1997.
XX
XX
PF 24-JAN-1997; 97WO-US001230.
XX
XX 24-JAN-1996; 96US-00590571.
XX
PA (UYVA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
XX Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
4 GTGGG 8

RESULT 43
AAT98848
ID AAT98848 standard; DNA; 10 BP.
XX
AC AAT98848;
XX
XX 20-MAR-1998 (first entry)
DT
DE Binding site BSN6 identified using the method of the invention.
XX
DE Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
PD
PD 31-JUL-1997.
XX
XX
PF 24-JAN-1997; 97WO-US001230.
XX
XX 24-JAN-1996; 96US-00590571.
XX
PA (UYVA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
XX Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
4 GTGGG 8

RESULT 44
AAT98864
ID AAT98864 standard; DNA; 10 BP.
XX
AC AAT98864;
XX
XX 20-MAR-1998 (first entry)
DT
DE Core-binding site clone 6-12-2R.
XX
XX Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
PD
PD 31-JUL-1997.
XX
XX 24-JAN-1997; 97WO-US001230.
XX
PA (UYVA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
XX Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
1 GTGGG 5

RESULT 44
AAT98864
ID AAT98864 standard; DNA; 10 BP.
XX
AC AAT98864;
XX
XX 20-MAR-1998 (first entry)
DT
DE Core-binding site clone 6-12-2R.
XX
XX Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
PD
PD 31-JUL-1997.
XX
XX 24-JAN-1997; 97WO-US001230.
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XX 24-JAN-1996; 96US-00590571.
XX (UYYA ) UNIV YALE.
XX Weissman SM, Kulkarni P, Nallur GN;
XX WPI; 1997-393714/36.
XX Identifying protein-binding sites for DNA-binding proteins - using
XX duplexes having 5' and 3' sequences for annealing to amplification
XX primers with an internal potential protein-binding site sequence.
XX Example 3; Page 22; 52pp; English.
XX This sequence represents a core-binding site identified using the method
XX of the invention. This sequence was identified using the 32P-labelled
XX oligonucleotide duplex shown in AAT76581 and the primers shown in
XX AAT76582-T76583 in the method of the invention. The method is for
XX simultaneously isolating protein-binding sites for DNA-binding proteins.
XX The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
XX having 5' and 3' sequences capable of annealing to primers for
XX amplification and an internal sequence having a potential protein-binding
XX site, a non-specific inhibitor and a sample containing DNA-binding
XX proteins; (b) separating unbound ON duplexes from ON duplexes complexed
XX with the DNA-binding proteins; (c) amplifying complexed duplexes to form
XX amplified duplexes; thereby isolating protein-binding sites for the DNA-
XX binding proteins. The methods can be used to identify protein-binding
XX sites which can be used to identify corresponding DNA-binding proteins in
XX an expression library. They can also be used to develop products to
XX inhibit the function of a given DNA-binding protein or for the
XX modification of transcription factors
XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
1 GTGGG 5

RESULT 45
AAT51668
ID AAT51668 standard; DNA; 10 BP.
XX AAT51668;
XX 12-NOV-1997 (first entry)
XX Viral integrase inhibiting oligonucleotide.
XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
XX herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
XX respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
XX integrase inhibition; guanosine tetrad; ss.
XX Synthetic.
XX WO9703997-A1.
XX 06-FEB-1997.
XX 17-JUL-1996; 96WO-US011786.
XX 19-JUL-1995; 95US-0001505P.
XX 23-OCT-1995; 95US-00535168.
XX 19-MAR-1996; 96US-0013688P.
XX 25-MAR-1996; 96US-0014007P.
XX 17-APR-1996; 96US-0015714P.
XX 23-APR-1996; 96US-0016271P.
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XX (ARON-) ARONEX PHARM INC.
XX Rando RF, Fennewald S, Zendequi JG, Ojwang JO, Hogan ME;
XX Pommier Y, Mazumder A;
XX WPI; 1997-132569/12.
XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit viral
XX enzyme responsible for integrating viral nucleic acid into the host
XX genome.
XX Claim 3; Page 168; 245pp; English.
XX AAT51619-T51698 are oligonucleotides used to inhibit the production of
XX viruses within a host cell. The oligonucleotides may form guanosine
XX tetrads (structures formed of eight hydrogen bonds by coordination of the
XX four oxygen atoms of guanine with alkali cations believed to bind to the
XX centre of a quadruplex, and by strong stacking interactions) and are used
XX to prevent the integration of viral nucleic acid into a host genome. The
XX oligonucleotides inhibit functioning of the integrase enzyme and hence
XX prevent viral infection. Viral infections that may be treated include
XX human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes
XX simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory
XX syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),
XX especially HIV-1 infection
XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db |||||
1 GTGGG 5

RESULT 46
AAT59107/c
ID AAT59107 standard; RNA; 10 BP.
XX AAT59107;
XX 25-MAR-2003 (revised)
XX 23-APR-1997 (first entry)
XX Activated H-ras mRNA antisense oligonucleotide 3283.
XX Activated H-ras; antisense; oligonucleotide; inhibition; affinity; ss.
XX Synthetic.
XX US5582972-A.
XX 10-DEC-1996.
XX 14-DEC-1992; 92US-00990303.
XX 14-JUN-1991; 91US-00715196.
XX (ISIS-) ISIS PHARM INC.
XX Ecker D, Freier S, Lima W, Monia B;
XX WPI; 1997-042296/04.
XX Anti-sense oligo:nucleotide(s) targeted to hairpin structure - of
XX activated H-ras mRNA, useful for inhibiting functions of Ras derived DNA
XX or RNA.
XX Claim 4; Col 13; 16pp; English.
XX
```

CC Oligonucleotides AAT59103-8 are antisense sequences targeted to  
CC nucleotides 18-64 of the activated H-ras mRNA (AAT59102). The  
CC oligonucleotides inhibit the function of RNA or DNA derived from the Ras  
CC gene. The oligonucleotides are selected by comparing the affinities of  
CC the oligonucleotides for their target region with the affinities for an  
CC oligonucleotide complement with the same number of nucleotides. Those  
CC oligonucleotides which have affinity for the target region not less than  
CC one thousandth of the affinity for the oligonucleotide complement are  
CC used to inhibit the H-ras sequence. (Updated on 25-MAR-2003 to correct PF  
CC field.)

XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db |||||  
8 GTGGG 4

RESULT 47

AAT59104/c  
ID AAT59104 standard; DNA; 10 BP.

XX  
AC AAT59104;

XX 25-MAR-2003 (revised)  
DT 23-APR-1997 (first entry)

XX Activated H-ras mRNA antisense oligonucleotide 3271.

XX Activated H-ras; antisense; oligonucleotide; inhibition; affinity; ss.

XX Synthetic.

XX US5582972-A.

XX 10-DEC-1996.

XX 14-DEC-1992; 92US-00990303.

XX 14-JUN-1991; 91US-00715196.

XX (ISIS-) ISIS PHARM INC.

XX Ecker D, Freier S, Lima W, Monia B;

XX WPI; 1997-042296/04.

XX Anti-sense oligo:nucleotide(s) targeted to hairpin structure - of  
PT activated H-ras mRNA, useful for inhibiting functions of Ras derived DNA  
PT or RNA.

XX Claim 4; Col 11; 16pp; English.

XX Oligonucleotides AAT59103-8 are antisense sequences targeted to  
CC nucleotides 18-64 of the activated H-ras mRNA (AAT59102). The  
CC oligonucleotides inhibit the function of RNA or DNA derived from the Ras  
CC gene. The oligonucleotides are selected by comparing the affinities of  
CC the oligonucleotides for their target region with the affinities for an  
CC oligonucleotide complement with the same number of nucleotides. Those  
CC oligonucleotides which have affinity for the target region not less than  
CC one thousandth of the affinity for the oligonucleotide complement are  
CC used to inhibit the H-ras sequence. (Updated on 25-MAR-2003 to correct PF  
CC field.)

XX Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db |||||  
8 GTGGG 4

RESULT 48

AAV10687/c  
ID AAV10687 standard; DNA; 10 BP.

XX  
AC AAV10687;

XX 21-JUL-1998 (first entry)

XX Human breast cancer gene differential display primer #5.

XX Breast cancer; malignant transformation; diagnostic; therapeutic;  
KW screening; primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9738085-A2.

XX 16-OCT-1997.

XX 09-APR-1997; 97WO-US005930.

XX 10-APR-1996; 96US-0015167P.

XX 05-JUN-1996; 96WO-US009286.

XX 06-JUN-1996; 96US-0019202P.

XX 11-JUL-1996; 96US-00678280.

XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX Smith H, Chen L;

XX WPI; 1997-512705/47.

XX Breast cancer genes - used to develop products to design or screen  
PT diagnostic reagents or therapeutic compounds.

XX Example 2; Page 46; 118pp; English.

XX Primers AAV10683-V10688 are used to obtain novel human breast cancer  
CC genes by differential display. The identified genes or fragments of these  
CC genes can be used for identifying genes and gene products that are  
CC intimately related to malignant transformation or maintenance of the  
CC malignant properties of cancer cells. It can also be used to design or  
CC screen diagnostic reagents or therapeutic compounds. Kits are included  
CC within the scope of the invention

XX Sequence 10 BP; 3 A; 6 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db |||||  
10 GTGGG 6

RESULT 49

AAT96115  
ID AAT96115 standard; RNA; 10 BP.

XX  
AC AAT96115;

XX 31-MAR-1998 (first entry)

XX Target site 1 sequence.



KW Determination; oligonucleotide; specific activity; therapy;  
KW target biomolecule; randomised oligonucleotide; diagnosis; research;  
KW target site; ss.  
XX  
OS Synthetic.  
XX  
PN US5686242-A.  
XX  
XX 11-NOV-1997.  
PD  
XX  
XX 27-OCT-1994; 94US-00330000.  
PF  
XX  
XX 05-SEP-1991; 91US-00755485.  
PR  
XX 04-SEP-1992; 92WO-US007489.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
XX  
PI Lima WF, Bruice TW;  
XX  
XX WPI; 1997-558135/51.  
DR  
XX  
XX Determination of oligo-nucleotide with specific activity for target bio-  
PT molecule - using set of randomised oligo-nucleotide(s).  
XX  
XX Example 17; Col 31-32; 22pp; English.  
PS  
XX The present sequence was used in the development of a method of  
CC determining an oligonucleotide having specific activity for a target  
CC biomolecule. The method comprises assaying a set of randomised  
CC oligonucleotides for activity against a target biomolecule, separating  
CC active from inactive oligonucleotides and recovering, amplifying and  
CC determining the nucleic acid sequence of the active oligonucleotides. The  
CC oligonucleotides can be used for therapeutic, diagnostic and research  
CC purposes  
XX  
XX Sequence 10 BP; 0 A; 2 C; 6 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db :|||  
3 GUGGG 7  
RESULT 50  
AAT96109/c  
ID AAT96109 standard; RNA; 10 BP.  
XX  
AC AAT96109;  
XX  
DT 31-MAR-1998 (first entry)  
XX  
DE Calibration oligonucleotide.  
XX  
KW Determination; oligonucleotide; specific activity; therapy;  
KW target biomolecule; randomised oligonucleotide; diagnosis; research;  
KW calibration oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
XX US5686242-A.  
XX  
XX 11-NOV-1997.  
PD  
XX  
XX 27-OCT-1994; 94US-00330000.  
PF  
XX  
XX 05-SEP-1991; 91US-00755485.  
PR  
XX 04-SEP-1992; 92WO-US007489.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX

PI Lima WF, Bruice TW;  
XX  
XX WPI; 1997-558135/51.  
DR  
XX  
XX Determination of oligo-nucleotide with specific activity for target bio-  
PT molecule - using set of randomised oligo-nucleotide(s).  
XX  
XX Example 12; Col 27-28; 22pp; English.  
PS  
XX The present sequence was used in the development of a method of  
CC determining an oligonucleotide having specific activity for a target  
CC biomolecule. The method comprises assaying a set of randomised  
CC oligonucleotides for activity against a target biomolecule, separating  
CC active from inactive oligonucleotides and recovering, amplifying and  
CC determining the nucleic acid sequence of the active oligonucleotides. The  
CC oligonucleotides can be used for therapeutic, diagnostic and research  
CC purposes  
XX  
XX Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db :|||  
8 GTGGG 4  
Search completed: January 7, 2005, 07:12:05  
Job time : 258.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GTGGG  
Perfect score: 5  
Sequence: 1 gtggg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues  
Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5	100.0	10	9	CL436411
C 2	5	100.0	10	9	CL436420
C 3	5	100.0	10	9	CL652677
C 4	5	100.0	11	5	BQ593914
C 5	5	100.0	11	9	CL675669
C 6	5	100.0	12	5	BQ592925
C 7	5	100.0	12	5	BQ594497
C 8	5	100.0	12	5	BQ595544
C 9	5	100.0	12	9	CL423646
C 10	5	100.0	13	1	AA910741
C 11	5	100.0	13	4	BG810452
C 12	5	100.0	13	5	BQ592041
C 13	5	100.0	13	5	BQ593629
C 14	5	100.0	13	5	BQ593844
C 15	5	100.0	13	5	BQ594526
C 16	5	100.0	13	5	BQ595480
C 17	5	100.0	13	7	CF542943
C 18	5	100.0	13	9	AJ588888
C 19	5	100.0	13	9	AJ593426
C 20	5	100.0	14	4	BM395358
C 21	5	100.0	14	5	BQ595292
C 22	5	100.0	14	5	BQ605961
C 23	5	100.0	14	9	AJ587271
C 24	5	100.0	15	1	AJ682954

25	5	100.0	15	5	BQ594756	BQ594756	E012441-0
26	5	100.0	15	5	BQ595235	BQ595235	E012708-0
C 27	5	100.0	15	6	CA851710	CA851710	D16F12_L2
C 28	5	100.0	15	7	CF543306	CF543306	S014668-0
C 29	5	100.0	15	7	CF543404	CF543404	S014668-0
C 30	5	100.0	16	1	AA937364	AA937364	OJ08F10.8
C 31	5	100.0	16	1	AI248882	AI248882	QU73E07.X
C 32	5	100.0	16	1	AI564478	AI564478	TQ57G09.X
C 33	5	100.0	16	1	AI569544	AI569544	TO28D10.X
C 34	5	100.0	16	1	AI590540	AI590540	TW11C02.X
C 35	5	100.0	16	1	AI684114	AI684114	TX79D02.X
C 36	5	100.0	16	1	AI735054	AI735054	AS88B02.X
C 37	5	100.0	16	1	AI749229	AI749229	AT41A02.X
C 38	5	100.0	16	2	BE586084	BE586084	Est#8PT7
C 39	5	100.0	16	4	BM396802	BM396802	5009-0-25
C 40	5	100.0	16	4	BM399406	BM399406	5009-0-57
C 41	5	100.0	16	5	BQ592176	BQ592176	E012696-0
C 42	5	100.0	16	5	BQ593213	BQ593213	E012795-0
C 43	5	100.0	16	5	BQ595114	BQ595114	E012708-0
C 44	5	100.0	16	7	CF543332	CF543332	S014665-0
C 45	5	100.0	16	9	AJ596548	AJ596548	Arabidops
C 46	5	100.0	17	1	AJ666397	AJ666397	Arabidops
C 47	5	100.0	17	4	BM395627	BM395627	5009-0-1-
C 48	5	100.0	17	4	BM397301	BM397301	5009-0-30
C 49	5	100.0	17	5	BQ590447	BQ590447	E012839-0
C 50	5	100.0	17	5	BQ594949	BQ594949	S015254-0
C 51	5	100.0	17	7	CF921142	CF921142	gmrhRww3-
C 52	5	100.0	17	9	AJ587423	AJ587423	Arabidops
C 53	5	100.0	17	9	AJ592362	AJ592362	Arabidops
C 54	5	100.0	18	4	BG925569	BG925569	HNC5-1-E2
C 55	5	100.0	18	4	BM399785	BM399785	5009-0-61
C 56	5	100.0	18	4	BM401236	BM401236	5009-0-84
C 57	5	100.0	18	5	BQ593882	BQ593882	E012763-0
C 58	5	100.0	18	5	BQ594466	BQ594466	E012442-0
C 59	5	100.0	18	5	BQ901245	BQ901245	hasp002xj
C 60	5	100.0	18	9	AJ591945	AJ591945	Arabidops
C 61	5	100.0	18	9	AJ595830	AJ595830	Arabidops
C 62	5	100.0	18	9	CL436272	CL436272	PST2635-N
C 63	5	100.0	19	1	AA878747	AA878747	of85b01.8
C 64	5	100.0	19	1	AA909236	AA909236	ol08a11.8
C 65	5	100.0	19	1	AA911671	AA911671	ol49f08.8
C 66	5	100.0	19	1	AA928040	AA928040	oi58g09.8
C 67	5	100.0	19	1	AI056541	AI056541	OY98C11.X
C 68	5	100.0	19	1	AI364573	AI364573	qw37g03.X
C 69	5	100.0	19	1	AI431460	AI431460	th40c01.X
C 70	5	100.0	19	1	AI537209	AI537209	tp06f07.X
C 71	5	100.0	19	1	AI641650	AI641650	fc22a01.X
C 72	5	100.0	19	1	AI718147	AI718147	as42f11.X
C 73	5	100.0	19	1	AI807936	AI807936	wf52e09.X
C 74	5	100.0	19	1	AJ649686	AJ649686	AJ649686
C 75	5	100.0	19	1	AJ662060	AJ662060	AJ662060
C 76	5	100.0	19	1	AJ686305	AJ686305	AJ686305
C 77	5	100.0	19	2	AW063940	AW063940	DP0975_KR
C 78	5	100.0	19	4	BM397569	BM397569	5009-0-34
C 79	5	100.0	19	4	BM399684	BM399684	5009-0-60
C 80	5	100.0	19	4	BM399791	BM399791	5009-0-61
C 81	5	100.0	19	5	BQ589613	BQ589613	E012681-0
C 82	5	100.0	19	5	BQ589692	BQ589692	E012679-0
C 83	5	100.0	19	6	CF293217	CF293217	3ODGS--02
C 84	5	100.0	19	7	D44776	D44776	HUMSUPY214
C 85	5	100.0	19	8	AZ307733	AZ307733	1M0009C12
C 86	5	100.0	19	8	AZ314143	AZ314143	1M0030K16
C 87	5	100.0	19	8	AZ314511	AZ314511	1M0031B20
C 88	5	100.0	19	8	AZ323681	AZ323681	1M0045E13
C 89	5	100.0	19	8	AZ324165	AZ324165	1M0046C06
C 90	5	100.0	19	8	AZ324865	AZ324865	1M0047G10
C 91	5	100.0	19	8	AZ341989	AZ341989	1M0074H13
C 92	5	100.0	19	8	AZ343228	AZ343228	1M0076M05
C 93	5	100.0	19	8	AZ351194	AZ351194	1M0089A08
C 94	5	100.0	19	8	AZ355195	AZ355195	1M0094G22
C 95	5	100.0	19	8	AZ368655	AZ368655	1M0118P13
C 96	5	100.0	19	8	AZ369361	AZ369361	1M0119I23
C 97	5	100.0	19	8	AZ369369	AZ369369	1M0119K19

C 98	5	100.0	19	8	AZ375581	1M0129E05	AZ375581	1M0129E05	171	5	100.0	20	8	AZ498694	1M0336B08
99	5	100.0	19	8	AZ379786	1M0135K09	AZ379786	1M0135K09	172	5	100.0	20	8	AZ511017	1M0355C19
100	5	100.0	19	8	AZ381798	1M0138G01	AZ381798	1M0138G01	173	5	100.0	20	8	AZ511024	1M0355D22
101	5	100.0	19	8	AZ412553	1M0186M03	AZ412553	1M0186M03	C 174	5	100.0	20	8	AZ514611	1M0361M20
102	5	100.0	19	8	AZ422531	1M0201E16	AZ422531	1M0201E16	C 175	5	100.0	20	8	AZ579536	1M0367I03
103	5	100.0	19	8	AZ435252	1M0222D11	AZ435252	1M0222D11	C 176	5	100.0	20	8	AZ582391	1M0374F17
C 104	5	100.0	19	8	AZ442378	1M0236K18	AZ442378	1M0236K18	177	5	100.0	20	8	AZ583699	1M0378G15
C 105	5	100.0	19	8	AZ445563	1M0241P18	AZ445563	1M0241P18	178	5	100.0	20	8	AZ590476	1M0400P06
C 106	5	100.0	19	8	AZ447936	1M0245O18	AZ447936	1M0245O18	179	5	100.0	20	8	AZ601843	1M0420M13
C 107	5	100.0	19	8	AZ452087	1M0251F18	AZ452087	1M0251F18	180	5	100.0	20	8	AZ609449	1M0434D20
108	5	100.0	19	8	AZ453412	1M0254I10	AZ453412	1M0254I10	181	5	100.0	20	8	AZ627848	1M0474G14
109	5	100.0	19	8	AZ466725	1M0277C09	AZ466725	1M0277C09	C 182	5	100.0	20	8	AZ628809	1M0481C17
C 110	5	100.0	19	8	AZ478164	1M0298I05	AZ478164	1M0298I05	183	5	100.0	20	8	AZ651800	1M0522N07
111	5	100.0	19	8	AZ478277	1M0298B16	AZ478277	1M0298B16	184	5	100.0	20	8	AZ652975	1M0526L20
112	5	100.0	19	8	AZ478905	1M0299E18	AZ478905	1M0299E18	C 185	5	100.0	20	8	AZ653361	1M0527D04
113	5	100.0	19	8	AZ482050	1M0306H20	AZ482050	1M0306H20	C 186	5	100.0	20	8	AZ663955	1M0543D22
114	5	100.0	19	8	AZ485264	1M0312O02	AZ485264	1M0312O02	187	5	100.0	20	8	AZ665998	1M0547F17
115	5	100.0	19	8	AZ489548	1M0322L05	AZ489548	1M0322L05	C 188	5	100.0	20	8	AZ666896	1M0549A24
C 116	5	100.0	19	8	AZ510143	1M0354P21	AZ510143	1M0354P21	189	5	100.0	20	8	AZ770749	1M0572B01
117	5	100.0	19	8	AZ512762	1M0358M04	AZ512762	1M0358M04	C 190	5	100.0	20	8	AZ776456	2M0010O03
C 118	5	100.0	19	8	AZ514405	1M0361L03	AZ514405	1M0361L03	C 191	5	100.0	20	8	AZ776807	2M0010H14
C 119	5	100.0	19	8	AZ579133	1M0363B04	AZ579133	1M0363B04	192	5	100.0	20	8	AZ782314	2M0022D03
120	5	100.0	19	8	AZ585820	1M0391I15	AZ585820	1M0391I15	193	5	100.0	20	8	AZ782816	2M0024F05
121	5	100.0	19	8	AZ626573	1M0466J24	AZ626573	1M0466J24	194	5	100.0	20	8	AZ793982	2M0047I05
122	5	100.0	19	8	AZ644418	1M0508B20	AZ644418	1M0508B20	195	5	100.0	20	8	AZ802167	2M0061A07
C 123	5	100.0	19	8	AZ646713	1M0512D20	AZ646713	1M0512D20	196	5	100.0	20	8	AZ808291	2M0071D09
124	5	100.0	19	8	AZ651870	1M0522M15	AZ651870	1M0522M15	197	5	100.0	20	8	AZ808381	2M0071F23
125	5	100.0	19	8	AZ656937	1M0532K13	AZ656937	1M0532K13	198	5	100.0	20	8	AZ828544	2M0105O04
126	5	100.0	19	8	AZ761834	1M0556E19	AZ761834	1M0556E19	C 199	5	100.0	20	8	AZ828665	2M0105I16
127	5	100.0	19	8	AZ768418	1M0568H23	AZ768418	1M0568H23	C 200	5	100.0	20	8	AZ830013	2M0109C05
128	5	100.0	19	8	AZ780591	2M0018B09	AZ780591	2M0018B09	201	5	100.0	20	8	AZ833488	2M0115B12
129	5	100.0	19	8	AZ782026	2M0021I23	AZ782026	2M0021I23	C 202	5	100.0	20	8	AZ835099	2M0129I07
C 130	5	100.0	19	8	AZ785573	2M0029L02	AZ785573	2M0029L02	203	5	100.0	20	8	AZ836147	2M0130O14
131	5	100.0	19	8	AZ786308	2M0031B17	AZ786308	2M0031B17	204	5	100.0	20	8	AZ846437	2M0146E10
132	5	100.0	19	8	AZ787717	2M0034A21	AZ787717	2M0034A21	205	5	100.0	20	8	AZ853944	2M0157B21
C 133	5	100.0	19	8	AZ788326	2M0035P16	AZ788326	2M0035P16	206	5	100.0	20	8	AZ859065	2M0164F06
134	5	100.0	19	8	AZ808178	2M0071A15	AZ808178	2M0071A15	C 207	5	100.0	20	8	AZ948873	2M0212P02
135	5	100.0	19	8	AZ819494	2M0091I10	AZ819494	2M0091I10	208	5	100.0	20	8	AZ990797	2M0274K12
C 136	5	100.0	19	8	AZ819577	2M0091H18	AZ819577	2M0091H18	C 209	5	100.0	20	9	CL656662	PR10127a-
137	5	100.0	19	8	AZ822954	2M0096I10	AZ822954	2M0096I10	C 210	5	100.0	20	9	CL660020	PR10135d
C 138	5	100.0	19	8	AZ824929	2M0099P16	AZ824929	2M0099P16	C 211	5	100.0	20	9	AG187876	Pan trogl
139	5	100.0	19	8	AZ834875	2M0117L13	AZ834875	2M0117L13	212	5	100.0	20	9	AG199663	Pan trogl
C 140	5	100.0	19	8	AZ837373	2M0132C07	AZ837373	2M0132C07	C 213	5	100.0	20	1	AJ662932	AJ662932
141	5	100.0	19	8	AZ859728	2M0165M22	AZ859728	2M0165M22	214	5	100.0	21	1	AJ662980	AJ662980
C 142	5	100.0	19	8	AZ864599	2M0174G17	AZ864599	2M0174G17	215	5	100.0	21	1	AU254493	AU254493
143	5	100.0	19	8	AZ967656	2M0238M09	AZ967656	2M0238M09	216	5	100.0	21	1	AU257028	AU257028
C 144	5	100.0	19	8	BH000474	2M0288B20	BH000474	2M0288B20	C 217	5	100.0	21	2	AW248836	2821108.3
145	5	100.0	20	1	AB088510	AB088510	AB088510	AB088510	C 218	5	100.0	21	4	BM395685	5009-0-10
146	5	100.0	20	4	BM395281	50072-2-8	BM395281	50072-2-8	219	5	100.0	21	4	BM396371	5009-0-21
C 147	5	100.0	20	6	CF296226	3DGS--06	CF296226	3DGS--06	220	5	100.0	21	4	BM400512	5009-0-74
148	5	100.0	20	6	CF302285	7LEAF--07	CF302285	7LEAF--07	221	5	100.0	21	5	BQ593572	BQ593572
C 149	5	100.0	20	6	CF315288	HD--04-C1	CF315288	HD--04-C1	222	5	100.0	21	7	CO785358	BL283B.D0
150	5	100.0	20	7	CO779101	BL005C.F0	CO779101	BL005C.F0	223	5	100.0	21	8	AZ313243	1M0029H16
C 151	5	100.0	20	7	D20001	HUMGS00971	D20001	HUMGS00971	C 224	5	100.0	21	8	AZ320581	1M0040P08
152	5	100.0	20	8	AZ307088	1M0008M23	AZ307088	1M0008M23	225	5	100.0	21	8	AZ324683	1M0046C13
C 153	5	100.0	20	8	AZ323748	1M0045B20	AZ323748	1M0045B20	226	5	100.0	21	8	AZ330987	1M0056D19
C 154	5	100.0	20	8	AZ330662	1M0056F15	AZ330662	1M0056F15	C 227	5	100.0	21	8	AZ345472	1M0080O11
C 155	5	100.0	20	8	AZ336487	1M0066J13	AZ336487	1M0066J13	228	5	100.0	21	8	AZ359241	1M0102D03
C 156	5	100.0	20	8	AZ345583	1M0080L18	AZ345583	1M0080L18	229	5	100.0	21	8	AZ365904	1M0112H20
157	5	100.0	20	8	AZ357114	1M0098B06	AZ357114	1M0098B06	230	5	100.0	21	8	AZ369855	1M0120G07
C 158	5	100.0	20	8	AZ368205	1M0118L07	AZ368205	1M0118L07	231	5	100.0	21	8	AZ375798	1M0129C22
159	5	100.0	20	8	AZ368843	1M0119C07	AZ368843	1M0119C07	232	5	100.0	21	8	AZ399828	1M0165A23
C 160	5	100.0	20	8	AZ369273	1M0119H13	AZ369273	1M0119H13	233	5	100.0	21	8	AZ422880	1M0201E12
161	5	100.0	20	8	AZ405596	1M0174B06	AZ405596	1M0174B06	C 234	5	100.0	21	8	AZ424095	1M0203E03
162	5	100.0	20	8	AZ447706	1M0245C06	AZ447706	1M0245C06	C 235	5	100.0	21	8	AZ426507	1M0208L03
C 163	5	100.0	20	8	AZ449127	1M0247A17	AZ449127	1M0247A17	236	5	100.0	21	8	AZ433959	1M0220B12
164	5	100.0	20	8	AZ466238	1M0276J16	AZ466238	1M0276J16	237	5	100.0	21	8	AZ435931	1M0223L15
C 165	5	100.0	20	8	AZ468486	1M0281G04	AZ468486	1M0281G04	238	5	100.0	21	8	AZ442444	1M0236N21
C 166	5	100.0	20	8	AZ478502	1M0298B09	AZ478502	1M0298B09	239	5	100.0	21	8	AZ443821	1M0238I07
167	5	100.0	20	8	AZ483003	1M0308G19	AZ483003	1M0308G19	C 240	5	100.0	21	8	AZ445481	1M0241P15
C 168	5	100.0	20	8	AZ487730	1M0317P04	AZ487730	1M0317P04	241	5	100.0	21	8	AZ451384	1M0250D13
169	5	100.0	20	8	AZ492477	1M0326D12	AZ492477	1M0326D12	C 242	5	100.0	21	8	AZ466379	1M0277I03
170	5	100.0	20	8	AZ495323	1M0331N07	AZ495323	1M0331N07	243	5	100.0	21	8	AZ468862	1M0282O04

244	5	100.0	21	8	AZ493166	AZ493166	1M0327K05
C 245	5	100.0	21	8	AZ495585	AZ495585	1M0331H02
C 246	5	100.0	21	8	AZ496015	AZ496015	1M0332P08
C 247	5	100.0	21	8	AZ503574	AZ503574	1M0343H19
248	5	100.0	21	8	AZ504494	AZ504494	1M0344O17
249	5	100.0	21	8	AZ510254	AZ510254	1M0354F10
C 250	5	100.0	21	8	AZ512534	AZ512534	1M0358B07
251	5	100.0	21	8	AZ514603	AZ514603	1M0361J24
C 252	5	100.0	21	8	AZ585597	AZ585597	1M0391J05
253	5	100.0	21	8	AZ596349	AZ596349	1M0409K03
254	5	100.0	21	8	AZ596843	AZ596843	1M0410C23
255	5	100.0	21	8	AZ598381	AZ598381	1M0413J11
C 256	5	100.0	21	8	AZ617284	AZ617284	1M0448C04
C 257	5	100.0	21	8	AZ628035	AZ628035	1M0476H15
258	5	100.0	21	8	AZ636817	AZ636817	1M0495C20
259	5	100.0	21	8	AZ645749	AZ645749	1M0511C20
260	5	100.0	21	8	AZ647787	AZ647787	1M0514P24
261	5	100.0	21	8	AZ648575	AZ648575	1M0517G07
C 262	5	100.0	21	8	AZ654730	AZ654730	1M0529P05
C 263	5	100.0	21	8	AZ660221	AZ660221	1M0538M09
264	5	100.0	21	8	AZ758704	AZ758704	1M0550A20
265	5	100.0	21	8	AZ768059	AZ768059	1M0567O18
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C 270	5	100.0	21	8	AZ778985	AZ778985	2M0014B14
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C 276	5	100.0	21	8	AZ812415	AZ812415	2M0079N04
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ALIGNMENTS

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VERSION	CL436411.1	GI:45571178			
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ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 10)				
JOURNAL	Hicks,G.G.				
COMMENT	www.EScells.ca				
	Unpublished (2002)				
	Contact: Hicks GG				
	Mammalian Functional Genomics Centre				
	Manitoba Institute of Cell Biology, University of Manitoba				
	ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada				
	Tel: 204 787 2133				
	Fax: 204 787 2190				
	Email: hicksgg@cc.umanitoba.ca				
	U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional				
	sequence information and target gene cloning can be generated. ES				
	cell line harboring insertion mutation of target gene is available.				
	Sequence analysis available from				
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FEATURES	Location/Qualifiers				

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Db 9 GTGGG 5

RESULT 2
CL436420/c
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CL436420
ACCESSION
VERSION
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Hicks,G.G.
TITLE
www.Escells.ca
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST2947-NR.Se
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Class: Gene Trap.
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Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 1

source
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST292-1.seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MIBC1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 1
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RESULT 3
CL652677/c
LOCUS
DEFINITION
PST2947-NR.Seq MIBC1 Mus musculus genomic clone PST2947-NR.Seq
similar to D130048F08RIK, genomic survey sequence.
CL652677
ACCESSION
VERSION
KEYWORDS
SOURCE
PRISTIONCHUS pristionchus
ORGANISM
PRISTIONCHUS pristionchus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .10
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 10 GTGGG 6

RESULT 4
BQ593914
LOCUS
DEFINITION
BQ593914
S015507-024-025-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-025-N20 5-PRIME, mRNA sequence.
ACCESSION
BQ593914
VERSION
BQ593914.1 GI:26123497
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
```



```
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaa@mpiz-koeln.mpg.de
              Insert Length: 11 Std Error: 0.00
              Plate: 25 row: N column: 20
              Seq primer: SP6; CATACGATTAGGTGACACTATAG.
              Location/Qualifiers
                1. .11
                  /organism="Beta vulgaris"
                  /mol_type="mRNA"
                  /cultivar="KWS2320 (double haploid, monogerm breeding
                  line)"
                  /db_xref="GABI:192937"
                  /db_xref="taxon:161934"
                  /clone="024-025-N20"
                  /tissue_type="developing root"
                  /lab_host="EMDH10B"
                  /clone_lib="MPIZ-ADIS-024-developing root"
                  /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
                  cDNA library from sugar beet, library provided by KWS
                  Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                  b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                  orientation:
                  SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                  Sequencing granted in the context of the GABI-Beet
                  project, local PI: Dr. Katharina Schneider, coordinator:
                  Prof. Christian Jung; Sequence submission managed by
                  RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
  Query Match      100.0%; Score 5; DB 5; Length 11;
  Best Local Similarity 100.0%; Pred. No. 9.4e+06;
  Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      1 GTGGG 5
          |||||
  Db      7 GTGGG 11

RESULT 5
CL675669/c
LOCUS
DEFINITION      CL675669 11 bp DNA linear GSS 09-JUL-2004
                  PRI0115C_C03_2 - PRI0115C.BR (11) Mixed stage fosmid library of P.
                  pacificus var. California Pristionchus pacificus genomic, genomic
                  survey sequence.
ACCESSION      CL675669
VERSION        CL675669.1 GI:50180372
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 11)
AUTHORS      Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE        AppADB: an AcedB database for the nematode satellite organism
              Pristionchus pacificus
JOURNAL      Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT      Contact: Sommer RJ
              Evolutionary Biology
              Max-Planck-Institute for Developmental Biology
              Spemannstr. 37-39, Tuebingen D-72076, Germany
              Tel: 00497071601371
              Fax: 00497071601498
              Email: ralf.sommer@tuebingen.mpg.de
              This library was generated at Caltech, Pasadena, USA and end
              sequenced at Vancouver, Canada.
              Seq primer: T7
              Class: fosmid ends.
              Location/Qualifiers
                1. .11

FEATURES
  source
    1. .11
      /organism="Pristionchus pacificus"
      /mol_type="genomic DNA"
      /strain="California"
      /db_xref="taxon:54126"
      /clone_lib="Mixed stage fosmid library of P. pacificus
      var. California"
      /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
  Query Match      100.0%; Score 5; DB 9; Length 11;
  Best Local Similarity 100.0%; Pred. No. 9.4e+06;
  Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      1 GTGGG 5
          |||||
  Db      5 GTGGG 1

RESULT 6
BQ592925/c
LOCUS
DEFINITION      BQ592925 12 bp mRNA linear EST 06-DEC-2002
                  E012123-024-028-F05-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
                  cDNA clone 024-028-F05 5-PRIME, mRNA sequence.
ACCESSION      BQ592925
VERSION        BQ592925.1 GI:26122508
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
REFERENCE
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL      MEDLINE
PUBMED      22362189
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaa@mpiz-koeln.mpg.de
              Insert Length: 12 Std Error: 0.00
              Plate: 28 row: F column: 05
              Seq primer: SP6; CATACGATTAGGTGACACTATAG.
              Location/Qualifiers
                1. .12
                  /organism="Beta vulgaris"
                  /mol_type="mRNA"
                  /cultivar="KWS2320 (double haploid, monogerm breeding
                  line)"
                  /db_xref="GABI:193933"
                  /db_xref="taxon:161934"
                  /clone="024-028-F05"
                  /tissue_type="developing root"
                  /lab_host="EMDH10B"
                  /clone_lib="MPIZ-ADIS-024-developing root"
                  /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
                  cDNA library from sugar beet, library provided by KWS
                  Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                  b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                  orientation:
                  SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                  Sequencing granted in the context of the GABI-Beet
                  project, local PI: Dr. Katharina Schneider, coordinator:
                  Prof. Christian Jung; Sequence submission managed by
                  RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
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Query Match 100.0%; Score 5; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
|  
Db 5 GTGGG 1

RESULT 7

BQ594497/c  
LOCUS  
DEFINITION  
E012444-024-024-P14-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-024-P14 5-PRIME, mRNA sequence.

ACCESSION  
BQ594497  
VERSION  
BQ594497.1 GI:26124080  
KEYWORDS  
EST.

SOURCE  
ORGANISM

Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS

Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED

Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

COMMENT

Contact: Weissshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 24 row: P column: 14  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers  
1. .12  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:192358"  
/db\_xref="taxon:161934"  
/clone="024-024-P14"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
|  
Db 5 GTGGG 1

RESULT 8

BQ595544  
LOCUS  
DEFINITION  
E012691-024-022-A12-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-022-A12 5-PRIME, mRNA sequence.

ACCESSION  
BQ595544  
VERSION  
BQ595544.1 GI:26125127  
KEYWORDS  
EST.

SOURCE  
ORGANISM

Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS

Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED

Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

COMMENT

Contact: Weissshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 22 row: A column: 12  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:191314"  
/db\_xref="taxon:161934"  
/clone="024-022-A12"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|  
|  
|  
|  
|  
Db 8 GTGGG 12

RESULT 9

CL423646/c  
LOCUS  
DEFINITION  
O1S0726-07C1-E03 UniformMu MutAIL Library Zea mays genomic clone  
O1S0726-07C1-E03, genomic survey sequence.

ACCESSION  
CL423646  
VERSION  
CL423646.1 GI:45501690  
KEYWORDS  
GSS.

SOURCE  
Zea mays

ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.  
TITLE Sequence tagged transposon insertions from the UniformMu maize population  
JOURNAL Unpublished (2003)  
COMMENT Contact: Donald R. McCarty  
Plant Molecular and Cellular Biology Program  
University of Florida  
PO 110690 Gainesville, FL 32611-0690, USA  
Tel: 352-392-1928 x322  
Email: drmc@ufl.edu  
Sequence Sequence flanking probable Mu insertion site in UniformMu line: 01S0726-07, Primer set: C  
Class: transposon insertion site.  
FEATURES  
source 1. .12  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="W22 (ACR, bz1-m9)"  
/cultivar="UniformMu"  
/db\_xref="taxon:4577"  
/clones="01S0726-07C1-E03"  
/clone\_lib="UniformMu MuTAIL Library"  
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."  
ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 10 GTGGG 6  
RESULT 10  
AA910741 13 bp mRNA linear EST 26-AUG-1998  
LOCUS 0124h01.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1524433 3' similar to TR:Q28584 Q28584 KAP5.5 KERATIN PROTEIN ;contains element MSR1 repetitive element ;, mRNA sequence.  
ACCESSION AA910741  
VERSION AA910741.1 GI:3050031  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 761 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
FEATURES  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1524433"  
/lab\_host="DH10B"  
/clone\_lib="Soares NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "  
ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 9 GTGGG 13  
RESULT 11  
BG810452/c 13 bp mRNA linear EST 22-MAY-2001  
LOCUS mgct006xc07f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe DEFINITION grisea cDNA clone mgct006xc07f 5', mRNA sequence.  
ACCESSION BG810452  
VERSION BG810452.1 GI:14181432  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Choi,W. and Dean,R.A.  
TITLE Construction and sequence analysis of an appressorium stage cDNA library in the rice blast fungus, Magnaporthe grisea Unpublished (2001)  
JOURNAL Contact: Ralph A. Dean  
COMMENT Fungal Genomics Laboratory  
North Carolina State University  
Campus Box 7251, Raleigh, NC 27695, USA  
Tel: 919-513-0020  
Fax: 919-513-0024  
Email: ralph.dean@ncsu.edu  
Seq primer: T3 primer (AATTAAACCTCACTAAAGGG).  
FEATURES  
source 1. .13  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
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/clone="mgct006xc07f"  
/dev\_stage="Germinated conidia on appressorium-inductive surface"  
/clone\_lib="Magnaporthe grisea Appressorium Stage cDNA"  
/note="Vector: pBluescript SK(+) Vector; Site 1: EcoRI; Site 2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."  
ORIGIN  
Query Match 100.0%; Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;



REFERENCE 1 (bases 1 to 13)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
Plate: 26 row: M column: 06  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
FEATURES  
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:193018"  
/db\_xref="taxon:161934"  
/clone="024-026-M06"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"  
ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 5 GTGGG 9  
RESULT 15  
BQ594526/c  
LOCUS E012443-024-024-L11-SP6 MPiZ-ADIS-024-developing root Beta vulgaris  
DEFINITION cDNA clone 024-024-L11 5-PRIME, mRNA sequence.  
ACCESSION BQ594526  
VERSION BQ594526.1 GI:26124109  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
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/clone="024-024-L11"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPiZ-ADIS-024-developing root"  
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SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"  
ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 5 GTGGG 1  
RESULT 16  
BQ595480  
LOCUS E012690-024-022-G15-SP6 MPiZ-ADIS-024-developing root Beta vulgaris  
DEFINITION cDNA clone 024-022-G15 5-PRIME, mRNA sequence.  
ACCESSION BQ595480  
VERSION BQ595480.1 GI:26125063  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00

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FEATURES	/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"	
	SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"	
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 13;	
	Best Local Similarity 100.0%; Pred. No. 9.5e+06;	
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ORIGIN	Db 8 GTGGG 12	
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FEATURES	S014678-024-030-I14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone	
	024-030-I14 5-PRIME, mRNA sequence.	
source	CF542943	
	CF542943.1 GI:34891383	
FEATURES	EST.	
	Beta vulgaris	
ORIGIN	Beta vulgaris	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.	
REFERENCE	1 (bases 1 to 13)	
	Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.	
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes	
	Plant J. 32 (5), 845-857 (2002)	
JOURNAL	MEDLINE	
	PUBMED	
COMMENT	12472698	
	Contact: Weisshaar B	
FEATURES	ADIS DNA core facility at MP12	
	Max-Planck-Institute for Plant Breeding Research	
source	Carl-von-Linne Weg 10, 50829 Koeln, Germany	
	Fax: 00492215062851	
FEATURES	Email: weisshaa@mpiz-koeln.mpg.de	
	Insert Length: 13 Std Error: 0.00	
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FEATURES	Location/Qualifiers	
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FEATURES	/db_xref="taxon:161934"	
	/clone="024-030-I14"	
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	/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"	
ORIGIN	SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"	
	Query Match 100.0%; Score 5; DB 7; Length 13;	
source	Best Local Similarity 100.0%; Pred. No. 9.5e+06;	
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
ORIGIN	QY 1 GTGGG 5	
	Db 7 GTGGG 11	
FEATURES	AJ588888	
	Arabidopsis thaliana T-DNA flanking sequence, right border, clone	
ORIGIN	540D02, genomic survey sequence.	
	AJ588888	
FEATURES	AJ588888.1 GI:37938512	
	GSS; right border; T-DNA flanking sequence.	
ORIGIN	Arabidopsis thaliana (chale cress)	
	Arabidopsis thaliana	
ORIGIN	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.	
	1	
REFERENCE	Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.	
	T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites	
JOURNAL	EMBO Rep. 3 (12), 1152-1157 (2002)	
	MEDLINE	
PUBMED	22363535	
	12446565	
REFERENCE	2 (bases 1 to 13)	
	Balzergue,S.	
AUTHORS	Direct Submission	
	Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue	
COMMENT	Gaston Cremieux, 91057 Evry cedex, FRANCE	
	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).	
FEATURES	Location/Qualifiers	
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source	/organism="Arabidopsis thaliana"	
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      8 GTGGG 12

RESULT 19
AJ593426
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380B04, genomic survey sequence.
ACCESSION
AJ593426
VERSION
AJ593426.1 GI:37943050
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1 Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 13)
AUTHORS
Balzergue,S.
TITLE
Direct Submission
SUBMITTED (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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Location/Qualifiers
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/note="T-DNA flanking sequence
left border"

ORIGIN
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Db      5 GTGGG 9

/note="T-DNA flanking sequence
right border"

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Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      8 GTGGG 12
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RESULT 20
BM395358
LOCUS
DEFINITION
50072-2-8-G03.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395358
VERSION
BM395358.1 GI:18195411
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
TITLE
Contact: Turkewitz AP
JOURNAL
COMMENT
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
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Location/Qualifiers
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
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Db      2 GTGGG 6

RESULT 21
BQ595292
LOCUS
DEFINITION
B012710-024-023-H07-SP6 MP12-AD15-024-developing root Beta vulgaris
cDNA clone 024-023-H07 5-PRIME, mRNA sequence.
ACCESSION
BQ595292
VERSION
BQ595292.1 GI:26124875
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
```



Email: weishaa@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 23 row: H column: 07  
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Location/Qualifiers  
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/lab\_host="EMDH10B"  
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 8 GTGGG 12

RESULT 22  
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LOCUS  
DEFINITION BQ605961 14 bp mRNA linear EST 25-JUN-2002  
BRY\_1556 wheat EST endosperm library Triticum aestivum cDNA 5', mRNA sequence.  
ACCESSION BQ605961.1 GI:21555112  
VERSION BQ605961.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.  
1 (bases 1 to 14)  
REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.  
AUTHORS Arabidopsis genomic information for interpreting wheat EST sequences  
TITLE Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
JOURNAL 22478026  
MEDLINE 12590341  
PUBMED  
COMMENT Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@acoma.stanford.edu.  
Location/Qualifiers  
1. .14  
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/db\_xref="taxon:4565"  
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FEATURES  
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misc\_feature 1. .14  
/note="T-DNA flanking sequence left border"

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 5 GTGGG 9

RESULT 24

ORIGIN  
Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 6 GTGGG 2

RESULT 23  
AJ587271  
LOCUS  
DEFINITION AJ587271 14 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 257B04, genomic survey sequence.  
ACCESSION AJ587271.1 GI:37936860  
VERSION AJ587271  
KEYWORDS GSS; left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 14)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

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/clone="257B04"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

misc\_feature 1. .14  
/note="T-DNA flanking sequence left border"

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Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
Db 5 GTGGG 9

RESULT 24

AJ682954/c  
LOCUS  
DEFINITION  
AJ682954 15 bp mRNA linear EST 29-JUN-2004  
AJ682954 CSEQRAN04 Sus scrofa cDNA clone C0001800\_K20, mRNA  
sequence.  
ACCESSION  
AJ682954  
VERSION  
AJ682954.1 GI:49415544  
KEYWORDS  
EST.  
SOURCE  
Sus scrofa (pig)  
ORGANISM  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE  
1 (bases 1 to 15)  
AUTHORS  
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
JOURNAL  
Unpublished (2004)  
COMMENT  
Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Sitel: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.  
FEATURES  
Location/Qualifiers  
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NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGGG 5  
|||||  
Db 13 GTGGG 9  
RESULT 25  
BQ594756  
LOCUS  
DEFINITION  
BQ594756 15 bp mRNA linear EST 06-DEC-2002  
E012441-024-024-I13-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-024-I13 5-PRIME, mRNA sequence.  
ACCESSION  
BQ594756  
VERSION  
BQ594756.1 GI:26124339  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 15)  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL  
Plant J. 32 (5), 845-857 (2002)  
MEDLINE  
22362189  
PUBMED  
12472698  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 24 row: I column: 13  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
FEATURES  
Location/Qualifiers  
source  
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/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:192102"  
/db\_xref="taxon:161934"  
/clone="024-024-I13"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGGG 5  
|||||  
Db 8 GTGGG 12  
RESULT 26  
BQ595235  
LOCUS  
DEFINITION  
BQ595235 15 bp mRNA linear EST 06-DEC-2002  
E012708-024-023-C01-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-023-C01 5-PRIME, mRNA sequence.  
ACCESSION  
BQ595235  
VERSION  
BQ595235.1 GI:26124818  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 15)  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL  
Plant J. 32 (5), 845-857 (2002)  
MEDLINE  
22362189  
PUBMED  
12472698  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 23 row: C column: 01  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
FEATURES  
Location/Qualifiers  
source  
1. .15

FEATURES  
source

/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:191628"  
/db\_xref="taxon:161934"  
/clone="024-023-C01"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 8 GTGGG 12

RESULT 27  
CA851710/c  
LOCUS  
DEFINITION  
CA851710  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE  
1 (bases 1 to 15)  
Alkharouf,N.W., Khan,R. and Matthews,B.F.  
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
Unpublished (2002)  
Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharouf@ars.usda.gov.

FEATURES  
source  
1. .15  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="D16F12"  
/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_lib="cDNA Peking library 2, 4 day SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 7 GTGGG 3

RESULT 28  
CF543306/c  
LOCUS  
DEFINITION  
CF543306  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
PUBMED  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 29 row: F column: 24  
Seq primer: SP6.

FEATURES  
source  
1. .15  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936441"  
/db\_xref="taxon:161934"  
/clone="024-029-F24"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 5 GTGGG 1

RESULT 29



/clone\_lib="NCI\_CGAP\_Brn35"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.33 kb. Tumor types include:  
 meningioma, oligodendroglioma, astrocytoma (grade II),  
 medulloblastoma, astrocytoma (grade IV). Life Technologies  
 catalog #: 11544-012"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||  
 Db 8 GTGGG 4

## RESULT 32

AI564478/c  
 LOCUS  
 DEFINITION  
 tc57g09.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2212960 3'  
 similar to TR:000599 O00599 CON1.; contains element MSRI repetitive  
 element.; mRNA sequence.

## ACCESSION

AI564478 1 GI:4522935

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 16)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Tumor Gene Index

## COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

## FEATURES

source

1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2212960"  
 /tissue\_type="well-differentiated endometrial  
 adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut1"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||  
 Db 14 GTGGG 10

## RESULT 33

AI569544/c

## LOCUS

## DEFINITION

AI569544 16 bp mRNA linear EST 12-MAY-1999  
 to28d10.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2180371 3'  
 similar to TR:Q18444 Q18444 COSMID C34D4.; contains MSRI.b2 MSRI

## ACCESSION

AI569544 1 GI:4532918

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 16)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Tumor Gene Index

## COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1683 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

1..16  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2180371"  
 /tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut4"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

|||||

Db 14 GTGGG 10

## RESULT 34

AI590540/c

## LOCUS

## DEFINITION

AI590540 16 bp mRNA linear EST 14-MAY-1999  
 tw1lc02.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259362 3'  
 similar to TR:O00599 O00599 CON1.; mRNA sequence.

## ACCESSION

AI590540 1 GI:4599588

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)  
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index Unpublished (1998)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Insert Length: 353 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

FEATURES  
source Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:2259362"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP Brn52"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; This library represents the normalized version of NCI CGAP Brn35. Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV). Constructed by Life Technologies."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 35  
AI684114/c  
LOCUS AI684114 16 bp mRNA linear EST 16-DEC-1999  
DEFINITION tx79d02.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2275779 3', similar to TR:Q09084 Q09084 EXTENSIN CLASS II PRECURSOR ;, mRNA sequence.  
ACCESSION AI684114 GI:4895408  
VERSION AI684114.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2335755"  
/sex="male"

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Insert Length: 1454 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers  
1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2275779"  
/tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Utl1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 15 GTGGG 11

RESULT 36  
AI735054/c  
LOCUS AI735054 16 bp mRNA linear EST 14-JUN-1999  
DEFINITION aa88b02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335755 3' similar to WP:T28C6.1 CE03746 ;contains MSR1.b2 MSR1 repetitive element ;, mRNA sequence.  
ACCESSION AI735054 GI:5056653  
VERSION AI735054.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers  
1..16  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2335755"  
/sex="male"



/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCAC TAGTAAT 3' and 5' ATTACTAGT 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 6 GTGGG 2

RESULT 37  
AI749229/c

LOCUS AI749229 16 bp mRNA linear EST 22-JUN-1999  
DEFINITION at41a02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374538 3' similar to TR:Q91810 Q91810 PROLINE RICH PROTEIN. ;contains MSR1.b3 MSR1 repetitive element ;, mRNA sequence.

ACCESSION AI749229 GI:5127493

VERSION AI749229.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 16)

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

TITLE Unpublished (1997)

JOURNAL Contact: Wilson RK

COMMENT Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2374538"  
/sex="male"

/dev\_stage="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCAC TAGTAAT 3' and 5' ATTACTAGT 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob

Barstead."

ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 14 GTGGG 10

RESULT 38  
BE586084/c

LOCUS BE586084

DEFINITION Est#8pt7\_G06\_g6\_040 KSU wheat Fusarium graminearum infected spike cDNA library Triticum aestivum cDNA clone Est#8pt7\_G06\_g6\_040, mRNA sequence.

ACCESSION BE586084.1

VERSION BE586084.1

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 16)

AUTHORS Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.

TITLE The structure and function of the expressed portion of the wheat genomes - Kansas State University. Fusarium graminearum infected spike cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: John Fellers

US Department of Agriculture, Agriculture Research Service, Plant Science and Entomology Unit

Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State University, Manhattan, KS 66506, USA

Tel: 785-532-2367

Fax: 785-532-6167

Email: jpf@alfalfa.ksu.edu

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: T7.

FEATURES

source

1. .16  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Sumai3"  
/db\_xref="taxon:4565"  
/clone="Est#8pt7\_G06\_g6\_040"  
/tissue\_type="Spike"  
/dev\_stage="Adult plant"  
/lab\_host="E. coli JM109"  
/clone\_lib="KSU wheat Fusarium graminearum infected spike cDNA library"  
/note="Vector: pGEM-T easy; Site\_1: SacII; Site\_2: SpeI; Plants were grown in the greenhouse. Spikes were sprayed with Fusarium graminearum (at what stage). Total RNA, and poly(A) RNA were prepared from infected spikes. cDNA was prepared using the SmartTM PCR cDNA synthesis kit from Clontech. cDNA was cloned into the pGEM-T easy vector from Promega."

ORIGIN

Query Match 100.0%; Score 5; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 5 GTGGG 1



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RESULT 39
BM396802
LOCUS
DEFINITION
  BM396802 16 bp mRNA linear EST 17-JAN-2002
  Tetrahymena thermophila cDNA (large fraction)
ACCESSION
  BM396802.1 GI:18196855
VERSION
  EST.
KEYWORDS
  Tetrahymena thermophila
SOURCE
  Tetrahymena thermophila
  ORGANISM
    Tetrahymena thermophila
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
    Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
  1 (bases 1 to 16)
  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
  Frankel,J. and Klobutcher,L.
  EST from Tetrahymena thermophila, strain CU428.1, growing cells
  Unpublished (2002)
COMMENT
  Contact: Turkewitz AP
  Molecular Genetics and Cell Biology
  University of Chicago
  920 E. 58th Street, Chicago, IL 60637, USA
  Tel: 773 702 4374
  Fax: 773 702 3172
  Email: apturkew@midway.uchicago.edu
  Seq primer: T3.
FEATURES
  source
    1..16
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /strain="CU428.1"
    /db_xref="taxon:5911"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /note="Vector: Bluescript2 SK+; Details on library
    preparation can be found in Chilcoat and Turkewitz (2001)
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
  Query Match 100.0%; Score 5; DB 4; Length 16;
  Best Local Similarity 100.0%; Pred. No. 9.5e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GTGGG 5
  Db |||||
  2 GTGGG 6
RESULT 40
BM399406
LOCUS
DEFINITION
  BM399406 16 bp mRNA linear EST 17-JAN-2002
  Tetrahymena thermophila cDNA (large fraction)
ACCESSION
  BM399406.1 GI:18199459
VERSION
  EST.
KEYWORDS
  Tetrahymena thermophila
SOURCE
  Tetrahymena thermophila
  ORGANISM
    Tetrahymena thermophila
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
    Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
  1 (bases 1 to 16)
  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
  Frankel,J. and Klobutcher,L.
  EST from Tetrahymena thermophila, strain CU428.1, growing cells
  Unpublished (2002)
COMMENT
  Contact: Turkewitz AP
  Molecular Genetics and Cell Biology
  University of Chicago
  920 E. 58th Street, Chicago, IL 60637, USA
  Tel: 773 702 4374
  Fax: 773 702 3172
  Email: apturkew@midway.uchicago.edu
  Seq primer: T3.
FEATURES
  source
    1..16
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /strain="CU428.1"
    /db_xref="taxon:5911"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /note="Vector: Bluescript2 SK+; Details on library
    preparation can be found in Chilcoat and Turkewitz (2001)
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
  Query Match 100.0%; Score 5; DB 4; Length 16;
  Best Local Similarity 100.0%; Pred. No. 9.5e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GTGGG 5
  Db |||||
  2 GTGGG 6
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/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
  Query Match 100.0%; Score 5; DB 4; Length 16;
  Best Local Similarity 100.0%; Pred. No. 9.5e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GTGGG 5
  Db |||||
  6 GTGGG 10
RESULT 41
BQ592176/c
LOCUS
DEFINITION
  BQ592176 16 bp mRNA linear EST 06-DEC-2002
  E012696-024-021-004-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
  cDNA clone 024-021-004 5-PRIME, mRNA sequence.
ACCESSION
  BQ592176
VERSION
  BQ592176.1 GI:26121759
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Beta vulgaris
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 16)
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaa@mpiz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 21 row: 0 column: 04
  Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
  Location/Qualifiers
    1..16
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultiivar="KWS2320 (double haploid, monogerm breeding
    line)"
    /db_xref="GABI:190799"
    /db_xref="taxon:161934"
    /clone="024-021-004"
    /tissue_type="developing root"
    /lab_host="EMDH10B"
    /clone_lib="MP1Z-ADIS-024-developing root"
    /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
    cDNA library from sugar beet, library provided by KWS
    Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
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Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||  
 Db 5 GTGGG 1

## RESULT 42

BQ593213

LOCUS

DEFINITION BQ593213 16 bp mRNA linear EST 06-DEC-2002  
 E012795-024-027-K15-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 cDNA clone 024-027-K15 5-PRIME, mRNA sequence.

ACCESSION

BQ593213

VERSION

BQ593213.1

GI:26122796

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 16)

AUTHORS

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

Plant J. 32 (5), 845-857 (2002)

MEDLINE

22362189

PUBMED

12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 27 row: K column: 15

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1..16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"

/db\_xref="GABI:193643"

/db\_xref="taxon:161934"

/clone="024-K15"

/tissue\_type="developing root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-developing root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match

Best Local Similarity

Matches

5; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 GTGGG 5

|||||

Db

6 GTGGG 10

## RESULT 43

BQ595114

LOCUS

DEFINITION

BQ595114

ACCESSION

BQ595114

VERSION

BQ595114.1

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 16)

AUTHORS

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

Plant J. 32 (5), 845-857 (2002)

MEDLINE

22362189

PUBMED

12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 23 row: M column: 09

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1..16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"

/db\_xref="GABI:191733"

/db\_xref="taxon:161934"

/clone="024-023-M09"

/tissue\_type="developing root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-developing root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match

Best Local Similarity

Matches

5; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 GTGGG 5

|||||

Db

8 GTGGG 12

## RESULT 44

CF543332

LOCUS

DEFINITION

CF543332

ACCESSION

CF543332

VERSION

CF543332.1

KEYWORDS

EST.

SOURCE ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert length: 16 Std Error: 0.00  
Plate: 29 row: 0 column: 21  
Seq primer: SP6.  
FEATURES source  
1. .16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936425"  
/db\_xref="taxon:161934"  
/clone="024-029-021"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"  
ORIGIN  
Query Match 100.0%; Score 5; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 12  
RESULT 45  
AJ596548  
LOCUS AJ596548.1 GI:37946176  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 435H06, genomic survey sequence.  
ACCESSION AJ596548  
VERSION AJ596548.1  
KEYWORDS GSS; left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 16)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).  
FEATURES source  
1. .16  
/organism="Arabidopsis thaliana"  
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/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="435H06"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature 1. .16  
/note="T-DNA flanking sequence  
left border"  
ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|||||  
Db 5 GTGGG 9  
RESULT 46  
AJ666397/c  
LOCUS AJ666397  
DEFINITION AJ666397 CSEQRAN09 Sus scrofa cDNA clone C000033\_K10, mRNA 17 bp mRNA linear EST 28-JUN-2004  
sequence.  
ACCESSION AJ666397  
VERSION AJ666397.1 GI:49350848  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
FEATURES source  
1. .17  
Location/Qualifiers



/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:189664"  
/db\_xref="taxon:161934"  
/clone="024-019-005"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
|||  
Db 8 GTGGG 12

RESULT 50  
BQ594949  
LOCUS  
DEFINITION BQ594949 17 bp mRNA linear EST 06-DEC-2002  
S015254-024-023-M09-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-023-M09 5-PRIME, mRNA sequence.  
ACCESSION BQ594949  
VERSION BQ594949.1 GI:26124532  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 23 row: M column: 09  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. .17

FEATURES  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGG 5  
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Db 8 GTGGG 12

Search completed: January 7, 2005, 11:01:27  
Job time : 2239.4 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GTGGG  
Perfect score: 5  
Sequence: 1 gtggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues  
Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10  
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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

Database : Issued\_Patents\_NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
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; Patent No. 5362864  
; GENERAL INFORMATION:  
; APPLICANT: Chua, Nam-Hai  
; TITLE OF INVENTION: Trans-Activating Factor-1  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/651,710A  
; FILING DATE: 19910206  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3288-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-8

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
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Db      5 GTGGG 9

RESULT 2
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/ Sequence 12, Application US/07651710A
/ Patent No. 5362864
/ GENERAL INFORMATION:
/ APPLICANT: Chua, Nam-Hai
/ TITLE OF INVENTION: Trans-Activating Factor-1
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/651,710A
/ FILING DATE: 19910206
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mirrock, S. Leslie
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3288-014
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 8698864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: NUCLEIC ACID
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/ TOPOLOGY: unknown
/ MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-12

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      6 GTGGG 10

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/ Sequence 27, Application US/08061697
/ Patent No. 5498696
/ GENERAL INFORMATION:
/ APPLICANT: Brown, Michael S.; Briggs, Michael R.; Wang,
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/ APPLICANT: Xiaodong; Goldstein, Joseph L.
/ TITLE OF INVENTION: Sterol Regulatory Element Binding Proteins
/ TYPE OF INVENTION: and Their Use in Screening Assays
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P. O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/061,697
/ FILING DATE: Concurrently Herewith
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: UTSD:347/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 320-7200
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-061-697-27

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Patent No. 5518885
/ GENERAL INFORMATION:
/ APPLICANT: RAZIUDIN
/ APPLICANT: SARKAR, FAZLUL H
/ TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
/ TITLE OF INVENTION: NEOPLASTIC DISEASE
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NEEDLE & ROSENBERG PC
/ STREET: 127 Peachtree Street, Suite 1200
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: usa
/ ZIP: 30303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/229,515A
/ FILING DATE: 19 APR 1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PERRYMAN, DAVID G
```

```
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-229-515A-17

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 2 GTGGG 6

RESULT 5
US-08-229-515A-18
; Sequence 18, Application US/08229515A
; Patent No. 551885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-229-515A-18

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 1 GTGGG 5

RESULT 6
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US-08-131-365B-27/c
; Sequence 27, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/131,365B
; FILING DATE: 01-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
;
US-08-131-365B-27

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 10 GTGGG 6

RESULT 7
US-08-131-365B-43
; Sequence 43, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
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; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/131.365B  
; FILING DATE: 01-OCT-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 474-7577  
; TELEFAX: (512) 418-3000  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-131-365B-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 3 GTGGG 7

RESULT 8  
US-07-990-303A-3/c  
; Sequence 3, Application US/07990303A  
; Patent No. 5582972  
; GENERAL INFORMATION:  
; APPLICANT: Lima, Walter F.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Ecker, David J.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES  
; TITLE OF INVENTION: TO THE ras GENE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz  
; ADDRESSEE: Mackiewicz & No. 5582972ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,303A  
; FILING DATE: 19921214  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 715,196  
; FILING DATE: June 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISIS-0786  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ANTI-SENSE: YES  
US-07-990-303A-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ANTI-SENSE: YES  
US-07-990-303A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 9  
US-07-990-303A-6/c  
; Sequence 6, Application US/07990303A  
; Patent No. 5582972  
; GENERAL INFORMATION:  
; APPLICANT: Lima, Walter F.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Ecker, David J.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES  
; TITLE OF INVENTION: TO THE ras GENE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz  
; ADDRESSEE: Mackiewicz & No. 5582972ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,303A  
; FILING DATE: 19921214  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 715,196  
; FILING DATE: June 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISIS-0786  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ANTI-SENSE: YES  
US-07-990-303A-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

```
Db          |||||
            8 GTGGG 4

RESULT 10
US-08-197-463-4/c
; Sequence 4, Application US/08197463
; Patent No. 5627047
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael
; APPLICANT: Besnard, Francois
; APPLICANT: Nakatani, Yoshihiro
; TITLE OF INVENTION: Astrocyte-Specific Transcription
; TITLE OF INVENTION: of Human Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Koslasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/769,626
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 1173-362P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 1..10
; OTHER INFORMATION: /function= "transcription enhancer"
; OTHER INFORMATION: /bound_moiety= "AP-2"
; OTHER INFORMATION: /standard_name= "AP-2 site"
US-08-197-463-4

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 GTGGG 5
            |||||
Db          6 GTGGG 2

RESULT 11
US-08-317-403A-44
; Sequence 44, Application US/08317403A
; Patent No. 5629155
; GENERAL INFORMATION:
; APPLICANT: WIEGAND, T., GOLD, L., AND TASSET, D.
; TITLE OF INVENTION: HIGH-AFFINITY

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO IMMUNOGLOBIN E
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,403A
; FILING DATE: 3-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-317-403A-44

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 GTGGG 5
            |:|||
Db          3 GUGGG 7

RESULT 12
US-08-202-927-20/c
; Sequence 20, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
```

;/ ZIP: 92715  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICANT: US/08/202,927  
;/ FILING DATE: 28-FEB-1994  
;/ CLASSIFICATION: 536  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Szekeres, Gabor L.  
;/ REGISTRATION NUMBER: 28,675  
;/ REFERENCE/DOCKET NUMBER: 491-07-PA  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (714) 854-5502  
;/ TELEFAX: (714) 854-4897  
;/ INFORMATION FOR SEQ ID NO: 20:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ FEATURE:  
;/ NAME/KEY: modified\_base  
;/ LOCATION: 10  
;/ OTHER INFORMATION: /mod\_base= OTHER  
;/ OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
;/ OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
;/ OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
;/ OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
;/ OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
;/ OTHER INFORMATION: formula 3)."  
;/  
;/ US-08-202-927-20

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
Db |||||  
5 GTGGG 1

## RESULT 13

US-08-202-927-38  
;/ Sequence 38, Application US/08202927  
;/ Patent No. 5646126  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Cheng, Yung-chi  
;/ APPLICANT: Lukhtanov, Eugeny A.  
;/ APPLICANT: Meyer Jr., Rich B.  
;/ APPLICANT: Pai, Balakrishna S.  
;/ APPLICANT: Reed, Michael W.  
;/ APPLICANT: Zhou, James H.  
;/ TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
;/ TITLE OF INVENTION: Anticancer Activity  
;/ NUMBER OF SEQUENCES: 70  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Klein & Szekeres  
;/ STREET: 4199 Campus Drive, Suite 700  
;/ CITY: Irvine  
;/ STATE: CA  
;/ COUNTRY: U.S.A.  
;/ ZIP: 92715  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICANT: US/08/202,927  
;/ FILING DATE: 28-FEB-1994

;/ CLASSIFICATION: 536  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Szekeres, Gabor L.  
;/ REGISTRATION NUMBER: 28,675  
;/ REFERENCE/DOCKET NUMBER: 491-07-PA  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (714) 854-5502  
;/ TELEFAX: (714) 854-4897  
;/ INFORMATION FOR SEQ ID NO: 38:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 10 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ FEATURE:  
;/ NAME/KEY: modified\_base  
;/ LOCATION: 10  
;/ OTHER INFORMATION: /mod\_base= OTHER  
;/ OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
;/ OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
;/ OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
;/ OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
;/ OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
;/ OTHER INFORMATION: formula 3)."  
;/  
;/ US-08-202-927-38

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
Db |||||  
1 GTGGG 5

## RESULT 14

US-08-202-927-38/c  
;/ Sequence 38, Application US/08202927  
;/ Patent No. 5646126  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Cheng, Yung-chi  
;/ APPLICANT: Lukhtanov, Eugeny A.  
;/ APPLICANT: Meyer Jr., Rich B.  
;/ APPLICANT: Pai, Balakrishna S.  
;/ APPLICANT: Reed, Michael W.  
;/ APPLICANT: Zhou, James H.  
;/ TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
;/ TITLE OF INVENTION: Anticancer Activity  
;/ NUMBER OF SEQUENCES: 70  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Klein & Szekeres  
;/ STREET: 4199 Campus Drive, Suite 700  
;/ CITY: Irvine  
;/ STATE: CA  
;/ COUNTRY: U.S.A.  
;/ ZIP: 92715  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICANT: US/08/202,927  
;/ FILING DATE: 28-FEB-1994  
;/ CLASSIFICATION: 536  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Szekeres, Gabor L.  
;/ REGISTRATION NUMBER: 28,675  
;/ REFERENCE/DOCKET NUMBER: 491-07-PA  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (714) 854-5502  
;/ TELEFAX: (714) 854-4897  
;/ INFORMATION FOR SEQ ID NO: 38:



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-38

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTGGG 5

Db 10 GTGGG 6

```
RESULT 15
US-08-645-865-17
; Sequence 17, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-17

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GTGGG 5

Db 10 GTGGG 6

```
Db 2 GTGGG 6

RESULT 16
US-08-645-865-18
; Sequence 18, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-18

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 1 GTGGG 5

RESULT 17
US-08-330-000-3/c
; Sequence 3, Application US/08330000
; Patent No. 5686242
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5686242ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 18  
US-08-330-000-4/c  
; Sequence 4, Application US/08330000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSES: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne

; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 8 GTGGG 4

RESULT 19  
US-08-330-000-6/c  
; Sequence 6, Application US/08330000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSES: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-6

Query Match 100.0%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
      |||||  
Db 8 GTGGG 4

RESULT 20  
US-08-330-000-9  
; Sequence 9, Application US/083300000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-330-000-9

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
      |||||  
Db 3 GUGGG 7

RESULT 21  
US-08-330-000-15/c  
; Sequence 15, Application US/083300000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.

; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-15

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
      |||||  
Db 8 GTGGG 4

RESULT 22  
US-08-471-985A-44  
; Sequence 44, Application US/08471985A  
; Patent No. 5686592  
; GENERAL INFORMATION:  
; APPLICANT: WIEGAND, Torsten Walter  
; APPLICANT: GOLD, Larry  
; APPLICANT: TASSET, Diane  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS TO  
; TITLE OF INVENTION: IMMUNOGLOBIN E  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 East Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage  
; COMPUTER: IBM compatible

```

; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,985A
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,403
; FILING DATE: 03-OCTOBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX23/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
;
US-08-471-985A-44

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 3 GUGGG 7

RESULT 23
US-08-171-718-30/c
; Sequence 30, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
```

```

; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-171-718-30

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 8 GTGGG 4

RESULT 24
US-08-463-660-13/c
; Sequence 13, Application US/08463660
; Patent No. 5759776
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHEN, LING-CHUN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,660
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 28888-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-463-660-13

Query Match 100.0%; Score 5; DB 1; Length 10;
```

Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
      |||||  
Db 10 GTGGG 6

RESULT 25

US-08-678-280-13/c  
; Sequence 13, Application US/08678280  
; Patent No. 5776683  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, HELENE S.  
; APPLICANT: CHUN, LING-CHEN  
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/678,280  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 28888-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-678-280-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
      |||||  
Db 10 GTGGG 6

RESULT 26

US-08-590-804-13  
; Sequence 13, Application US/08590804  
; Patent No. 5780273  
; GENERAL INFORMATION:  
; APPLICANT: Burg, J. Lawrence  
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE  
; TITLE OF INVENTION: NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corporation  
; STREET: 55 Shuman Blvd., Suite 600  
; CITY: Naperville  
; STATE: Illinois

; COUNTRY: USA  
; ZIP: 60563  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,804  
; FILING DATE: 24-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/357,779  
; FILING DATE:  
; APPLICATION NUMBER: US 08/045,587  
; FILING DATE: 09-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Galloway, No. 5780273val B  
; REGISTRATION NUMBER: 33,595  
; REFERENCE/DOCKET NUMBER: 32,468  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-717-2447  
; TELEFAX: 708-717-2430  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-590-804-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
      |||||  
Db 4 GTGGG 8

RESULT 27

US-08-590-804-18  
; Sequence 18, Application US/08590804  
; Patent No. 5780273  
; GENERAL INFORMATION:  
; APPLICANT: Burg, J. Lawrence  
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE  
; TITLE OF INVENTION: NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corporation  
; STREET: 55 Shuman Blvd., Suite 600  
; CITY: Naperville  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60563  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/590,804  
; FILING DATE: 24-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/357,779  
; FILING DATE:  
; APPLICATION NUMBER: US 08/045,587  
; FILING DATE: 09-APR-1993  
; ATTORNEY/AGENT INFORMATION:

/ NAME: Galloway, No. 5780273val B  
/ REGISTRATION NUMBER: 33,595  
/ REFERENCE/DOCKET NUMBER: 32,468  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 708-717-2447  
/ TELEFAX: 708-717-2430  
/ INFORMATION FOR SEQ ID NO: 18:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 10 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
US-08-590-804-18

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|:|:|  
Db 6 GTGGG 10

RESULT 28  
US-08-540-448-16  
/ Sequence 16, Application US/08540448  
/ Patent No. 5786145  
/ GENERAL INFORMATION:  
/ APPLICANT: KARN, JONATHAN  
/ APPLICANT: GAIT, MICHAEL J.  
/ APPLICANT: HEAPHY, SHAUN  
/ APPLICANT: DINGWALL, COLIN  
/ TITLE OF INVENTION: VIRAL GROWTH INHIBITION  
/ NUMBER OF SEQUENCES: 25  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
/ ADDRESSEE: P.C.  
/ STREET: 1755 S. Jefferson Davis Highway, Suite 400  
/ CITY: Arlington  
/ STATE: Virginia  
/ COUNTRY: U.S.A.  
/ ZIP: 22202

/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/540,448  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/030,102  
/ FILING DATE: 18-MAR-1993  
/ APPLICATION NUMBER: GB 9020541.0  
/ FILING DATE: 20-SEP-1990  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Oblon, No. 5786145man F.  
/ REGISTRATION NUMBER: 24,618  
/ REFERENCE/DOCKET NUMBER: 3077-007-0 PCT  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (703) 413-3000  
/ TELEFAX: (703) 413-2220  
/ TELEX: 248855 OPAT UR  
/ INFORMATION FOR SEQ ID NO: 16:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 10 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: unknown  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: Other nucleic acid;

/ DESCRIPTION: RNA (synthetic)  
US-08-540-448-16  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|:|:|  
Db 2 GUGGG 6

RESULT 29  
US-08-729-447-3/C  
/ Sequence 3, Application US/08729447  
/ Patent No. 5789174  
/ GENERAL INFORMATION:  
/ APPLICANT:  
/ TITLE OF INVENTION: DETECTION OF PERIODONTAL PATHOGENS INCLUDING  
/ TITLE OF INVENTION: BACTEROIDES FORSYTHUS, PORPHYROMONAS GINGIVALIS,  
/ TITLE OF INVENTION: PREVOTELLA INTERMEDIA AND PREVOTELLA NIGRESCENS  
/ NUMBER OF SEQUENCES: 20  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/729,447  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 10 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "AP-PCR primer for P.  
/ DESCRIPTION: intermedia and P. nigrescens"  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
US-08-729-447-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGG 5  
|:|:|  
Db 10 GTGGG 6

RESULT 30  
US-08-597-467-9  
/ Sequence 9, Application US/08597467  
/ Patent No. 5824787  
/ GENERAL INFORMATION:  
/ APPLICANT: Singer, Paul A.  
/ TITLE OF INVENTION: POLYNUCLEOTIDE SIZING REAGENT  
/ NUMBER OF SEQUENCES: 20  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Spensley Horn Jubas & Lubitz  
/ STREET: 1880 Century Park East, Suite 500  
/ CITY: Los Angeles  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 90067  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,467
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,901
; FILING DATE: 03-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: EP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..10
; US-08-597-467-9

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 6 GTGGG 10

RESULT 31
US-08-590-571-17
; Sequence 17, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-17

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
Db 1 GTGGG 5

RESULT 33
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
```



```
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-29

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 34
US-08-590-571-45
; Sequence 45, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-45

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 35
US-08-590-571-48
; Sequence 48, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-48

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 36
US-08-590-571-49
; Sequence 49, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
```

STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-49

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 1 GTGGG 5

RESULT 37  
US-08-276-567A-6/c  
Sequence 6, Application US/08276567A  
Patent No. 5866699  
GENERAL INFORMATION:  
APPLICANT: Adrienne Smyth  
TITLE OF INVENTION: Oligonucleotides Having Anti-MDR-1 Gene Activity  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusmer  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,567A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-022  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-276-567A-6  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 10 GTGGG 6

RESULT 38  
US-08-668-123-27/c  
Sequence 27, Application US/08668123  
Patent No. 5891631  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,123  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/131,365  
FILING DATE: 01-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-668-123-27

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 10 GTGGG 6

RESULT 39  
US-08-668-123-43  
; Sequence 43, Application US/08668123  
; Patent No. 5891631  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Briggs, Michael R.  
; APPLICANT: Wang, Xiaodong  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/668,123  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/131,365  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-668-123-43

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||  
Db 3 GTGGG 7

RESULT 40  
US-08-403-888A-108  
; Sequence 108, Application US/08403888A  
; Patent No. 5952490  
; GENERAL INFORMATION:  
; APPLICANT: Hanecak et al.  
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
; TITLE OF INVENTION: Sequence  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia

STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,888A  
; FILING DATE: 12-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/954,185  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul K. Legaard  
; REGISTRATION NUMBER: 38,534  
; REFERENCE/DOCKET NUMBER: ISIS-1229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-403-888A-108

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||  
Db 3 GTGGG 7

RESULT 41  
US-08-481-658B-19/c  
; Sequence 19, Application US/08481658B  
; Patent No. 5955075  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,658B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-481-658B-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 8 GTGGG 4

RESULT 42
US-08-477-504A-19/c
; Sequence 19, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-477-504A-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 8 GTGGG 4

RESULT 43
US-08-486-756A-19/c
; Sequence 19, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-486-756A-19

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 GTGGG 4

RESULT 44
US-08-485-862B-19/c
; Sequence 19, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
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QY 1 GTGGG 5
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; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-485-862B-19
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Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTGGG 5
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Db 8 GTGGG 4
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RESULT 45
US-08-265-484B-15
; Sequence 15, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
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; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-15
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QY 1 GTGGG 5
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Db 5 GUGGG 9
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RESULT 46
US-08-388-353-84
; Sequence 84, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-84
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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTGGG 5
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Db          6 GTGGG 10

RESULT 47
US-08-388-353-85
; Sequence 85, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-86

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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           |||||
Db          5 GTGGG 9

RESULT 48
US-08-388-353-86
; Sequence 86, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City

Query Match      100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GTGGG 5
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Db          5 GTGGG 9

RESULT 49
US-08-388-353-87
; Sequence 87, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-86

Query Match      100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          5 GTGGG 9

RESULT 49
US-08-388-353-87
; Sequence 87, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
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Search completed: January 7, 2005, 11:05:41  
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; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
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; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-87

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-388-353-88  
; Sequence 88, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-88

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GTGGG 6



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
106.177 Million cell updates/sec

Title: GTGGG  
Perfect score: 5  
Sequence: 1 gtggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10  
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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	5	100.0	10	9	US-09-989-789-562
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	4	5	100.0	10	9	US-09-989-789-625
	5	5	100.0	10	9	US-09-989-789-630
	6	5	100.0	10	9	US-09-989-789-1273
	7	5	100.0	10	9	US-09-989-789-1645
	8	5	100.0	10	9	US-09-989-789-1646
	9	5	100.0	10	9	US-09-989-789-1668
	10	5	100.0	10	9	US-09-989-789-1669
	11	5	100.0	10	9	US-09-989-789-1670
	12	5	100.0	10	9	US-09-989-789-1673
						Sequence 9, Appli
						Sequence 562, App
						Sequence 624, App
						Sequence 625, App
						Sequence 630, App
						Sequence 1273, Ap
						Sequence 1645, Ap
						Sequence 1646, Ap
						Sequence 1668, Ap
						Sequence 1669, Ap
						Sequence 1670, Ap
						Sequence 1673, Ap



232	5	100.0	10	18	US-10-487-934-282	Sequence 282, App	305	5	100.0	11	17	US-10-450-797-972	Sequence 972, App
c 233	5	100.0	10	18	US-10-602-494-372	Sequence 372, App	306	5	100.0	11	17	US-10-450-797-1039	Sequence 1039, Ap
c 234	5	100.0	10	18	US-10-602-494-379	Sequence 379, App	307	5	100.0	11	17	US-10-450-797-1124	Sequence 1124, Ap
235	5	100.0	11	9	US-09-772-719-73	Sequence 73, Appl	c 308	5	100.0	11	17	US-10-450-797-1175	Sequence 1175, Ap
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c 238	5	100.0	11	10	US-09-918-715-137	Sequence 137, App	311	5	100.0	11	17	US-10-781-055-28	Sequence 28, Appl
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c 240	5	100.0	11	10	US-09-249-155-38	Sequence 38, Appl	c 313	5	100.0	11	18	US-10-474-794-137	Sequence 137, App
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c 242	5	100.0	11	10	US-09-249-155-72	Sequence 72, Appl	315	5	100.0	11	18	US-10-733-878-318	Sequence 318, App
c 243	5	100.0	11	10	US-09-249-155-142	Sequence 142, App	316	5	100.0	11	18	US-10-149-109A-109	Sequence 109, App
c 244	5	100.0	11	10	US-09-249-155-175	Sequence 175, App	317	5	100.0	11	18	US-10-149-109A-120	Sequence 120, App
245	5	100.0	11	10	US-09-249-155-188	Sequence 188, App	c 318	5	100.0	11	18	US-10-149-109A-153	Sequence 153, App
246	5	100.0	11	10	US-09-249-155-237	Sequence 237, App	319	5	100.0	11	18	US-10-149-109A-159	Sequence 159, App
247	5	100.0	11	10	US-09-967-237-73	Sequence 73, Appl	c 320	5	100.0	11	18	US-10-149-109A-160	Sequence 160, App
c 248	5	100.0	11	14	US-10-146-354A-5	Sequence 5, Appli	321	5	100.0	11	18	US-10-149-109A-163	Sequence 163, App
c 249	5	100.0	11	14	US-10-146-354A-6	Sequence 6, Appli	c 322	5	100.0	11	18	US-10-149-109A-164	Sequence 164, App
250	5	100.0	11	14	US-10-224-836-245	Sequence 245, App	c 323	5	100.0	11	18	US-10-149-109A-165	Sequence 165, App
c 251	5	100.0	11	15	US-10-193-938-15	Sequence 15, Appl	c 324	5	100.0	11	18	US-10-715-844-35	Sequence 35, Appl
c 252	5	100.0	11	15	US-10-193-938-16	Sequence 16, Appl	325	5	100.0	12	9	US-09-245-026-15	Sequence 15, Appl
c 253	5	100.0	11	15	US-10-266-138B-18	Sequence 18, Appl	c 326	5	100.0	12	9	US-09-757-049A-41	Sequence 41, Appl
c 254	5	100.0	11	15	US-10-265-509B-18	Sequence 18, Appl	c 327	5	100.0	12	9	US-09-263-959-698	Sequence 698, App
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ALIGNMENTS

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; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
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; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
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; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
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US-09-989-789-624

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; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
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; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
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; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-625

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 5
US-09-989-789-630
; Sequence 630, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-630

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 6
US-09-989-789-1273
; Sequence 1273, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
```



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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1273

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 7
US-09-989-789-1645
; Sequence 1645, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1645

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 8
US-09-989-789-1646
; Sequence 1646, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1646

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 9
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 10
US-09-989-789-1669
; Sequence 1669, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1669

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      5 GTGGG 9
```

```

; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1646

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 9
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 10
US-09-989-789-1669
; Sequence 1669, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1669

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      5 GTGGG 9
```



```
RESULT 11
US-09-989-789-1670
; Sequence 1670, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1670

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 5 GTGGG 9

RESULT 12
US-09-989-789-1673
; Sequence 1673, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1673
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1673

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 5 GTGGG 9

RESULT 13
US-09-989-789-1687
; Sequence 1687, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
```

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; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1687
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1687

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 4 GTGGG 8

RESULT 14
US-09-989-789-1705
; Sequence 1705, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1705
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1705

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5
   |||||
Db 3 GTGGG 7

RESULT 15
US-09-989-789-1706
; Sequence 1706, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
```

US-09-989-789-1706

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 3 GTGGG 7

RESULT 16

US-09-761-116-2  
; Sequence 2, Application US/09761116  
; Patent No. US20020102552A1  
; GENERAL INFORMATION:  
; APPLICANT: American Home Products Corp.  
; APPLICANT: Susulic, Vedrana S.  
; APPLICANT: Duzic, Edmir  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN  
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE  
; FILE REFERENCE: 0630/0E791  
; CURRENT APPLICATION NUMBER: US/09/761,116  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/243,335  
; PRIOR FILING DATE: 1999-02-01  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-761-116-2

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 3 GTGGG 7

RESULT 17

US-09-942-325A-5/c  
; Sequence 5, Application US/09942325A  
; Patent No. US20020106794A1  
; GENERAL INFORMATION:  
; APPLICANT: Iacovitti, Lorraine  
; APPLICANT: Kessler, Mark  
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter  
; TITLE OF INVENTION: Sequence and Related Methods and Compositions  
; FILE REFERENCE: IAC01.NP001  
; CURRENT APPLICATION NUMBER: US/09/942,325A  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/228931  
; PRIOR FILING DATE: 2000-02-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-942-325A-5

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||

Db 8 GTGGG 4

RESULT 18

US-09-816-763-110/c  
; Sequence 110, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: SREBP1  
; NAME/KEY: misc\_binding  
; LOCATION: (0)---(0)  
; OTHER INFORMATION: non E-Box consensus binding sequence  
US-09-816-763-110

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 10 GTGGG 6

RESULT 19

US-09-772-719-19/c  
; Sequence 19, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
;
US-09-772-719-19

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      8 GTGGG 4

RESULT 20
US-09-846-033B-140
; Sequence 140, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; TITLE OF INVENTION: Finger Proteins
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
;
US-09-846-033B-140

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 21
US-09-990-186-562
; Sequence 562, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
```

```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 562
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
;
US-09-990-186-562

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 22
US-09-990-186-624
; Sequence 624, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
;
US-09-990-186-624

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 23
US-09-990-186-625
; Sequence 625, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-625

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 24
US-09-990-186-630
; Sequence 630, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 25
US-09-990-186-1273
; Sequence 1273, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1273

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
```

```
Db      4 GTGGG 8

RESULT 26
US-09-990-186-1645
; Sequence 1645, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1645

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 27
US-09-990-186-1646
; Sequence 1646, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1646

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 28
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1668

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 29
US-09-990-186-1669
; Sequence 1669, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1669

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 30
US-09-990-186-1670
; Sequence 1670, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1670

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      5 GTGGG 9

RESULT 31
US-09-990-186-1673
; Sequence 1673, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1673
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1673

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      5 GTGGG 9

RESULT 32
US-09-990-186-1687
; Sequence 1687, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1687
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1687

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8
```

```
; OTHER INFORMATION: DNA
US-09-990-186-1670

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      5 GTGGG 9

RESULT 31
US-09-990-186-1673
; Sequence 1673, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1673
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1673

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 32
US-09-990-186-1687
; Sequence 1687, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1687
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1687

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8
```

```

RESULT 33
US-09-990-186-1705
; Sequence 1705, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1705
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1705

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 34
US-09-990-186-1706
; Sequence 1706, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1706

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 35
US-09-996-484-62
; Sequence 62, Application US/09996484
; Publication No. US20030092010A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: ULLMAN, Christopher G.
; TITLE OF INVENTION: MOLECULAR SWITCHES
; FILE REFERENCE: 8325-2004 / G8-US1
; CURRENT APPLICATION NUMBER: US/09/996,484
; PRIOR FILING DATE: 2000-01-03

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 36
US-09-748-710-14
; Sequence 14, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; TITLE OF INVENTION: FROM SAGE TAGS FOR GENE IDENTIFICATION
; FILE REFERENCE: ARCD:343US
; CURRENT APPLICATION NUMBER: US/09/748,710
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-748-710-14

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 37
US-09-748-710-27
; Sequence 27, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; TITLE OF INVENTION: FROM SAGE TAGS FOR GENE IDENTIFICATION
; FILE REFERENCE: ARCD:343US
; CURRENT APPLICATION NUMBER: US/09/748,710
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
```

```
; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-748-710-27

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      3 GTGGG 7

RESULT 38
US-09-989-994-562
; Sequence 562, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 562
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-562

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 39
US-09-989-994-624
; Sequence 624, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
```

```
US-09-989-994-624

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 40
US-09-989-994-625
; Sequence 625, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-625

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 41
US-09-989-994-630
; Sequence 630, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8
```



```
RESULT 42
US-09-989-994-1273
; Sequence 1273, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1273

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 43
US-09-989-994-1645
; Sequence 1645, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1645

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 44
US-09-989-994-1646
; Sequence 1646, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
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; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1646

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 45
US-09-989-994-1668
; Sequence 1668, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1668

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGGG 5
      |||||
Db      1 GTGGG 5

RESULT 46
US-09-989-994-1669
; Sequence 1669, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1669
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Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 5 GTGGG 9

## RESULT 47

US-09-989-994-1670  
; Sequence 1670, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1670  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1670

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 5 GTGGG 9

## RESULT 48

US-09-989-994-1673  
; Sequence 1673, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1673  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1673

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 4 GTGGG 8

## RESULT 49

US-09-989-994-1687

; Sequence 1687, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1687  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1687

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 4 GTGGG 8

## RESULT 50

US-09-989-994-1705  
; Sequence 1705, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1705  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1705

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
Db 3 GTGGG 7

Search completed: January 7, 2005, 11:31:26  
Job time : 272.2 secs

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